Access DB# 89382



## SEARCH REQUEST FORM

Scientific and Technical Information Center

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Inventors (please provide full name	s): Japan	le étal.	villebrand fuctor et	
Earliest Priority Filing Date: *For Sequence Searches Only* Please is	nclude all pertinent information	<del></del>	ed nates t numbers) along with the	
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STAFF USE ONLY  Searcher Phone #:  Searcher Location:  Date Searcher Picked Up: 3/2 0  Date Completed: 3/2 0  Searcher Prep & Review Time: 10  Clerical Prep Time: 11	Type of Search  NA Sequence (#)  AA Sequence (#)  Structure (#)  Bibliographic  Litigation  Fulltext  Patent Family  Other	Vendors and cost  STN		

PTO-1590 (8-01)

segid\_1\_15fused.rspt

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Q98014 streptomyce
Q93h87 streptomyce
Q23551 caenorhabdi
Q93h86 streptomyce
Q9406 transmissib
O9v467 drosophila
O9v493 drosophila
Q8v493 drosophila
Q8v493 drosophila
Q8v493 drosophila
Q8v493 drosophila
Q8v493 drosophila
Q8581 etreptomyce
Q28733 oryctolagus
G58297 streptomyce
G58497 streptomyce
G5840 polyangium
Q93nx8 streptomyce
G93940 polyangium
Q93nx8 streptomyce
G8873 museuju
                                                                                                                                                                                                                                                                                                                                                                                Q9alm2 saccharopol
Q9nyq8 homo sapien
Q95714 homo sapien
Q93n87 streptomyce
019791 caenorhabdi
09kid7 streptomyce
09z4x6 streptomyce
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X PubMed=11557746;

A PubMed=11557746;

A Fulkawa K.;

Rushuckere of von Willebrand Factor-cleaving Protesse (ADAMTS13), a "Structure of von Willebrand Factor-cleaving Reprotesse (ADAMTS13), a "Structure of PROTESSE (ADAMTS13), a "Structure of von Willebrand Factor-cleaving Reprotesse (ADAMTS13), a "Structure of von Willebrand Factor-cleaving Protesse (ADAMTS13), a "Structure of von William Protesse (ADAMTS1), a "Structure of von Wi
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NON WILLEBRAND FACTOR-CLEAVING PROTEASE.
153632 MW; EBIBC3AABC1A4442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Von Willebrand factor-cleaving protease precursor.
ADAMTS13
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Best Local Similarity
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08wzb3 homo sapien
09ewa1 streptomyce
09164 tolypocladi
093nw6 streptomyce
09163 drosophila
08x840 ralstonia s
04226 streptomyce
085168 pseudomonas
0914w3 streptomyce
018559 centorhabdi
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                            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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PROSITE; PS00038; HELIX LOOP HELIX; UNKNOWN_1.
PROSITE; PS00290; IG_MHG; UNKNOWN 1.
PROSITE; PS00013; PEROXIDARE 1; UNKNOWN 1.
PROSITE; PS00019; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.
SEQUENCE 34350 AA; 3816262 MW; 581120058A7CE58A CRC64;
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Best Local Similarity 0.4*
Matches 112; Conservative
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EMBL, AJ27892; CAD12456.1, -.

InterPro; IPR00019; Euk_PKinase.

InterPro; IPR001991; FW_PKINASE.

InterPro; IPR001961; FN_III.

InterPro; IPR001961; FN_III.

InterPro; IPR001961; FN_III.
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MEDLINE=20309627; PubMed=10850961;
Freiburg A., Trombicas K., Hell W., Cazorla O., Fougerousse F.,
Granzier T., Kohmerer B., Witt C., Beckmann J.S., Gregorio C.C.,
Granzier H., Labeit S.;
"Series of exon-skipping events in the elastic spring region of
as the structural basis for myofibrillar elastic diversity.";
Circ. Res. 86:1114-1121(2000).
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MEDLINE=2117839; PubMed=11717165;
Bang M.L. Centner T., Fornoff F., Geach A.J., Gotthardt M.,
McNabb M., Witt C.C., Labeit D., Gregorio C.C., Granzier H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelv
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00060; FN3; I33.
SMART; SM00409; IG, 167.
SMART; SM00406; IG.2; 148.
SMART; SM00406; IGV; 23.
SMART; SM00220; STKC; 1.
PROSITE; PS00933; FGGY_KINASES_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 34350 AA
                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR002016; Peroxidase.
InterPro; IPR004168; PPAK motif.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                         121 VTQLGGACSPTWSCLITEDTGFDLGVTI 148
                                                                                                                                                                                                                                                                                     VTQLGGACSPTWSCLITEDTGFDLGVTI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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IPR003006; 19_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, 1) Titin.
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Pfam, PF00041, ig, 146.
Pfam, PF00069; pkinase; 1.
Pfam, PF02818; PPAK; 53.
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR003006; Ig
nterPro; IPR003596; Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000001; Euk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                    Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
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q	4031	NVVMPPDQIIESKREFVAIKKVQEVQGRDLLSKESLLSGIPEEQRLNLKIQICRALQAAV 4090
ò	12	11
g	4091	ASEQPGLFSEWLRNIEKVEVEAVNITQEPRHIMCMYLVTSAKSVTEEVTIIIEDVDPQMA 4150
ò	12	11
g	4151	4151 NLKMELRDALCAIIYEEIDILTAEGPRIQQGAKTSLQEEMDSFSGSQKVEPITEPEVESK 4210
ે	12	
gg	4211	YLISPEEVSYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKPSEEKEESSSESGTEE 4270
ò	12	
g	4271	4271 VATVKIQEAEGGFIKEDGPMIHTPLVDTVSEEGDIVHLTTSITNAKEVNWYFENKLVPSD 4330
ò	12	11
q	4331	EKFKCLQDQNTYTLV1DKVNTEDHQGEYVCEALNDSGKTATSAKLTVVKRAAPV1KRK1E
ò	12	
g	4391	4391 PLEVALGHLAKFTCEIQSAPNVRFQWFKAGREIYESDKCSIRSSKYISSLEILRTQVVDC 4450
ò	16	15
g	4451	GEYTCKASNEYGSVSCTATLTVTEAYPPTFLSRPKSLTTFVGKAAKFICTVTGTPVIETI 4510
ò	16	
q	4511	4511 WQKDGAALSPSPNWKISDAENKHILELSNLTIQDRGVYSCKASNKFGADICQAELIIIDK 4570
ò	16	15
g	4571	PHFIKELEPVQSAINKKVHLECQVDEDRKVTVTWSKDGQKLPPGKDYKICFEDKIATLEI 4630
ò	16	15
g	4631	PLAKLKDSGTYVCTASNEAGSSSCSATVTVREPPSFVKKVDPSYLMLPGESARLHCKLKG 4690
ò	16	15
QQ	4691	SPVIQVTWFKNNKELSESNTVRMYFVNSEAILDITDVKVEDSGSYSCEAVNDVGSDSCST 4750
ò	16	15
g	4751	. EIVIKEPPSFIKTLEPADIVRGTNALLQCEVSGTGPFEISWFKDKKQIRSSKKYRLFSOK 4810
ઠે	16	15
음	4811	SLVCLEIFSFNSADVGEYECVVANEVGKCGCMATHLLKEPPTFVKKVDDLIALGGQTVTL 4870
ò	16	
qq	4871	QAAVRGSEPISVTWMKGQEVIREDGKIKMSFSNGVAVLIIPDVQISFGGKYTCLAENEAG 4930
δ	19	
g	4931	SQTSVGELIVKEPAKIIERAELIQVTAGDPATLEYTVAGTPELKPKWYKDGRPLVASKKY.
ò	19	9
g	4991	RISFKNNVAQLKFYSAELHDSGQYTFEISNEVGSSSCETTFTVLDRDIAPFFTKPLRNVD
ò	19	9
g	5051	1 SVVNGTCRLDCKIAGSLPMRVSWFKDGKEIAASDRYRIAFVEGTASLEIIRVDMNDAGNF 5110
ò	19	9 18
q		5111 TCRATNSVGSKDSSGALIVQEPPSFVTKPGSKDVLPGSAVCLKSTFQGSTPLTIRWFKGN 5170

ò	
Dp	5171 KELVSGGSCYITKEALESSLELYLVKTSDSGTYTCKVSNVAGGVECSANLFVKEPATFVE 5230
ò	19
g	5231 KLEPSQLLKKGDATQLACKVTGTPP1KITWFANDREIKESSKHRMSFVESTAVLRLTDVG 5290
ò	- 18
Op	5291 IEDSGEYMCEAQNEAGSDHCSSIVIVKESPYFTKEFKPIEVLKEYDVMLLAEVAGTPPFE 5350
ò	19
Q	5351 ITWFKDNTILRSGRKYKTFIQDHLVSLQILKFVAADAGEYQCRVTNEVGSSICSARVTLR 5410
ò	21
qq	5411 EPPSFIKKIESTSSLRGGTAAFQATLKGSLPITVTWLKDSDEITEDDNIRMTFENNVASL 5470
ò	
qq	5471 YLSGIEVKHDGKYVCQAKNDAGIQRCSALLSVKEPATITEEAVSIDVTQGDPATLQVKFS 5530
ò	22 21
q	5531 GTKEITAKWFKDGQELTLGSKYKISVTDTVSILKIISTEKKDSGEYTFEVQNDVGRSSCK 5590
ò	22 21
QQ	5591 ARINVLDLIIPPSFTKKLKKMDSIKGSFIDLECIVAGSHPISIQWFKDDQEISASEKYKF 5650
ò	22 21
QQ	5651 SFHDNTAFLEISQLEGTDSGTYTCSATNKAGHNQCSGHLTVKEPPYFVEKPQSQDVNPNT 5710
ò	22 21
셤	5711 RVQLKALVGGTAPMTIKWFKDNKELHSGAARSVWKDDTSTSLELFAAKATDSGTYICQLS 5770
ò	22 21
q	5711 NDVGTATSKATLFVKEPPQFIKKPSPVLVLRNGQSTTFECQITGTPKIRVSWYLDGNEIT 5830
ò	22 21
; A	5831 AIOKHGISFIDGLATFQISGARVENSGTYVCEARNDAGTASCSIELKVKEPPTFIRELKP 5890
Š	
}	5801 VEVVKYSDVELECEVTGTPPFEVTWLKNNREIRSSKKYTLTDRVSVFNLHITKCDPSDTG 5950
8	
: A	5951 EYOCIVSNEGGSCSCSTRVALKEPPSFIKKIENTTTVLKSSATFQSTVAGSPPISITWLK 6010
8	
; A	6011 DDOILDEDDNVYISFVDSVATLQIRSVDNGHSGRYTCQAKNESGVERCYAFLLVQEPAQI 6070
}	22
5 2	22 COLI VIEKRKSVIDVITEKDPMTLECVVAGTPELKVKWLKDGKQI VPSRYFSMSFENNVASFRIQSV 6130
9 8	
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5	6191 LPISAOWFKDGKEISTSAKYRLVCHERSVSLEVNNLELEDTANYTCKVSNVAGDDACSGI 6250

g G	7331 ELHESWKYNMSFINSVALLTINEASAEDSGDYICEAHNGVGDASCSTALTVKAPPV	FTOK 7390
ò	44	43
Q	7391 PSPVGALKGSDVILQCEISGTPPFEVVMVKDRKQVRNSKKFKITSKHFDTSLHI	LNLEAS 7450
ò	44	43
Q	7451 DVGEYHCKATNEVGSDTCSCSVKFKEPPRFVKKLSDTSTLIGDAVELRAIVEGFQPI	SW 7510
ò		43
q	7511 WLKDRGEVIRESENTRISFIDNIATLQLGSPEASNSGKYICQIKNDAGMRECSAVLTVLE	VLE 7570
ò	44	43
qq	7571 PARIIEKPEPMTVTTGNPFALECVVTGTPELSAKWFKDGRELSADSKHHITFINKVASLK	SLK 7630
δ	44	43
g	7631 IPCAEMSDKGLYSFEVKNSVGKSNCTVSVHVSDRIVPPSFIRKLKDVNAILGASVVLECR	ECR 7690
ò	44	43
qq	7691 VSGSAPISVGWFQDGNEIVSGPKCQSSFSENVCTLNLSLLEPSDTGIYTCVAANVAGSDE	SDE 7750
ò	/ 44	43
q	7751 CSAVLTVQEPPSFEQTPDSVEVLPGMSLTFTSVIRGTPPFKVKWFKGSRELVPGESCNIS	NIS 7810
ò		43
q	7811 LEDFVTELELFEVQPLESGDYSCLVTNDAGSASCTTHLFVKEPATFVKRLADFS	VETGSP 7870
ò		43
q	7871 IVLEATYTGTPPISVSWIKDEYLISQSERCSITMTEKSTILEILESTIEDYAQYS	CLIEN 7930
ò		43
qq	7931 EAGQDICEALVSVLEPPYFIEPLEHVEAVIGEPATLQCKVDGTPEIRISWYKEHTKLRSA	RSA 7990
ò	/	43
g	7991 PAYKNQFKNNVASLVINKVDHSDVGEYSCKADNSVGAVASSAVLVIKERKLPPFFARKLK	1KLK 8050
ò	, the second sec	43
qq	8051 DVHETLGFPVAFECRINGSEPLQVSWYKDGVLLKDDANLQTSFVHNVATLÖT	LQTDQSHI 8110
ò	,	43
g	B111 GQYNCSASNPLGTASSSAKLILSEHEVPPFFDLKPVSVDLALGESGTFKCHVTGTAPIKI	91KI 8170
ò	A 44	43
g	b 8171 TWAKDNREIRPGGNYKMTLVENTATLTVLKVGKGDAGQYTCYASNIAGKDSCSAHLGVQE	3VQE 8230
ò	γ 44	43
q	b 8231 PPRFIKKLEPSRIVKQDEFTRYECKIGGSPEIKVLWYKDETEIQESSKFRMSFVDS	VAVL 8290
ò	λ 44	43
QQ	b 8291 EMHNLSVEDSGDYTCEAHNAAGSASSSTSLKVKEPPIFRKKPHPIETLKGADVHLECELQ	CELO 8350
ò	λ 44	43
qq	b 8351 GTPPFHVSWYKDKRELRSGKKYKIMSENFLTSIHILNVDAADIGEYQCKATNDVGSDTCV	DTCV 8410
ò	γ	43

GSIALKAPPRFVKKLSDISTVVGKEVQLQTTIEGAEPISVVWFKDKGEIVRESDNIWISY 8470	43	SENIATLQFSRVEPANAGKYTCQIKNDAGMQECFATLSVLEPATIVEKPESIKVTTGDTC 8530	43	TLECTVAGTPELSTKWFKDGKELTSDNKYKISFFNKVSGLKIINVAPSDSGVYSFEVQNP 8590	43	VGKDSCTASLQVSDRTVPPSFTRKLKETNGLSGSSVVMECKVYGSPPISVSWFHEGNEIS 8650	43	SGRKYQTTLIDNTCALTVAMLEESÖSGDYTCIATNMAGSDECSAPLTVREPPSFVQKPDP 8710	43	MDVLTGTNVTFTSIVKGTPPFSVSWFKGSSELVPGDRCNVSLEDSVAELELFDVDTSQSG 8770	43	EYTCIVSNEAGKASCTTHLYIKAPAKFVKRLNDYSIEKGKPLILEGTFTGTPPISVTWKK 8830	43	NGINVTPSQRCNITTTEKSAILEIPSSTVEDAGQYNCYIENASGKDSCSAQILILEPPYF 8890	43	VKQLEPVKVSVGDSASLQCQLAGTPEIGVSWYKGDTKLRPTTTYKMHFRNNVATLVFNQV 8950		DINDSGEYICKAENSVGEVSASTFLTVQEQKLPPSFSRQLRDVQETVGLPVVFDCAISGS 9010	51	EPISVSWYKDGKPLKDSPNVQTSFLDNTATLNIFKTDRSLAGQYSCTATNPIGSASSSAR 9070	51	LILTEGKNPPFFDIRLAPVDAVVGESADFECHVTGTQPIKVSWAKDSREIRSGGKYQISV 9130	51	LENSAHLTVLKVDKGDSGQYTCYAVNEVGKDSCTAQLNIKERLIPPSFTKRLSETVEETE 9190	13	GNSFKLEGRVAGSQPITVAWYKNNIEIQPTSNCEITFKNNTLVLQVRKAGMNDAGLYTCK 9250	51	VSNDAGSALCTSSIVIKEPKKPPVFDQHLTPVTVSEGEYVQLSCHVQGSEPIRIQWLKAG 9310	51	REIKPSDRCSFSFASGTAVLELRDVAKADSGDYVCKASNVAGSDTTKSKVTIKDKPAVAP 9370	51	ATKKAAVDGRLFFVSEPQSIRVVEKTTATFIAKVGGDPIPNVKWTKGKWRQLNQGGRVFI 9430	51	HQKGDEAKLEIRDTTKTDSGLYRCVAFNEHGEIESNVNLQVDERKKQEKIEGDLRAMLKK 9490		TPILKKGAGEBEBIDIMELLKNVDPKEYEKYARMYGITDFRGLLQAFELLKÖSQEBETHR 9550
GSIALKAPPRFVKKLSDISTVVGKEVQL		SENIATLQFSRVEPANAGKYTCQIKNDA		TLECTVAGTPELSTKWFKDGKELTSDNK		VGKDSCTASLQVSDRTVPPSFTRKLKET		SGRKYQTTLTDNTCALTVNMLEESDSG		MDVLTGTNVTFTSIVKGTPPFSVSWFKC					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			DINDSGEYICKAENSVGEVSASTFLTV																		
8411	44	8471	4	8531	4 4	8591	44	8651	4	8711	4	8771	44	8831	44	8891	4	8951	52	9011	52	9071	52	9131	52	9191	52	9251	52	9311	52	9371	52	9431	52	9491
g	ò	qq	ò	gg	ò	q	ò	qq	ò	q	ò	g	ò	q	ò	g	ò	q	ò	g	ò	qq	ò	q	ò	g	ò	g	ò	g	ò	g	ò	g	ò	đ

ò	- 25	51	
a	9551 L	LEIEEIERSERDEKEFEELVSFIQQRLSQTEPVTLIKDIENQTVLKDNDAVFEIDIKINY 96	9610
ò	52 -	51	
d	9611 F	PEIKLSWYKGTEKLEPSDKFEISIDGDRHTLRVKNCQLKDQGNYRLVCGPHIASAKLTVI 96	0496
ò	52 .	51	ą
අු	9671 E	EPAWERHLQDVTLKEGQTCTMTCQFSVPNVKSEWFRNGRILKPQGRHKTEVEHKVHKLŢI 97	9730
ò	52 .	51	r.
g	9731 #	ADVRAEDQGQYTCKYEDLETSAELRIEAEPIQFTKRIQNIVVSEHQSATFECEVSFDDAI 97	9790
ò	52	51	<u>.</u>
g	9791	VTWYKGPTELTESQKYNFRNDGRCHYMTIHNVTPDDEGVYSVIARLEPRGEARSTAELYL 98	9850
ò	52	51	ជ
g	9851	TTKEIKLELKPPDIPDSRVPIPTMPIRAVPPEEIPPVVAPPIPLLLPTPEEKKPPPKRIE 99	9910
ò	52	(8)	51
셤	9911	VTKKAVKKDAKKVVAKPKEMTPREEIVKKPPPPTTLIPAKAPEIIDVSSKAEEVKIMTIT 99	9970
ò	25	[9]	51
유	9971	RKKEVQKEKEAVYEKKQAVHKEKRVPIESPEBPYDELEVEPYTEPPEQPYYEBPDEDYEE 1(	10030
ò	52	[5]	51
q	10031	IKVEAKKEVHEEWEEDFEEGQEYYEREEGYDEGEEEWEEAYQEREVIQVQKEVYEESHER 1(	10090
ò	52	(S)	51
g	10001	KVPAKVPEKKAPPPPKVIKKPVIEKIEKTSRRMEEEKVQVTKVPEVSKKIVPQKPSRTPV 1	10150
ò	52	SVHTVKWVI	65
a	10151		10210
ò	9	5	59
: 名	10211	PPPKVPELPEKPAPEEVAPVPIPKKVEPPAPKVPEVPKKPVPEEKKPVPVPKKEPAAPPK 1	10270
ò	9		59
셤	10271	VPEVPKKPVPEEKIPVPVAKKKEAPPAKVPEVQKRVVTEEKITIVTQREESPPPAVPEIP 1	10330
ò	9	5	59
g	10331	KKKVPEERKPVPRKEEEVPPPFKVPALPKKPVPEEKVAVPVPVAKKAPPPRAEVSKKTVV 1	10390
ò	9	5	59
q	10391	EEKRFVAEEKLSFAVPQRVEVTRHEVSAEEEWSYSEEEEGVSISVYREEEREEEEABVT 1	10450
ò	9	5	59
g	10451	EYEVMEEPEEYVVEEKLHIISKRVEAEPAEVTERQEKKIVLKPKIPAKIEEPPPAKVPEA 1	10510
ò	9		23
ద	10511	PKKIVPEKKVPAPVPKKEKVPPPKVPEEPKKPVPEKKVPPKVIKMEEPLPAKVTERHMQI 1	10570
ò	9		59
q	10571	TQEEKVLVAVTKKEAPPKARVPEEPKRAVPEEKVLKLKPKREEEPPAKVTEFRKRVVKEE	10630

ò	09		59
qq	10631	KVSIEAPKREPQPIKEVTIMEEKERAYTLEEEAVSVQREEEYEEYEEYEFTE	10690
ò	09	.	64
g	10691	EYDQY BEYEEREYERY EEH EEY I TEPEKPI PVKPVPEEPVPTKPKAPPAKVLKKAVPEEK	10750
ò	65		64
g	10751	<b>VPVPIPKKLKPPPPKVPEEPKKVFEEKIRISITKREKEQVTEPAAKVPWKPKRVVAEEKV</b>	10810
ò	. 65		64
g	10811	PVPRKEVAPPVRVPEVPKELEPÇEVAFEEEVVTHVEEYLVEEBEEYIHEEEEFITEEEVV	10870
ò	65		64
QQ	10871	PVI PVKVPEVPRKPVPEEKKPVPVPKKKEAPPAKVPEVPKKPEEKVPVLI PKKEKPPPAK	10930
ઠે	65		64
Q	10931	<b>VPEVPKKPVPEEKVPVPVPKKVEAPPAKVPEVPKKPVPEKKVPVPAPKKVJEAPPAKVPEV</b>	10990
ò	65		64
QQ	10991	PKKLI PEEKKPTPVPKKVEAPPPKVPKKREPVPVAL PQEEEVLFEEEI VPEEEVLPEE	11050
ò	65		64
엄	11051	<b>EEVLPEEEEVLPEEEEVLPEEEE1PPEEEEVPPEEETVPFEEEFVPEEEEVLPEVKPKVPV</b>	11110
ò	65		64
qq	11111	PAPVPEIKKKVTEKKVVI PKKEEAPPAKVPEVPKKVEEKRIILPKEEEVLPVEVTEEPEE	. 07111
ò	65		64
QQ	11111	EPISEEEIPEEPPSIEEVEEVAPPRVPEVIKKAVPEAPTPVPKKVEAPPAKVSKKIPEEK	11230
ò	65		64
CD	11231	<b>VPVPVQKKEAPPAKVPEVPKKVPEKKVLVPKKEAVPPAKGRTVLEEKVSVAFRQEVVVKE</b>	11290
ò	65		64
g	11291	RLELEVVEAEVEEI PEEEEFHEVEEY FEGGEFHEVEEFIKLEQHRVEEHRVEKVHRVIE	11350
ò	65		64
g	11351	VFEAEEVEVFEKPKAPPKGPEISEKIIPPKKPPTKVVPRKEPPAKVPEVPKKIVVEEKVR	11410
ò	65		64
g	11411	<b>VPEEPRVPPTKVPDVLPPKEVVPEKKVPVPPAKKPEAPPPKVPEAPKEVVPEKKVPVPPP</b>	11470
ò	65		64
Q	11471	KKPEVPPTKVPEVPKAAVPEKKVPEAI PPKPESPPPEVPEAPKEVVPEKKVPAAPPKKPE	11530
ò	65		64
g	11531	VTPVKVPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVPKVAVPEKKVPEAI PPKPESPPP	11590
ò	65		64
б	11591	EVFEEPEEVALEEPPAEVVEEPEPAAPPQVTVPPKKPVPEKKAPAVVAKKPELPPVKVPE	11650
ò	65		64
g	11651	<b>VPKEVVPEKKVPLVVPKKPEAPPAKVPEVPKEVVPEKKVAVPKKPEVPPAKVPEVPFKKPV</b>	11710
ò	65		64

qq	11711	LEEKPAVPVPERAESPPPEVYEEPEEIAPEEEIAPEEEKPVPVAEEEEPEVPPPAVPEEP	11770
ò	, 59		64
g	11771	KKII PEKKVPVI KKPEAPPPKEPEFKVI EKPKLKPRPPPPPPPPPREDVKEKI FQLKAI	11830
ò	. 59		64
q	11831	PKKKVPEKPQVPEKVELTPLKVPGGEKKVRKLLPBRKPEPKEEVVLKSVLRKRPEBEBPK	11890
ò	. 59		64
q	11891	VEPKKLEKVKKPAVPEPPPPRPVEEVEVPTVTKRERKI PEPTKVPEIKPAI PLPAPEPKP	11950
ò	. 99	GAP.	67
q	11951	kpeaevktikpppvepeptpiaapvtvpvvgkkaeakapkeeaakpkgpikgvpkktpsp	12010
ò	. 89		67
qq	12011	I EAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDI ILTESEFVGSSAI FECLVS	12070 .
ò	89		67
q	12071	PSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAGEYTCVLRLGNKEKTSTA	12130
ò	89		67
g	12131	KLVVEELPVRFVKTLEEEVTVVKGQPLYLSCELNKERDVVWRKDGKIVVEKPGRIVPGVI	12190
ò	89		67
සු	12191	GLMRALTINDADDTDAGTYTVTVENANNLECSSCVKVVEVIRDWLVKPIRDQHVKPKGTA	12250
ò	68		
đ	12251	IFACDIAKDTPNIKWFKGYDEIPAEPNDKTEILRDGNHLYLKIKNAMPEDIAEYAVEIEG	12310
ò	68		29
q	12311	KRYPAKLTLGEREVELLKPIEDVTIYEKESASFDAEISEADIPGQWKLKGELLRPSPTCE	12370
ò	89		67
Q	12371	IKAEGGKRFLTLRKVKLDQAGEVLYQALNAITTAILTVKEIELDFAVPLKDVTVPERRQA	12430
ò	68		67
qq	12431	RFECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILVINDSQFDDEGVFTAEVEGKKT	12490
ò	68		67
qq	12491	SARLFVTGIRLKFMSPLEDQTVKEGETATFVCELSHEKMHVVMFKNDAKLHTSRTVLISS	12550
ò	68		63
q	12551	EGKTHKLEMKEVTLDD18Q1KAQVKELSSTAQLKVLEADPYFTVKLHDKTAVBKDE1TLK	12610
ò	68		29
g	12611	CEVSKDVPVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLKDKGEYVCDCGTDKTKAN	12670
ò	68		29
qq	12671	VTVEARLIKVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEI1EDGK	12730
ò	68		. 67
QQ	12731	KHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIPITPLSDVKVFEKDEAKFECEV	12790
ò	68		67

KKYMFEAEDKHTSGKLI 12850	67	NLHTTRSVSMQDEGKTH 12910	67	(TGVEKDEVILQCEISK 12970	67	TCDCGTDKTSGKLDIE 13030	29 62	COTPDCEIKEEGKIHSL 13090	67	VTAGETATFDCELSYED 13150	67	LTAKDFKTHANLFVKEP 13210		SKKYEIVADGRVRKLVI 13270	67	EKEMARFECELSRENAK 13330		VRTARTSGMLTVLEEEA 13390	67	RYEILTEGRKRILVIQN 13450		EKAEFVCSISKESFPVQ 13510	67	AARAAAHLTVIEKLRIV 13570	67	ILQKDLVYTLRIRDAHL 13630	67	EKKSVTFWCKVNRLNVT 13690	67	AGQDKSVAELLIIEAPT 13750	67	KYKFEKDGSIHRLIIKD 13810	67	SADVVFLAELNKDKVEVQ 13870	67	
SREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDEAKYMFEAEDKHTSGKLI		IEGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQRLHTTRSVSMQDEGKTH		SITFKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGKLQDYTGVEKDEVILQCEISK		ADAPVKWFKDGKEIKPSKNAVIKADGKKRMLILKKALKSDIGQYTCDCGTDKTSGKLDIE		DREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEALLQTPDCEIKEEGKIHSL		VLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVTVTAGETATFDCELSYED		I PVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVQLTAKDFKTHANLFVKEP		PVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILKSKKYEIVADGRVRKLVI		HDCTPEDIKTYTCDAKDFKTSCNLNVVPPHVEFLRPLTDLQVREKEMARFECELSRENAK		VKWFKDGAEIKKGKKYDIISKGAVRILVINKCLLDDEAEYSCEVRTARTSGMLTVLEEEA		VFTKNLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIETGRYEILTEGRKRILVIQN		AHLEDAGNYNCRLPSSRTDGKVKVHELAAEFISKPQNLEILEGEKAEFVCSISKESFPVQ		WKRDDKTLESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVGAARAAAHLTVIEKLRIV		VPLKDTRVKEQQEVVFNCEVNTEGAKAKAFRNEEAI FDSSKYIILGKDLVYTLRIRDAHL		DDQANYNVSLTNHRGENVKSAANLIVEEEDLRIVEPLKDIETMEKKSVTFWCKVNRLNVT		LKWTKNGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDEGEYIVTAGQDKSVAELLIIEAPT		EFVEHLEDQTVTEFDDAVFSCQLSREKANVKWYRNGREIKEGKKYKFEKDGSIHRLIIKD		CRLDDECEYACGVEDRKSRARLFVEEIPVEIIRPPQDILEAPGADVVFLAELNKDKVEVQ		
12791 S	69	12851 I	- 89	12911 S	- 89	12971 A	- 89	13031	- 89	13091	. 89	13151	89	13211	. 89	13271	. 89	13331	. 89	13391	89	13451	89	13511	89	13571	89	13631	68	13691	68	13751	99	13811	68	
. දු	ò	g	ò	Q	ò	g	ò	Вр	ò	Q Q	ò	qq	ò	đ	ò	g	ò	q	ò	q	ò	q	ò	g	ò	đ	ò	q	ò	Ω	ò	Q	ò	ď	δ	

ò	89		
q	13931	TADQDLVVDVGKPLTMVVPYDAYPKAEAEWFKENEPLSTKTIDTTAEQTSFRILEAKKGD 13	3990
ò	89	29	,
පි	13991	KGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNLEVTETFDGEVSLAWEEPLTDGGSKIIG 14	14050
ò	68	49	7
쥠	14051	YVVERRDIKRKTWVLATDRAESCEFTVTGLQKGGVEYLFRVSARNRVGTGEPVETDNPVE 14	14110
ò	68	04NIN	0
සි	14111	:    ARSKYDVPGPPLNVTITDVNRFGVSLTWEPPEYDGGAEITNYVIELRDKTSIRWDTAMTV 14	14170
ò	7.1	76 SNLTSS 76	9,
쉱	14171	RAEDLSATVTDVVEGQEYSFRVRAQNRIGVGKPSAATPFVKVADPIERPSPPVNLTSSDQ 14	14230
ò	77	9.	9,
g	14231	TOSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLVPELTYKVTGLEKGNKYL 14	14290
ò	77	9.	9,
qq	14291	YRVSAENKAGVSDPSEILGPLTADDAFVEPTMDLSAFKDGLEVIVPNPITILVPSTGYPR 14	14350
ò	77	9.	9.
ą	14351	PTATWCFGDKVLETGDRVKMKTLSAYAELVISPSERSDKGIYTLKLENRVKTISGEIDVN 14	14410
ò	77	9.	92
d d	14411	VIARPSAPKELKFGDITKDSVHLTWEPPDDDGGSPLTGYVVEKREVSRKTWTKVMDFVTD 14	14470
ò	77	81	81
qq	14471	LEFTVPDLVQGKEYLFKVCARNKCGPGEPAYVDEPVNMSTPATVPDPPENVKWRDRTANS 14	14530
ò	82	8]	81
셤	14531	IFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKMEVTGLEEGKWYAYRVKA 14	14590
ò	82	[8]	81
qq	14591	LNRQGASKPSRPTEEIQAVDTQEAPEIFLDVKLLAGLTVKAGTKIELPATVTGKPEPKIT 1	14650
ò	82	[8	81
ద	14651	WTKADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYIIEAVNVCGRATAVVEVNVLDK 1	14710
ò	82	.00	81
셤	14711	PGPPAAFDITDVTNESCLLTWNPPRDDGGSKITNYVVERRATDSEVWHKLSSTVKDTNFK 1	14770
ò	82		81
q	14771	ATKLIPNKEYIFRVAAENMYGVGEPVQASPITAKYOFDPPGPPTRLEPSDITKDAVTLTW 1.	14830
ò	82	8	81
q	14831	CEPDDDGGSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKGLTNKKKYRFRVLAENLA 1.	14890
ò	82	8	81
q	14891	GPGKPSKSTEPILIKDPIDPPWPPGKPTVKDVGKTSVRLNWTKPEHDGGAKIESYVIEML 1	14950
ò	82	8	81
£	14951	KTGTDEWYRVAEGVPTTOHLLPGLMEGOEYSFRVRAVNKAGESEPSEPSDPVLCREKLYP 1	15010

5		,
82		•
15011	PSPPRWLEVINITKNTADLKWTVPEKDGGSPITNYIVEKRDVRRKGWQTVDTTVKDTKCT 1	15070
82		81
15071	VTPLTEGSLYVFRVAAENAIGQSDYTEIEDSVLAKDTFTTPGPPYALAVVDVTKRHVDLK	15130
82		81
15131	WEPPKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNFRVTDVIEGTEVQFQVRAENE	15190
82		81
15191	AGVGHPSEPTE1LS1EDPTSPP&PPLDLHVTDAGRKH1A1AWKPPEKNGGSP11GYHVEM	15250
82		81
15251	CPVGTEKWMRVNSRP1KDLKFKVEEGVVPDKEYVLRVRAVNA1GVSEPSE1SENVVAKDP	15310
82		81
15311	DCKPT1DLETHD11V1EGEKLS1PVPFRAVPVPTVSWHKDGKEVKASDRLTMKNDH1SAH	15370
82		81
15371	LEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDIKASDITKSSCKLTWEPP	15430
82		81
15431	EFDGGTP1LHYVLERREAGRRTY1PVMSGENKLSWTVKDL1PNGEYFFRVKAVNKVGGGE	15490
82		81
15491	YIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYDGGSKIMGYIIEKIAKGE	15550
82		81
15551	ERWKRCNEHLVPILTYTAKGLEEGKEYQFRVRAENAAGISEPSRATPPTKAVDPIDAPKV	15610
82		81
15611	1LRTSLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEEIKKRAAPLVRRRKGEVQEE	15670
82		. 18
15671	EPFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVENDHGIAKAPCTVSVLDTPG	15730
82		81
15731	PPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKPDSEWIVVTSTLRHCKYS	15790 .
82		81
15791	VTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAPDKPIVEDVTSNSMLVKM	15850
82		81
15851	NEPKDNGSPILGYWLEKREVNSTHWSRVNKSLLNALKANVDGLLEGLTYVFRVCAENAAG	15910
82		81
15911	PGKFSPPSDPKTAHDPISPPGPPIPRVTDTSSTTIELEWEPPAFNGGGEIVGYFVDKQLV	15970
82		81
15971	GTNEWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGPPGETQPVTVAEPQEPPA	16030
82		81
16031	VELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELDKDRVVIDNVGTKSELII	16090
82	2	81

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4 60	1 POSKRSDIGLYTITAVNNLGIASKEMKLNVLGKFFVGFINE BSVSAUGHILDSHE	171	<u>අ</u> ද
83	84	80	ò
17110	51 EFMEVEEGTHVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLYDTHVNKLVVDDTCTLVI	170	g
83	84	ω	ò
17050	11 RQCNKRDVEELQFTVEDLVEGGEYEFRVKAVNAAGVSKPSATVGPCDCQRPDMPPSIDLK	16991	g
	4	œ	ò
16990	.1 TARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHYIVECLAWDPTGTKKEAW	16931	g
83		å	ò
16930	1 KGYVIEKRTIDGKAMTKVNPDCGSTTFVVPDLLSEQQYFFRVRAENRFGIGPPVETIQRT	16871	q
83	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	84	ò
16870	1 SHTGKYSITAKNKAGQKTANCRVKVMDVPGPPKDLKVSDITRGSCRLSWHMPDDDGGDRI	16811	QQ
83	,	84	ò
16810	1 AGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQLETAENSSVIIIPECKR	16751	g
83	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	8	ò
16750	1 CECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIQEEPEVPIDIGAQDCLVCK	16691	g
83	7	8	ઠે
16690		16631	: 음
83		88	8
16630	1 YWSRVSRAPITKVGLKGVEFNVPRLLEGVKYQFRAWAINAAGIGPPSEPSDPEVAGDPIF	16571	음
81	2	82	ò
16570	1 ECKSDKVVIQDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNGGSPITGYWLEKREEGSP	16511	QQ
81	2	82	ò
16510	1 NGGSEITHYVIDKRDASRKKAEWEEVTNTAVEKRYGIWKLIPNGQYEFRVRAVNKYGISD	16451	đ
81	2	82	ò
16450	1 IPKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPPRNLAVTDIKAESCYLTWDAPLD	16391	g
81	2	82	ò
16390	1 RGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDALQITKEEVSRSEAKTELS	16331	d
81	2	82	ò
16330	1 VNKRLCPTTSFLVENLDEHQMYEFRVKAVNEIGESEPSLPLNVVIQDDEVPPTIKLRLSV	16271	g
81		82	ò
16270	I GPILAVDPLGPPTSPERLTYTERTKSTITLDWKEPRSNGGSPIQGYIIEKRRHDKPDFER	16211	qq
81		82	ò
16210	GGSEITGFIIERKDAKMHTWRQPIETERSKCDITGLLEGGEYKFRVIAKNKFGCGPPVEI	16151	g
81		82	ò
16150	. KDALRKDHGRYVITATNSCGSKFAAARVEVFDVPGPVLDLKPVVTNRKMCLLNWSDPEDD	16091	g

임	17171 DG	DGGSKI TNYVI EKREANRKTWVHVSSEPKECTYTI PKLLEGHEYVFRIMAQNKYGIGEPL	17230
ò	84	NILOS	88
q	17231 DS		17290
ò	68		88
g	17291 KR	KRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPASLPSDPATARDPIAPPG	17350
ò	68		88
QQ	17351 PF	PPFPKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEEWEKGKDKEVRGTKLVVT	17410
ò	68		88
g	17411 GI	<b>GLKEGAFYKFRVSAVNIAGIGEPGËVTDVIEMKDRLVSPDLQLDASVRDRIVVHAGGVIR</b>	17470
ò	68		88
g	17471	IIAYVSGKPPPTVTWNMNERTLPQEATIETTAISSSMVIKNCQRSHQGVYSLLAKNEAGE	17530
ò	68	PEDD	92
g	17531 RE	RKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGSPITNYVIEKRESDRRAW	17590
ò	93		92
g	17591 TE	<b>TPVTYTVTRQNATVQGLIQGKAYFFRIAAENSIGMGPFVETSEALVIREPITVPERPEDL</b>	17650
ò	93 -		92
8		EVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIGTEKFHKVTNDNLLSRKYTVKGLKE	17710
ò	93 -		92
දු		GDTYEYRVSAVNIVGQGKPSFCTKPITCKDELAPPTLHLDFRDKLTIRVGEAFALTGRYS	17770
ò	93		92
: A		GKPKPKVSWFKDEADVLEDDRTHIKTTPATLALEKIKAKRSDSGKYCVVVENSTGSRKGF	17830
6			92
8		CQVNVVDRPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKITNYIIEKKEVGKDVMMPVT	17890
8	93 -		92
. ද		SASAKTTCKVSKLLEGKDYIFRIHAENLYGISDPLVSDSMKAKDRFRVPDAPDQPIVTEV	17950
ò	93 .		92
셤	17951 T	<b>TKDSALVTWNKPHDGGKPITNYILEKRETMSKRWARVTKDPIHPYTKFRVPDLLEGCQYE</b>	18010
ò	93 -		. 92
윱	18011 F	FRVSAENEIGIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTCNSVDLTWQPPRHDGGSK	C 18070
ò	- 66	-HDFQT	. 97
g	18071 I	ILGYIVEYQKVGDEEWRRANHTPESCPETKYKVTGLRDGQTYKFRVLAVNAAGESDPAHV	7 18130
ò	- 86		- 97
g	18131 F	PEPVLVKDRLEPPELILDANMAREQHIKVGDTLRLSAIIKGVPFPKVTWKKEDRDAPTKA	A 18190
ò	86		- 97
g	18191	RIDVTPVGSKLEIRNAAHEDGGIYSLTVENPAGSKTVSVKVLVLDKPGPPRDLEVSEIRK	K 18250
ò	. 86		- 97
ç	18251	DSCYLTWKEPLDDGGSVITNYVVERRDVASAQWSPLSATSKKKSHFAKHLNEGNQYLFRV	v 18310

ò	96		97
q	18311	AAENQYGRGPFVETPKP1KALDPLHPPGPPKDLHHVDVDKTEVSLVWNKPDRDGGSP1TG	18370
ò	6		97
3 2	16221	VI VIEVOEEGTODWIKEKTVTNLECVVTGLOOGKTYRFRVKAENIVGLGLPDTTIPIECOE	18430
3 8	0		97
à á	-	NO SECUEL DUKI. I EGI JUKAGTTUR PA I IRGV PV PTAKWTT DGSEI KT DEHYTVET DN	18490
9	18431		4.4
ઠે	98	TEMPORENT THREE CHARGEST STREET	 האמנ
Q	18491	FSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGPPTGFINILDVIFEHMIL	^
ò	98		93
đ	18551	SWQPPKDDGGSPVINYIVEKQDTRKDTWGVVSSGSSKTKLKIPHLQKGCEYVFRVRAENK	18610
ò	98		97
qq	18611	IGVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAATVSWTLPKSDGGSPITGYYMERR	18670
ò	98		97
Q	18671	EVTGKWVRVNKTPIADLKFRVTGLYEGNTYEFRVFAENLAGLSKPSFSSDPIKACRPIKP	18730
ò	98	-ADIV	101
q	18731		18790
ò	102		101
q	18791	FRVPGLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILHPPEVELDVTCRDVITVRVG	18850
ò	102		101
යි	18851	QTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVELQIKEAVRADHGKYIISA	18910
Š	102		101
: 2	1 1 9 9 1	KNSSCHAQGSAIVNVLDRPGPCQNLKVTNVTKENCTISWENPLDNGGSEITNFIVEYRKP	18970
àè	102		101
3 2	1897	NOKGWSIVASDVTKRLIKANLLANNEYYFRVCAENKVGVGPTIETKTPILAINPIDRPGE	19030
3 8			101
<b>3</b>	70 0	GVMYHERILKGSDWGSSDWLSYHVERRILKGSDDWGGGGGWLWWGGSLKGSDWGRWHYWWD	19090
පු	19031		
ò	102		2 6
g	19091	. RCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQKPVLDLKLSGVLTVKAGDTIRLEA	
ò	102		101
g	19151	. GVRGKPFPEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKAKRSDGGKYVVTATNTAG	19210
ò	102		101
යි	19211	. SFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGCEIQNYILEKCETKRMVW	19270
ò	102		. 101
qq	19271	L STYSATVLTPGTTVTRLIEGNEYIPRVRAENKIGTGPPTESKPVIAKTKYDKPGRPDPPE	19330
ò	102		101
q	19331	1 VTKVSKEEMTVVWNPPEYDGGKSITGYFLEKKEKHSTRWVPVNKSAIPERRMKVQNLLPD	19390

	HEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEPPGPPTNFRVVDTTKHSITLGWGKPVYD	19450 101
		0.01
		70.
	GGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTSLDENQEYEFRVCAQNQV	19510
		101
19511 GIG	GIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRLFAIVRGRPAPKVTWRKV	19570
102		101
19571 GI	GIDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLVNPAGEKAVFVNVRVLDTPGPVS	19630
102		101
19631 DL	DLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWSTVTPEVKKTSFHVTNLV	19690
102		101
19691 PG	PGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLEVTEMTKNSATLAWLPPL	19750
102		101
19751 RD	RDGGAKIDGYITSYREEEQPADRWTEYSVVKDLSLVVTGLKEGKKYKFRVAARNAVGVSL	19810
102		101
19811 PR	PREAEGUYEAKEQLLPPKILMPEQITIKAGKKLRIEAHVYGKPHPTCKWKKGEDEVVTSS	19870
102		101
19871 HL	HLAVHKADSSSILIIKDVTRKDSGYYSLTAENSSGTDTQKIKVVVMDAPGPPQPPFDISD	19930
102		101
19931 ID	IDADACSLSWHIPLEDGGSNITNYIVEKCDVSRGDWVTALASVTKTSCRVGKLIPGQEYI	19990
102		101
19991 FR	FRVRAENRFGISEPLTSPKMVAQFPFGVPSEPKNARVTKVNKDCIFVAMDRPDSDGGSPI	20050
102		101
20051 IG	IGYLIERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFRIYALNKAGSSPPSKPTEY	20110
102		101
20111 VT	VTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFVEACKLPGDKWVRCNTAP	20170
102		101
20171 HC	HQIPQEEYTATGLEEKAQYQFRAIARTAVNISPPSEPSDPVTILAENVPPRIDLSVAMKS	20230
102		101
20231 LI	LLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAMQRNLCTLELFSVNRKDS	20290
102		101
20291 GE	GDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAMLSWEPPLEDGGSEITNY	20350
102		101
20351 IN	IVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYQFRICAENKYGVGDPVFTEPAIAKN	20410
102		101
20411 P	PYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEKRETQAVNWTKVNRKPII	20470
102 -		101

CD	20471	ERTLKATGLQEGTEYEFRVTAINKAGPGKPSDASKAAYARDPQYPPAPPAFPKVYDTTRS 205	0230
ò	102	100	01
q	20531	SVSLSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPQNLQKTRFEVTGLMEDTQYQFR 205	0830
ò	102	101	01
q	20591	VYAVNKIGYSDPSDVPDKHYPKDILIPPEGELDADLRKTLILRAGVTMRLYVPVKGRPPP	20650
ò	102	101	01
q	20651	KITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYILTLENSCGKKEYTIVVKV	20710
ò	102	101	01
Q	20711	LDTPGPPVNVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKRDAERKSWSTVTTECSKT	20770
ò	102	0.00	101
QQ	20771	SFRVANLEEGKSYFFRVFAENEYGIGDPGETRDAVKASQTPGPVVDLKVRSVSKSSCS1G	20830
ò	102	101	10
qq	20831	WKKPHSDGGSR11GYVVDFLTEENKWQRVMKSLSLQYSAKDLTEGKEYTFRVSAENENGE	20890
ò	102		101
q	20891	GTPSEITVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPIKGKPAPSVSWKKGEDPL	20950
ò	102		101
d	20951	ATDTRVSVESSAVWTTLIVYDCQKSDAGKYTITLKNVAGTKEGTISIKVVGKPGIPTGPI	21010
ò	102		101
q	21011	KFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTCASAVQKTTFRVTRLHEG	21070
ò	102		101
Q	21071	MEYTFRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPPNIVDVRHDSVSLTWTDPKKTG	21130
ò	102		101
qq	21131	GSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEYEFRVMAINLAGVGKPSL	21190
ò	102		101
Q	21191	PSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLTGYIVEKROLPSKSWMKA	21250
ò	102		101
qq	21251	NHVNVPECAFTVTDLVEGGKYEFRIRAKNTAGAISAPSESTETIICKDEYEAPTIVLDPT	21310
ò	102		101
qq	21311	IKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDITQITSTPTSSMLTIKYAT	21370
ò	102		101
q	21371	RKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSAEKATLTWTPPLEDGGSP	21430
ò	102		101
g	21431	IKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRVSAVNHYGKGEPVQSEPV	21490
ò	102		101
đ	21491	KAYUDRFGPPGPPEKPEVSNVTKATATVSWKRPVDDGGSEITGYHVERREKKSLRWVRAIK	21550
ò	, 102		101

g	21551	TPVSDLRCKVTGLQEGSTYEFRVSAENRAGIGPPSEASDSVLMKDAAYPPGPPSNPHVTD 21610	
ò	102	107	
qq	21611	TTKKSASLAWGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGTALRITQFVVPDLQTKEK 21670	
ò	108	107	
g	21671	YNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTLVVRAGLSIRIFVPIKGR 21730	
ઠે	108	107	
qq	21731	PAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFVMTIENPAGKKSGFVNVR 21790	
ò	108	107	
g	21791	VLDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEKREATRKSYSTATTKCHK 21850	
ò	108	107	
g	21851	CTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASEAPSPPDSLNIMDITKSTVSL 21910	
ò	108	107	
g	21911	AWPKPKHDGGSKITGYVIEAQRKGSDQWTHITTVKGLECVVRNLTEGEEYTFQVMAVNSA 21970	
ò	108	107	
g	21971	GRSAPRESRPVIVKEQTWLPELDLRGIYQKLVIAKAGDNIKVEIPVLGRPKPTVTWKKGD 22030	
ó	108	107	
g	22031	QILKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGEVGDVITIQVHDIPGPPT 22090	
ò	108	101	
8	22091	GPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTWVELATTVIRTTYKATRL 22150	
ò	108	107	
දු	22151	TTGLEYQFRVKAQNRYGVGPGITSACIVANYPFKVPGPPGTPQVTAVTKDSMTISWHEPL 22210	
ò	108		
g	22211	SDGGSPILGYHVERKERNGILWQTVSKALVPGNIFKSSGLTDGIAYEFRVIAENMAGKSK 22270	
ò	108	107	
g	22271	. PSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGFKITSYIVEKRDLPNGRW 22330	
ò	108	107	
g	22331	L LKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDVEAPKIKV 22390	
ò	108	107	
g	22391	I DVKFKDTVILKAGEAFRLEADVSGRPPPTMEWSKDGKELEGTAKLEIKIADFSTNLVNKD 22450	-
ò	108	9	
g	22451	1 STRRDSGAYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTEVTSEKCVLSWFPPLDDG 22510	
ò	108	8	
q	22511	1 GAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYIFRVMAVNKYGVGEPLES 22570	
ò	108	8	
g	22571	1 EPVLAVNPYGPPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEIINYIVERRDKAGGRWIK 22630	-
ò	108	8	
g	22631	1 CNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPFYKACDTVFKPGPPGNPR 22690	_

ò	108		107
g	22691	VLDTSRSSISIAWNKPIYDGGSEITGYMVEIALPEEDEWQIVTPPAGLKATSYTITGLTE	22750
ò	108		107
; d	22751	NOEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADLRKVVTIRACCTLRLFVP	22810
8	108		101
2 8	22811	1KGRPAPEVKWARDHGESLDKASIESTSSYTLL1VGNVNRFDSGKY1LTVENSSGSKSAF	22870
ò	108		107
연	22871	VNVRVLDTPGPPQDLKVKEVTKTSVTLTWDPPLLDGGSKIKNYIVEKRESTRKAYSTVAT	22930
ò	108		107
qq	22931	NCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKASERPLPPGKITLMDVTRN	22990
ò	108		107
g	22991	SVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEATITGLIQGEEYSFRVSA	23050
ò	108		107
q	23051	QNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLKVDVPFIGRPTPAVTWHK	23110
ò	108		107
q	23111	DNVPLKQTTRVNAESTENNSLLTIKDACREDVGHYVVKLTNSAGEAIETLNVIVLDKPGP	23170
ò	108		101
qq	23171	PTGPVKMDEVTADSITLSWGPPKYDGGSSINNYIVEKRDTSTTTWQIVSATVARTTIKAC	
ò	108		107
q	23231	RLKTGCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGTPVVTLSSRDSMEVQWNE	23290
ò	108		101
q	23291	PISDGGSRVIGYHLERKERNSILWVKLNKTPIPQTKFKTTGLEEGVEYEFRVSAENIVGI	23350
ò	108		101
d	23351	GKPSKVSECYVARDPCDPPGRPEAIIVTRNSVTLQWKKPTYDGGSKITGYIVEKKELPEG	23410
è			101
ģ · ģ	,	bwmxasftniidthfevtglvedhryefrviarnaagvfsepsestgaitardevdppri	23470
3 2			101
7	í	VSTATE TO THE TERMINATION OF THE TOTAL CONTRIBUTION OF THE TRANSPORT OF TH	7 23530
g	23		107
ò	108		
q	23531	. KDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVISGVTAEKCTLAWKPPLQ	
ò	108		
đ	23591	DGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNEYTFRIMAVNKYGVGEPL	
ò	108		- 107
g	23651	1 BSEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGSEILGYVLEKRDKEGIRW	
ò	108		- 107
q	23711	1 TRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPSAYQKACDPIYKPGPPNN	N 23770

ò	108	101	i		177.17
Ę	17775	PKVIDITRSSVFLSWSKPIYDGGCEIOGYIVEKCDVSVGEWTMCTPPTGINKTNIEVEKL 23830	2	1419411 15947	1
3			ò	131	
ò	108		දු	24911 KLTEHQI	EHOI
g G	23831	LEKHEYNFRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLDLELKKIINIKAGGSLKLF 23890	ò	131	i
ò	112		Q	24971 IHIPFK	PFK(
d Q	23891	VPIKGRPTPEVKWGKVDGEIRDAAIIDVTSSFTSLVLDNVNRYDSGKYTLTLENSSGTKS 23950	ò	134	1
ò	112	111	qq	25031 KSAFVT	FVT
q	23951	AFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIKNYIVEKREATRKSYAAV 24010	ò	134	1
ò	112	111	QC	25091 NVSSKC	SKC
đ	24011	VINCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIKVAEVPQPPGKITVDDVT 24070	ò	134	:
ò	112	111	QQ	25151 VSQTSA	TSA
QQ	24071	RNSVSLSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSLQAVITNLTQGEEYLFRV 24130	ò	134	- {
ò	112	111	qq	25211 RVKAYN	AYN
Q	24131	24131 VAVNEKGRSDPRSLAVPIVAKDLVIEPDVKPAFSSYSVQVGQDLKIEVPISGRPKPTITW 24190	ò	134	i
ò	112	111	đ	25271 SWVKDG	KDG
q	24191	TKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVANVVGQKTASIEIVTLDKP 24250	ò	134	:
ò	112	111	q	25331 KPGPPV	۸dd
q	24251	DPPKGPVKFDDVSAESITLSWNPPLYTGGCQITNYIVQKRDTTTTVWDVVSATVARTTLK 24310	ò	134	
ò	112		q	25391 IKITKL	TKL
g	24311	VTKLKTGTEYQFRIFAENRYGQSFALESDPIVAQYPYKEPGPPGTPFATAISKDSMVIQW 24370	ò		
ò	112	111	qq	25451 QWH	QWHEPV
g	24371	HEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTQFKAQNLEEGIEYEFRVYAENIV 24430	ò	134	- }
ò	112	111	qq	25511 IVG	IVGIGK
q	24431	GVGKASKNSECYVARDPCDPPGTPEPIMVKRNEITLQWTKPVYDGGSMITGYIVEKRDLP 24490	ò	134	
ò	112		q	25571 LPD	LPDGRW
ద	24491	DGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISKPSDSTGPITAKDEVELP 24550	ò	134	
ò	112		q	25631 APN	APNASL
a	24551	RISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEIEESARCEIKNTDFKALL	ò	134	
ò	112	:	đ	25691 TTI	TTLW
g	24611	IVKDAIRIDGGQYILRASNVAGSKSFPVNVKVLDRPGPPEGPVQVTGVTSEKCSLTWSPP	ò	134	
ò	123	-01.03	q	25751 NPPLQE	570
å	24671	LÓDGGSDISHYVVEKRETSRLAWTVVASEVVTNSLKVTKLLEGNEYVFRIMAVNKYGVGE	ò	134	Ì
ò	127		q	25811 IGE	IGEPLE
đ	24731	PLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDGGSEIIGYIVEKRDRSGI	ò	134	
ò	127	ACSP	qa	25871 EG	EGVRWI
g	24791	RWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSPATVYYKACDPVFKPGPP	ò	134	į
ò	131	1			

g	24851	TNAHIVDTTKNSITLAWGKPIYDGGSEILGYVVEICKADEEEWQIVTPQTGLRVTRFEIS 2	24910
ò	131	1	130
g	24911	KLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDLDSELRKGIVVRAGGSAR 2	24970
ò	131	1TWS	133
Q	24971		25030
ò	134	1	133
ф	25031	KSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAKVKNYVIDKRESTRKAYA	25090
ò	134	1	133
g	25091	NVSSKCSKTSFKVENLTEGAIYYFRVMAENEFGVGVPVETVDAVKAAEPPSPPGKVTLTD	25150
ò	134	1	133
g	25151	VSQTSASLMWEKPEHDGGSRVLGYVVEMQPKGTEKWSIVAESKVCNAVVTGLSSGQEYQF	25210
ò	134		133
g	25211	RVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAGEDLKIEIPVIGRPRPNI	25270
ò	134	1	133
q	25271	SWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDFGKYTVTATNSAGTATENLSVIVLE 2	25330
ò	134	1	133
q	25331	KPGPPVGPVRFDEVSADFVVISWEPPAYTGGCQISNYIVEKRDTTTTWHMVSATVARTT	25390
ò	134	1	133
Q	25391	IKITKLKTGTEYQFRIFAENRYGKSAPLDSKAVIVQYPFKEPGPPGTPFVTSISKDOMLV	25450
ò	134		133
qq	25451	QWHEPVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIQDTKFKTTGLDEGLEYEFKVSAEN	25510
ò	134		133
qq	25511	IVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKPAYDGGSKITGYIVEKKD	25570
ò	134		133
q	25571	LPDGRWMKASFTNVLETEFTVSGLVEDQRYEFRVIARNAAGNFSEPSDS94AITARDEID	25630
ò	134		133
a a	25631	APNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGKELEETAARMEIKSTIOK	25690
ò	134		133
đ	25691	TTLVVKDCIRTDGGQY1LKLSNVGGTKSIP1TVKVLDRPGPPEGPLKVTGVTAEKCYLAW	25750
ò	134		133
qq	25751	NPPLQDGGANISHYIIEKRETSRLSWTQVSTEVQALNYKVTKLLPGNEYIFRVMAVNKYG	25810
ò	134		133
q	25811	IGEPLESGPVTACNPYKPPGPPSTPEVSAITKDSMVVTWARPVDDGGTEIEGYILEKRDK	25870
ò	134		133
đ	25871	EGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENAAGVGEPSEPSVFYRACDALYPP	25930
			111

g	25931	GPPSNPKVTDTSRSSVSLAMSKPIYDGGAPVKGYVVEVKEAAADEWTTCTPPTGLQGKQF	25990
6	134		133
a	25991	TVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPEIELDADLRKVVVLRASA	26050
ò	134		133
g	26051	TLRLFVT1KGRPEPEVKWEKAEGILTDRAQ1EVTSSFTMLV1DNVTRFDSGRYNLTLENN	26110
ò	134		133
q	26111	SGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDGGAKITNYIVEKRETTRK	26170
ò	134		133
g	26171	AYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAETTEPVKVSEPPLPPGRVT	26230
ò	134		133
g	26231	LVDVTRNTATIKWEKPESDGGSKITGYVVEMQTĶGSEKWSTCTQVKTLEATISGLTAGEE	26290
ò	134		133
g	26291	YVFRVAAVNEKGRSDPRQLGVPVIARDIEIKPSVELPFHTFNVKAREQLKIDVPFKGRPQ	26350
ò	134		133
엄	26351	ATVNWRKDGQTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYELCVSNSAGSITVPITII	26410
ò	134		133
q	26411	VLDRPGPPGPIRIDEVSCDSITISWNPPRYDGGCQISNYIVEKKETTSTTWHIVSQAVAR	26470
ò	134		133
g	26471	TSIKIVRLTTGSEYQFRVCAENRYGKSSYSESSAVVAEYPFSPPGPPGTPKVVHATKSTM	26530
ò	134		133
q	26531	. LVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQMKVSGLDEGLMYEYRVYA	26590
ò	134		133
g	26591	. ENIAGIGKCSKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWSKPHYDGGAKITGYIVER	26650
ò	134		133
පු	26651	I RELPDGRWLKCNYTNIQETYFEVTELTEDQRYEFRVFARNAADSVSEPSESTGPIIVKDD	26710
ò	134		133
g	26711	1 VEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKDGIEIEERARTEIISTDN	26770
ò	134	7	133
qq	26771	1 HTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPPAGPLEINGLTAEKCSLS	26830
ò	134	þ	133
g	26831	MGRPQEDGGADIDYYIVEKRETSHLAWTICEGELQMTSCKVTKLLKGNEYIFRVTGVNKY	26890
ò	134	t	133
q	26891	1 GVGEPLESVAIKALDPFTVPSPPTSLEITSVTKESMTLCWSRPESDGGSEISGYIIERRE	26950
ò	134	,	. 133
윱	26951	1 KNSLRWVRVNKKPVYDLRVKSTGLREGCEYEYRVYAENAAGLSLPSETSPLIRAEDPVFL	27010
ò	134		. 133
g	27011	1 PSPPSKPKIVDSGKTTITIAWVKPLFDGGAPITGYTVEYKKSDDTDWKTSIQSLRGTEYT	r 27070

ò	134	MM
g	27071	ISGLTTGAEYVFRVKSVNKVGASDPSDSSDPQIAKEREEEPLFDIDSEMRKTLIVKAGAS 27130
ò	134	133
qq	27131	FIWIVPFRGRPVPNVLWSKPDTDLRTRAYVDTTDSRTSLTIENANRNDSGKYTLTIQNVL 27190
ò	134	133
셤	27191	SAASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVPENDGGAPVKNYHIEKREASKKA 27250
ò	134	133
g	27251	WVSVTNNCNRLSYKVTNLQEGAIYYFRVSGENEFGVGIPAETKEGVKITEKPSPPEKLGV 27310
ò	134	133
Q	27311	TSISKDSVSLTWLKPEHDGGSRIVHYVVEALEKGQKNWVKCAVAKSTHHVVSGLRENSEY 27370
ò	134	133
Q	27371	FFRVFAENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTVYVRAGSNLKVDIPISGK 27430
ò	134	133
g	27431	PLPKYTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFIN 27490
ò	134	133
g	27491	IVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSQVTNYILLKRETSTAVWTEVSAT 27550
ò	134	133
q	27551	VARTWMKVMKLTTGEEYQFRIKAENRFGISDHIDSACVTVKLPYTTPGPPSTPWVTNVTR 27610
ò	134	
g	27611	ESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWQKANKLVIRTTHFKVTTISAGLIYEFR 27670
à	134	133
Q	27671	VYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSLSWQQPAFDGGSKITGYI 27730
ò	134	133
음	27731	VERRDLPDGRWTKASFTNVTETQFIISGLTQNSQYEFRVFARNAVGSISNPSEVVGPITC 27790
ò	134	133
; A	2779	IDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEWYKDDKELQTNALVCVEN 27850
ò		133
QQ	27851	TTDLASILIKDADRLNSGCYELKLRNAMGSASATIRVQILDKPGPPGGPIEFKTVTAEKI 27910
ò		137
셤	27	1:   TLLWRPPADDGGAKITHYIVEKRETSRVVWSMVSEHLEECIITTTKIIKGNEYIFRVRAV 27970
ò		
: සි	27	NKYGIGEPLESDSVVAKNAFVTPGPPGIPEVTKITKNSMTVVWSRPIADGGSDISGYFLE 28030
ò	138	137
g	28031	KRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAAGOGPFSEPSEFYKAADP 28090
õ	138	137
q	28091	IDPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIRQGEEEEWTTVSTKGEVR 28150

ò	138 -	137		q	2923
Q	28151 T	TTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDILEAPEIDLDVALRTSVIA 28210		ò	13
ò	138 -	137		. d	2926
a	28211 K	KAGEDVQVLIPFKGRPPTVTWRKDEKNLGSDARYSIENTDSSSLLTIPQVTRNDTGKYI 28270		ò	1
ò	138 -	137		අ	293
ΩP	28271 L	LTIENGVGEPKSSTVSVKVLDTPAACQKLQVKHVSRGTVTLLMDPPLIDGGSPIINYVIE 28330		ò	급
ò	138 -	137		đ	294
g	28331 K	KRDATKRTWSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENBIGIGEPCETTEPVKAAEVP 28390		ò	ä
ò	138 -	137		q	294.
g	28391 A	APIRDLSMKDSTKTSVILSWTKPDFDGGSVITEYVVERKGKGEQTWSHAGISKTCEIEVS 28450		ò	H
ò	138 -	137		g	295
g	28451 C	QLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELIITPEVDLSDIPGAQVTVRIGHNVHL 28510		ò	H
ò	138 -	137		음	295
g	28511 E	ELPYKGKPKPSISWLKDGLPLKESEFVRFSKTENKITLSIKNAKKEHGGKYTVILDNAVC 28570		ò	7
ò	138 -	137		qq	296
đ	28571 F	RIAVPITVITLGPPSKPKGPIRFDEIKADSVILSWDVPEDNGGGEITCYSIEKRETSQTN 28630	20.	ò	H
ò	138	137		q	297
8	28631 4	WKMVCSSVARTTFKVPNLVKDAEYQFRVRAENRYGVSQPLVSSIIVAKHQFRIPGPPGKP 28690		ò	1
ò	138	137		<u> </u>	297
g	28691	VIYNVTSDGMSLTWDAPVYDGGSEVTGFHVEKKERNSILWQKVNTSPISGREYRATGLVE 28750		ò	7
ò	138	137		g	298
g	28751 (	GLDYQFRVYAENSAGLSSPSDPSKFTLAVSPVDPPGTPDYIDVTRETITLKWNPPLRDGG 28810		ò	-
ò	138	137		q	298
g	28811	SKIVGYSIEKRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEFRIIARNAVGTISPPSQS 28870	_	ò	-
ò	138	137		e d	299
g	28871	SGIIMTRDENVPPIVEFGPEYFDGLIIKSGESLRIKALVQGRPVPRVTWFKDGVEIEKRM 28930		ò	-
ò	138			q	300
දු	28931	NMEITDVLGSTSLFVRDATRDHRGVYTVEAKNASGSAKAEIKVKVQDTPGKVVGPIRFTN 28990		ò	-
ò	138	137		q	300
Q	28991	ITGEKMTLWWDAPLNDGCAPITHYIIEKRETSRLAWALIEDKCEAQSYTAIKLINGNEYQ 29050		ò	-
ò	138	137		qq	301
g	29051	FRVSAVNKFGVGRPLDSDPVVAQIQYTVPDAPGIPEPSNITGNSITLTWARPESDGGSEI 29110		ò	-
ò	138	137	_	g	301
g	29111	QQYILERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEFHVMAENAAGVGPASGISR 29170		ò	-
ò	138			g	303
셤	29171	29171 LIKCREPVNPPGPPTVVKVTDTSKTTVSLEWSKPVFDGGMEIIGYIIEMCKADLGDWHKV 29230		ò	-
č	138	111111111111111111111111111111111111111	_		

g	29231 N	NAEACVKTRYTVTDLQAGEEYKFRVSAINGAGKGDSCEVTGTIKAVDRLTAPELDIDANF 29290
ò	138 -	137
g	29291 F	KQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHTTDSFSTLTVENCNRNDA 29350
ò	138 -	137
g	29351 (	GKYTLTVENNSGSKSITFTVKVLDTPGPPGPITFKDVTRGSATLMMDAPLLDGGARIHHY 29410
ò	138	137
qq	29411	VVEKREASRRSWQVISEKCTRQIFKVNDLAEGVPYYFRVSAVNEYGVGEPYEMPEPIVAT 29470
ò	138	137
g	29471	EQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQKGSDFWVEAGHTKQLTF 29530
ò	138	137
g	29531	TVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVIIKEPQIEPTADLTGITNQLITCKAGS 29590
ò	138	137
ď	29591	PFTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLTVKDSMRGDSGRYFLTLE 29650
ò	138	137
g	29651	NTAGVKTFSVTVVVJGRPGPVTGPIEVSSVSAESCVLSWGEPKDGGGTEITNYIVEKRES 29710
ò	138	137
g	29711	GTTAWQLVNSSVKRTQIKVTHLTKYMEYSFRVSSENRFGVSKPLESAPIIAEHPFVPPSA 29770
ò	138	137
g	29771	PTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTILWVKENKVPCLECNYKVT 29830
ò	138	137
g	29831	GLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPEVTDVTRSTVSLIWSAPA 29890
ò	138	137
QQ	29891	YDGGSKVVGYIIERKPVSEVGDGRWLKCNYTIVSDNFFTVTALSEGDTYEFRVLAKNAAG 29950
ò	138	137
g	29951	VISKGSESTGPVTCRDEYAPPKAELDARLHGDLVTIRAGSDLVLDAAVGÖKPEPKIIWTK 30010
ò	138	137
g	30011	GDKELDLCEKVSLQYTGKRATAVIKFCDRSDSGKYTLTVKNASGTKAVSVMVKVLDSPGP 30070
ò	138	137
g	30071	CGKLTVSRVTQEKCTLAMSLPQEDGGAEITHYIVERRETSRLNWVIVEGECPTLSYVVTR 30130
ò	138	137
q	30131	LIKNNEYIFRVRAVNKYGPGVPVESEPIVARNSFTIPSPPGIPEEVGTGKEHIIIQWTKP 30190
ò	138	137
đ	30191	ESDGGNEISNYLVDKREKKSLRWTRVNKDYVVYDTRLKVTSLMEGCDYQFRVTAVNAAGN 30250
ò	138	137
g	30251	SEPSEASNFISCREPSYTPGPPSAPRVVDTTKHSISLAWTKPMYDGGTDIVGYVLEMQEK 30310
ò	138	137

a D	30311	DTDOWYRVHTNATIRNTEFTVPDLKMGQKYSFRVAAVNVKGMSEYSESIAEIEFVERIEI	30370
ò	138		137
QQ	30371	PDLELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQGIDLASRAIIDTTESYSLLI	30430
ò	138		137
q	30431	VDKVNRYDAGKYTIEAENQSGKKSATVLVKVYDTPGPCPSVKVKEVSRDSVTITWEIPTI	30490
ò	138		137
QQ	30491	DGGAPVNNYIVEKREAAMRAFKTVTTKCSKTLYRISGLVEGTMYYFRVLPENIYGIGEPC	30550
ò	138	•	137
g	30551	ETSDAVLVSEVPLVPAKLEVVDVTKSTVTLAWEKPLYDGGSRLTGYVLEACKAGTERWMK	30610
ò	138		137
qq	30611	WYTLKPTVLEHTVTSLNEGEQYLFRIRAQNEKGVSEPRETVTAVTVQDLRVLPTIDLSTM	30670
ò	138		137
g	30671	POKTIHVPAGRPVELVIPIAGRPPPAASWFFAGSKLRESERVTVETHTKVAKLTIRETTI	30730
ò	138	EDŢĞ	141
g	30731	   RDTGEYTLELKNVTGTTSETIKVIILDKPGPPTGPIKIDEIDATSITISWEPPELDGGAP	30790
ò	142		141
g	30791	LSGYVVEQRDAHRPGWLPVSESVTRSTFKFTRLTEGNEYVFRVAATNRFGIGSYLQSEVI	30850
ò	142		141
g	30851	ECRSSIRIPGPPETLQ1FDVSRDGMTLTWYPPEDDGGSQVTGY1VERKEVRADRWVRVNK	30910
ઠે	142		141
q	30911	VPVTMTRYRSTGLTEGLEYEHRVTAINARGSGKPSRPSKPIVAMDPIAPPGKPQNPRVTD	30970
ò	142		141
g	30971	TTRTSVSLAWSVPEDEGGSKVTGYLIEMQKVDQHEWTKCNTTPTKIREYTLTHLPQGAEY	31030
ઠે	142		. 141
g	31031	RFRVLACNAGGPGEPAEVPGTVKVTEMLEYPDYELDERYQEGIFVRQGGVIRLTIPIKGK	31090
ò	142		. 141
g	31091	PFPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYDLVLENKCGKKAVYIKVR	31150
ò	142		. 141
q	31151	VIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADILGYILERREVPKAAWYTIDSRVR	31210
ò	142		. 141
g	31211	GTSLVVKGLKENVEYHFRVSAENQFGISKPLKSEEPVTPKTPLNPPEPPSNPPEVLDVTK	K 31270
ò	142		- 141
Q	31271	. SSVSLSWSRPKDDGGSRVTGYYIERKETSTDKWVRHNKTQITTTMYTVTGLVPDAEYQFR	31330
ò	142		- 141
g	31331	. IIAQNDVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKDSVTLQWEKPECDGGKEIL	L 31390
ò	142		- 141
g	31391	. GYWVEYROSGDSAWKKSNKERIKDKOFTIGGLLEATEYEFRVFAENETGLSRPRRTAMSI	I 31450

ò	142		141
임	31451	KTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKWYRFGKELIQSRKYKMSS	31510
ò	142		141
g	31511	DGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATPQFHPGYPLKEKYYGAVG	31570
ò	142		141
d d	31571	STLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHLVMKNVQRKTHAGKYKVQ	31630
ò	142		141
qq	31631	LSNVFGTVDA1LDVE1QDKPDKPTGP1V1EALLKNSAVISWKPPADDGGSW1TNYVVEKC	31690
ò	142		141
QQ	31691	EAKEGAEWQLVSSAISVTTCRIVNLTENAGYYPRVSAQNTFGISDPLEVSSVVIIKSPFE	31750
ò	142		141
a	31751	KPGAPGKPT1TAVTKDSCVVAWKPPASDGGAKIRNYYLEKREKKQNKWISVTTEE1RETV	31810
ò	142		141
g	31811	FSVKNL1EGLEYEFRVKCENLGGESEWSE1SEP1TPKSDVP1QAPHFKEELRNLNVRYQS	31870
ò	142		141
g	31871	NATLVCKVTGHPKPIVKMYRQGKEIIADGLKYRIQEFKGGYHQLIIASVTDDDATVYQVR	31930
ò	142		141
g	31931	ATNOGGSVSGTASLEVEVPAKIHLPKTLEGMGAVHALRGEVVSIKIPFSGKPDPVITWQK	31990
ò	142		141
d d	31991	GQDLIDNNGHYQVIVTRSFTSLVFPNGVERKDAGFYVVCAKNRFGIDQKTVELDVADVPD	32050
ò	142		141
<b>Q</b>	32051	PPRGVKVSDVSRDSVNLTWTEPASDGGSKITNYIVEKCATTAERWLRVGQARETRYTVIN	32110
ò	142		141
. a	32111	LFGKTSYQFRVIAENKFGLSKPSEPSEPT1TKEDKTRAMNYDEEVDETREVSMTKASHSS	32170
ò	142		141
: a	32171	TKELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEISILNIAR	32230
ò	142		141
d d	32231	HRNILHLHESFESMEELVMIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLH	32290
ò	142		144
: සි	32	: SHNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKPGDNFRLLFTAPEYYAPEVHQHDV	32350
ò	145		144
d	32351	VSTATDMWSLGTLVYVLLSGINPFLAETNOQIJENIMNAEYTFDEEAFKEISJEAMDFVD	32410
ò	145		. 144
q	32411	RLLVKERKSRMTASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARI	1 32470
ò	145		. 144
ద	32471	SCGGAIRSQKGVSVAKVKVASIEIGPVSGQIMHAVGEEGGHVKYVCKIENYDQSTQVTWY	32530

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CONFLICT
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                    32531 FGVRQLENSEKYEITYEDGVAILYVKDITKLDDGTYRCKVVNDYGEDSSYAELFVKGVRE 32590
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95331314; PubMed=7607248; Gautel M., Motta A., Pastore A.; Cautel M., Castiglione-Morelli M.A., Pfuhl M., Motta A., Pastore A.; A calmodulian-binding sequence in the C-terminus of human cardiac titin kinase.; But. J. Blochem. 230:752-750:1007.
   ------ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112 IMMUNOGLOBULIN C2-LIKE DOWAINS AND 132 FIBRONECTIN TYPE III-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: MUSCLE-SPECIFIC. SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 Labeit S., Kolmer B.; "Titins: giant proteins in charge of muscle ultrastructure and
                                                         32591 VYDYYCRRTMKKIKRRTDTMRLLERPPEFTLPLYNKTAYVGENVRFGVTI 32640
                                        GVTI 148
                                                                                                                                                                                                                                                                                                                                                                   Labeit S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Titin, heart isoform N2-B (EC 2.7.1.-) (Connectin).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                   MEDLINE=92259380; PubMed=158240;
Labeit S., Gautel M., Lakey A., Trinick J.;
"Towards a molecular understanding of titin.";
EMBO J. 11:1711-1716 (1992).
                                                                                                            PRT; 26926 AA
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Interpro; IPR000719; Buk pkinase.
Interpro; IPR000577; FGGY kin.
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FnIII repeat.
FN III.
HLH basic.
19_62.
                                                                                                                                                                                                                                TISSUE=HEART;
MEDLINE=96026330; Pubmed=7569978;
                                                                                                                                                                                                                                                                                             SEQUENCE OF 22277-25376 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1976-2014 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X83270; CAA58243.1; -. EMBL; X64697; CAA45938.1; -. EMBL; X90569; CAA62188.1; -. EMBL; X64699; CAA45940.1; -. HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X64698; CAA45939.1; -.
                                                                                                                                                                                                                                                                    elasticity.";
Science 270:293-296(1995).
                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003598;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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R InterPro; IPR001560; Ig_like.

R InterPro; IPR00120; Peptidase_S24.

R InterPro; IPR00129; Peptidase_S24.

R InterPro; IPR00129; Peptidase.

R InterPro; IPR00220; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; PF00041; fin3; 132.

R Pfam; PF000041; fin3; 132.

R PRINTS; PR00126; LEXASERPTASE.

R PRINTS; PR00126; LEXASERPTASE.

R PRINTS; PR00126; LEXASERPTASE.

R PRART; SM00060; FN3; 127.

R SWART; SM00060; FN3; 127.

R SWART; SM00410; IG_11ke; 79.

R SWART; SM00410; IG_11ke; 79.

R PROSITE; PS000933; FGGY KINASES 1; UNKNOWN 1.

R PROSITE; PS00093; PROTEIN KINASE 1; UNKNOWN 1.

R PROSITE; PS00109; PROTEIN KINASE 1; UNKNOWN 1.

R PROSITE; PS00109; PROTEIN KINASE TVP; 1.

R PROSITE; PS00109; PROTEIN KINASE; TVP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKSRTKEIITTKQEQMHVTHEQIRKETEKTFVPKVVISAAKAKEQETRISEEITKKQKQ 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 AARISTSPIRSVRSPLLMRKTQASTVATGPEVPPPWKQEGYVASSSEAEMRETTLTTSTQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 IRTEERWEGRYGVQEQVTISGAAGAAASVSASASYAAEAVATGAKEVKQDADKSAAVATV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ÈLLVQGEEEVPAKKTKTIVSTAQISESRQTRIEKKIEAHFDARSIATVENWIDGAAGQQL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 PHKTPPRIPPKPKSRSPTPPSIAAKAQLARQQSPSPIRHSPSPVRHVRAPTPSPVRSVSP 309
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PHOSPHORYLATION (BY PDPK) (POTENTIAL).
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E -> G (IN REF. 2).
T -> Q (IN REF. 2).
S -> L (IN REF. 2).
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0.4%; Pred. No. 10;
tive 16; Mismatches
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28;

ą	550 V	VTQEA I MKETRKTVVPKVI VATPKVKEQDLVSRGREGITTKREQVQI TQEKMRKEAEKTA	609
à	19 -		18
ą	610 L	LSTI AVATAKAKEQETILRTRETMATRQEQI OVTHGKVDVGKKAEAVATVVAAVDQARVR	699
à	19 -		18
g	670 E	EPREPGHLEESYAQQTTLEYGYKERI SAAKVAEPPQRPASEPHVVPKAVKPRVI QAPSET	729
ઠે	19 -		18
유	730 H	HIKTTDQKGMHISSQIKKTTDLTTERLVHVDKRPRTASPHFTVSKISVPKTEHGYEASIA	789
à	19 -	•	18
g	790 G	GSA1ATLQKELSATSSAQKITKSVKAPTVKPSETRVRAEPTPLPQFPFADTPDTYKSEAG	849
ò	19 -		18
q	950 V	VEVKKEVGVSITGTTVREERFEVLHGREAKVTETARVPAPVEI PVTPPTLVSGLKNVTVI	606
ò	19 -	-VAHOEDTERYV-	30
a	910 E	EGESVTLECHISGYPSPTVTWYREDYQIESSIDFQITFQSGIARLMIREÄFAEDSGRFTC	696
કે	31 -		30
요	970	SAVNEAGTVSTSCYLAVQVSEEFEKETTAVTEKFTTEËKRFVESRDVVMTDTSLTEEQAG	1029 ·
ò	31		30
g	1030 E	PGEPAAPYFITKPVVQKLVEGGSVVFGCQVGGNPKPHVYWKKSGVPLTTGYRYKVSYNKQ	1089
ò	31		30
යු	1090 1	TGECKLVISMTFADDAGEYTIVVRNKHGETSASASLLEEADYELLMKSQQEMLYQTQVTA	1149
ò	31		30
g	1150	FVQEPEVGETAPGFVYSEYEKEYEKEQALIRKKMAKDTVVVRTYVEDQEFHISSFEERLI	1209
ò	31		30
g	1210	KEIEYRIIKTTLEELLEEDGEEKMAVDISESEAVESGFDLRIKNYRILEGMGVTFHCKMS	1269
ò	31		30
a	1270 (	GYPLPKIAWYKDGKRIKHGERYQMDFLQDGRASLRIPVVLPEDEGIYTAFASNIKGNAIC	1329
ò	31		30
q	1330	SGKLYVEPAAPLGAPTYIPTLEPVSRIRSLSPRSVSRSPIRMSPARMSPARMSPARMSPARMSPA	1389
ò	31		30
g	1390	RMSPGRRLEETDESQLERLYKPVFVLKPVSFKCLEGANCRFDLKVVGRPMPETFWFHDGO	1449
ò	31		30
q	1450	QIVNDYTHKVVIKEDGTQSLIIVPATPSDSGEWTVVAQNRAGRSSISVILTVEAVEHQVK	1509
ò	31	INTERIOR	. 96
g	1510		1569
ò	37		36
g G	1570	KIDSTVSQDSAWYTATAINKAGRDTTRCKVNVEVEFAEPEPERKLIIPRGTYRAKEIAAP	1629
ò	37		36
8	1630	<b>ELEPLHLRYGQEQWEEGDLYDKEKQQKPFFKKKLTSLRLKRFGPAHFECRLTPISDPTMV</b>	1689

ò	37 -	07
qq	1690 V	VEWLHDGKPLEAANRLRMINEFGYCSLDYGVAYSRDSGIITCRATNKYGTDHTSATLIVK 1749
ò	37 -	
q	1750 D	DEKSLVEESQLPEGRKGLQRIEELERMAHEGALTGVTTDQKEKQKPDIVLYPEPVRVLEG 1809
ò	39 -	38
CC	1810 E	ETARFRCRVTGYPQPKVNWYLNGQLIRKSKRFRVRYDGIHYLDIVDCKSYDTGBVKVTAE 1869
ò	. 68	38
о С	1870 N	NPEGVIEHKVKLEIQOREDFRSVLRRAPEPRPEFHVHEPGKLOFEVOKVDRPVDTTETKE 1929
ò	39 -	42 
QQ	1930 V	VVKLKRAERITHEKVPEESEELRSKFKRRTEEGYYEAITAVELKSRKKDESYEELLRKTK 1989
. <b>6</b>	43 -	42
g	1990	DELLHWTKELTEEEKKALAEEGKITIPTFKPDKIELSPSMEAPKIFERIQSQTVGOGSDA 2049
ò	43	45
q	2050 F	HFRVRVVGKPDPECEMYKNGVKIERSDRIYMYMPEDNVCELVIRDVTAEDSASIMVKAIN 2109
ò	46	45
q	2110 1	IAGETSSHAFLLVQAKQLITFTQELQDVVAKEKDTMATFECETSEPFVKVKWYKDGMEVH 2169
ò	46	45
q	2170	EGDKYRMHSDRKVHFLSILTIDTSDAEDYSCVLVEDENVKTTAKLIVEGAVVEFVKELQD 2229
ò	46	45
QQ	2230	IEVPESYSGELECIVSPENIEGKWYHNDVELKSNGKYTITSRRGRQNLTVKDVTKEDQGE 2289
ò	. 46	45
QQ	2290	YSFVIDGKKTTCKLKMKPRPIAILQGLSDQKVCEGDIVQLEVKVSLESVEGVWMKDGQEV 2349
ò	4.6	45
Q	2350 (	QPSDRVHIVIDKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSGRVSVYSVDVITPLKDVN 2409
ઠે	4 6	45
qq	2410	VIEGTKAVLECKVSVPDVTSVKMYLNDEQIKPDDRVQAIVKGTKQRLVINRTHASDEGPY 2469
ò	46	45
QQ	2470	KLIVGRVETNCNLSVEKIKIIRGLRDLTCTETQNVVFEVELSHSGIDVLMNFKDKEIKPS 2529
ò	46	45
qq	2530	SKYKİEAHGKIYKLIVLNAMKDDEGKYTFYAGENMISGKLIVAGGAISKPLIDQIVAESQ 2589
ó	46	59
g	2590	EAVFECEVANPDSKGEWLRDGKHLPLTNNIRSESDGHKRRLIIAATKLDDIGEYTYKVAT 2649
ò	46	45
QQ .	2650	SKTSAKLKVEAVKIKKTLKNLTVTETQDAVFTVELTHPNVKGVQWIKNGVVLESNEKYAI 2709
ò	46	LGAQFRVHLVXVV
qq	2710	SVKGTIYSLRIKNCAIVDESVYGFRLGRLGASARLHVETVKIIKKPKDVTALENATVAFE 2769

	85		
ò		റ്റ	3850 YPQSSIEPPMHSYL
qq	2770 VSVSHDTVPVKWFHKSVEIKPSDKHRLVSERKVHKLMLQNISPSDAGEYTAVVGQLECKA 2829	δ	
ò	85 65	qo	3910 ESLQSPDVMISQVN
qq	2830 KLEVETLHITKTMKNIEVPETKTASFECEVSHFNVPSMMLKNGVEIEMSEKFKIVVQGKL 2889	ò	99
ò	85 58	q	3970 ALEEKQVLLKEEHS
g	2890 HQLIIMNTSTEDSAEYTFVCGNDQVSATLTVTPIMITSMLKDINAEEKDTITFEVTVNYE 2949	ò	
ò	85 65	q	4030 LNLKIQICRALQAA
q	2950 GISYKWLKNGVEIKSTDKCQMRÇKKLTHSLNIRNVHFGDAADYTFVAGKATSTATLYVEA 3009	ò	99
ò	85 65	Q	4090 EEVTIIIEDVDPOM
qq	3010 RHIEFRKHIKDIKVLEKKRAMFECEVSEPDITVQWMKDDQELOITDRIKIQKEKYVHRLL 3069	ò	99
ò	85 65	g	4150 SQKVEPITEPEVES
q	3070 IPSTRMSDAGKYTVVAGGNVSTAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDV 3129	ò	99
ò	85 65	q	4210 SEEKEESSSESGTE
đ	3130 DAHWYKDGIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYTFVAGRNRSSVTLYVNA 3189	ò	
ò	85	g	4270 KEVNWYFENKLVPS
8	3190 PEPPQVLQELQPVTVQSGKPARFCAMISGRPQPKISWYKEEQLLSTGFKCKFLHDGQEYT 3249	ò	99
ò	85 28	q	4330 TVVKRAAPVIKRK
q	3250 LLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEVPEVVSPDQEMPVYPPAIITPLQDTV 3309	ò	04
ò	85 65	qq	4390 YISSLEILRTQVVI
q	3310 TSEGQPARFQCRVSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLEIAEAYPEDEGTYT 3369	ò	70
ò	85 65	QQ	4450 VVLKSVLRKRPEE
g	3370 FVANNAVGQVSSTANLSLEAPESILHERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLS 3429	ò	70
ò	65	q	4510 VPEIKPAIPLPAP
Q	3430 KINETLELLSESPVYPTKFDSEKEGTGPIFIKEVSNADISMGDVATLSVTVIGIPKPKIQ 3489	ò	70
ò	85 68	q	4570 AKPKGPIKGVPKK
q	3490 WFFNGVLLTPSADYKFVFDGDDHSLIILFTKLEDEGEYTCMASNDYGKTICSAYLKINSK 3549	ò	70
ò	85 28	g	4630 TESEFVGSSAIFE
g	3550 GEGHKDTETESAVAKSLEKLGGPCPPHFLKELKPIRCAQGLPAIFEYTVVGEPAPTVTWF 3609	ò	04
ò		QQ	4690 EYTCVLRLGNKEK
g	3610 KENKOLCTSVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENMLGESTCAAELLVLLED	ò	70
ò		අු	4750 DGKIVVEKPGRIV
g	3670 TDMTDTPCKAKSTPEAPEDFPQTPLKGPAVEALDSEQEIATFVKDTILKAALITEENQQL	ò	70
ò	65	q	4810 WLVKPIRDQHVKE
g	3730 SYEHIAKANELSSQLPLGAQELQSILEQDKLTPESTREFLCINGSIHFQPLKEPSPNLQL 3789	ò	02
ò	-53431711	a	4870 KNAMPEDIAEYAN
g	3790 QIVQSQKTFSKEGILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPLKTLLAEPEGN	ò	04
ò	69		

g	3850 YPQSSIEPPMHSYLTSVAEEVLSLKEKTV	SDTNREQRVTLOKQEAQSALILSOSLAEGHV 3909	õ
ò		3 6	
g	3910 ESLQSPDVMI	D.	D O
ò	λ 99 λ	59	
a	b 3970 ALEEKQVLLKEEHSDNVVMPPDQIIESKREPVAIKKVQEVQGRDLLSKESLLS	GIPEEOR 402	29
ò	99	99	
QQ	D 4030 LNLKIQICRALQAAVASEQPGLFSEWLRNIEKVEVEAVNITQEPRHIMCMYLVTSAKSVT	408	68
ò		65	
Q	3b 4090 EEVTIIIEDVDPQMANLKMELRDALCAIIYEEIDILTAEGPRIQQGAKT	SLQEEMDSFSG 414	<b>4</b> 0
ò	λ(	9	
g	3b 4150 SQKVEPITEPEVESKYLISTEEVSYFNVQSRVKYLDAT	PVTKGVASAVVSDEKODESLKP 420	
ò	99 K		
q	35 4210 SEEKEESSSESGTEEVATVKIQEAEGGLIKEDGPMIHT	PLVDTVSEEGDIVHLTTSITNA 426	69
ò	99	59 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10
g	4270 KEVNWYFENKLVPSDEKFKCLQDQNTY	TLVIDKVNTEDHQGEYVCEALNDSGKTATSAKL 432	329
ò	99	APNI 69	m
q	330 TVVKRAAPVIKRKIEPLEVALGHLAKFTCEIOSAPNVRFQWFKAGRE	PNVRFQWFKAGREIYESDKCSIRSSK 438	389
ò	07 YC	69	o.
g	4390 YISSLEILRTQVVDCGEYTCKASNEYGSVS	CTATLTVTVPGGEKKVRKLLPERKPEPKEE 444	449
ò	yc yc	69	o.
QQ	Db 4450 VVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEP	PPPKPVEEVEVPTVTKRERKIPEPTK 450	209
ò	VO YO	69	6
qq	Db 4510 VPEIKPAIPLPAPEPKPKPEAEVKTIKPPPVEPEPTPIAA	PVTVPVVGKKAEAKAPKEEA 45	569
ò		69	6
ු සු	4570 AKPKGPIKGVPKKTPSPI	EAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDIIL 462	629
ò		69	σ,
. a	4630 TESEFVGSSAIFECLVSPSTAITT	WMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAG 468	689
ò	, vo	69	o.
q	4690 EYTCVLRLGNKEKTSTAKLVVEELPVRFVKT	LEEEVTVVKGQPLYLSCELNKERDVVWRK 474	749
ò	07 VO	69	0
a	Db 4750 DGKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYTVTVENANNLECS	SCVKVVEVIRD 48	809
ò	VQ VQ	69	6
g	4810 WLVKPIRDQHVKPKGTAIFACDIAKDT	PNIKWFKGYDEIPAEPNDKTEILRDGNHLYLKI 480	1869
ò	yo yo	69	6
d d	Db 4870 KNAMPEDIAEYAVEIEGKRYPAKLTLGEREVELLKPIEDVTIYEKESASFDAEISEADI	P 49	929
;			0

ĝ	GOWKLKGELLRPSPTCEIKAEGGKRFLTLHKVKLDOAGEVLYQALNAITTAILTVKEIEL 4989	61
	69	-
DFA1	DFAVPLKDVTVPERRQARFECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILVINDS 504	6
÷	69	
OFI	QFDDEGVYTAEVEGKKTSARLFVTGIRLKFMSPLEDQTVKEGETATFVCELSHEKMHVVW 5109	60
	69	
Ϋ́	FKNDAKLHTSRTVLISSEGKTHKLEMKEVTLDDISQIKAQVKELSSTAQLKVLEADPYFT 516	69
1	69	
>	VKLHDKTAVEKDEITLKCEVSKDVPVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLK 522	62
i	69	
ã	DKGEYVCDCGTDKTKANVTVEARLIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLK 5289	39
•	69	
ŏ	GQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIFITPL 5349	61
•	69	
S	SDVKVFEKDEAKFECEVSREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDE 5409	60
	69	
Ø	AKYMFEAEDKHTSGKLIIEGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQ 5469	69
1	69	
5470 R	RLHTTRSVSMQDEGKTHSITFKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGKLQD 5529	59
•	69	
5530 Y	YTGVEKDEVILQCEISKADAPVKWFKDGKEIKPSKNAVIKTDGKKRMLILKKALKSDIGQ 5589	68
'	69	
5590 Y	YTCDCGTDKTSGKLDIEDREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEAL 5649	49
,	69	
1 0595	LQTPDCEIKEEGKIHSLVLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVT 5709	60
70 -	69	
5710 \	VTAGETATFDCELSYEDIPVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVQ 576	69
70	69	
5770 1	LTAKDFKTHANLFVKEPPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILK 582:	29
. 07	69	
5830	SKKYEIVADGRVRKLVIHDCTPEDIKTYTCDAKDFKTSCNLNVVPPHVEFLRPLTDLQVR 588	68
70	69	
5890	EKEMARFECELSRENAKVKWFKDGAEIKKGKKYDIISKGAVRILVINKCLLDDEAEYSCE 594	49
70	69	
5950 \	VRTARTSGMLTVLEEEAVFTKNLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIETG 6009	60
70	69	
6010 R	RYEILTEGRKRILVIQNAHLEDAGNYNCRLPSSRTDGKVKVHELAAEFISKPQNLEILEG 6069	691

ò	- 01	9	69
Q	6070 E	EKAEFVCSISKESFPVQWKRDDKTLESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVG 6	6129
ò	- 04	9	69
qq	6130 #	AARAAAHLTVIEKLRIVVPLKDTRVKEQQEVVFNCEVNTEGAKAKWFRNEEAIFDSSKYI 6	6189
ò	70	9	69
đ	6190 ]	ILQKDLVYTLRIRDAHLDDQANYNVSLTNHRGENVKSAANLIVEEEDLRIVEPLKDIETM 6	6249
ò	70	9	69
qq	6250 E	EKKSVTFWCKVNRLNVTLKWTKNGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDEGEYIVT 6	6309
ò	70		69
qq	6310 4	AGODKSVAELLIIBAPTEFVEHLEDQTVTEFDDAVFSCQLSREKANVKWYRNGREIKEGK 6	6369
ò	70	9	69
q	6370 1	KYKFEKDGSIHRLIIKDCRLDDECEYACGVEDRKSRARLFVEEIPVEIIRPPQDILEAPG 6	6429
ò	. 07	9	69
qq	6430 /	ADVVFLAELNKDKVEVQWLRNNMVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIAK 6	6489
ò	70		69
qq	6490	DKEARAKLELAAAPKIKTADQDLVVDVGKPLTMVVPYDAYPKAEAEWFKENEPLSTKTIO 6	6549
ò	70	9	69
qq	6550	TTAEQTSFRILEAKKGDKGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNLEVTETFDGEV 6	6099
ò	70	9	69
q	6610	SLAWEEPLTDGGSKIIGYVVERRDIKRKTWVLATDRAESCEFTVTGLQKGGVEYLFRVSA 6	6999
ò	20	9	69
q	6670	RNRVGTGEPVETDNPVEARSKYDVPGPPLNVTITDVNRFGVSLTWEPPEYDGGAEITNYV 6	6729
ò	70	9	69
QQ	6730	IELRDKISIRWDTAMTVRAEDLSATVTDVVEGQEYSFRVRAQNRIGVGKPSAATPFVKVA 6	6189
ò	70	TANLTSS	94
Q	6790	 DPIERPSPPVNLTSSDQTQSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLV (	6849
ò	77		94
g	6850	PELTYKVTGLEKGNKYLYRVSAENKAGVSDPSEILGPLTADDAFVEPTMDLSAFKDGLEV (	6069
ò	77		92
g	6910	IVPNPITILVPSTGYPRPTATWCFGDKVLETGDRVKWKTLSAYAELVISPSERSDKGIYT (	6969
ò	77		92
q	6970	LKLENRVKTISGEIDVNVIARPSAPKELKFGDITKDSVHLTWEPPDDDGGSPLTGYVVEK	7029
ò	77	LLSVC	81
q	7030	REVSRKTWTKVMDFVTDLEFTVPDLVQGKEYLFKVCARNKCGPGEPAYVDEPVNMSTPAT	7089
ò	82		81
g	7090	VPDPPENVKWRDRTANSIFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKM	7149

ઠે	82		81
g	7150 EVTGLEEGKWYAYRVKTLNRQGASKPSRPTEEIQAVDTQEAPEI	FLDVKLLAGLTVKAGT	7209
ò	82		81
g	7210 KIELPATVTGKPEPKITWTKADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYIIEAV		7269
ò	8		81
g	7270 NVCGRATAVVEVNVLDKPGPPAAFDITDVTNESCLLTWNPPRDDGGSKITNYVVERRATD	SCLLTWNPPRDDGGSKITNYVVERRATD	7329
ò			81
g	7330 SEVWHKLSSTVKDTNFKATKLIPNKEYIFRVAAENMYGAGEPVQASPITAKYQFDPPGPP	<b>AENMYGAGEPVQASPITAKYQFDPPGPP</b>	7389
ઠે			81
g	7390 TRLEPSDITKDAVTLTWCEPDDDGGSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKG	VERLDPDTDKWVRCNKMPVKDTTYRVKG	7449
ò	85		81
a	7450 LTNKKKYRFRVLAENLAGPGKPSKSTEPILIKDPIDPPWPPGKPTVKDVGKTSVRLNWTK	DPIDPPWPPGKPTVKDVGKTSVRLNWTK	7509
ò			81
q	7510 PEHDGGAKIESYVIEMLKTGTDEWVRVAEGVPTTQHLLPGLMEGQEYSFRVRAVNKAGES	TTQHLLPGLMEGQEYSFRVRAVNKAGES	7569
ò	, 82		81
g	D 7570 EPSEPSDPVLCREKLYPPSPPRWLEVINITKNTADLKWTVPEKDGGSPITNYIVEKRDVR	TADLKWTVPEKDGGSPITNYIVEKRDVR	7629
ઠે	, 82		81
g	<ul> <li>7630 RKGWQTVDTTVKDTKCTVTPLTEGSLYVFRVAAENAIGQSDYTEIEDSVLAKDTFTTPGP</li> </ul>	AENAIGQSDYTEIEDSVLAKDTFTTPGP	7689
ò	у 82		81
셤	D 7690 PYALAVVDVTKRHVDLKWEPPKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNFRVT	VIEKKERLGTRWVKAGKTAGPDCNFRVT	7749
ò	у 82		81
음	b 7750 DVIEGTEVQFQVRAENEAGVGHPSEPTEILSIEDPTSPPSPPLDLHVTDAGRKHIAIAWK	EDPTSPPSPPLDLHVTDAGRKHIAIAWK	7809
ò	γ 82γ		81
g	b 7810 PPEKNGGSPIIGYHVEMCPVGTEKWMRVNSRPIKDLKFKVEEGVVPDKEYVLRVRAVNAI	IKDLKFKVEEGVVPDKEYVLRVRAVNAI	7869
ò	у 82		81
g	b 7870 GVSEPSEISENVVAKDPDCKPTIDLETHDIIVIEGEKLSIPVPFRAVPVPTVSWHKDGKE	I EGEKLSI PVPFRAVPVPTVSWHKDGKE	7929
ò	у 82		81
ద	b 7930 VKASDRLTMKNDHISAHLEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDI	1TLENKLGSATASINVKVIGLPGPCKDI	7989
ò	у 82у		81
g	D 7990 KASDITKSSCKLTWEPPEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWTVKDLIPN	REAGRRTYIPVMSGENKLSWTVKDLIPN	8049
ò	у 82		81
g	8050 GEY	FFRVKAVNKVGGGEYIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYD	8109
ò	γ 82γ		81
q	D 9110 GGSKIMGYIIEKIAKGEERWKRCNEHLVPILTYTAKGLEEGKEYQFRVRAENAAGISEPS	rytakgleegkeyQfrvraenaagiseps	8169
ò	γγ 82		81
g	3D 8170 RATPPTKAVDPIDAPKVILRTSLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEEIK	ALDASISGSPYPTITWIKDENVIVPEEIK	8229
ò	, 82		81

ф	8230	KRAAPLVRRRKGEVQEEEPFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVEND 8	3289
ò	82	8	31
qq	8290	HGIAKAPCTVSVLDTPGPPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKP 8	8349
ò	82	8	81
g	.8350	DSEWIVVTSTLRHCKYSVTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAP 8	8409
ò	82	8	81
gg .	8410	DKPIVEDVTSNSMLVKWNEPKDNGSPILGYWLEKREVNSTHWSRVNKSLLNALKANVDGL 8	8469
ò	82	8	81
q	8470	LEGLTYVFRVCAENAAGPGKFSPPSDPKTAHDPISPPGPPIPRVTDTSSTTIELEWEPPA 8	8529
ò	82		81
qq	8530	FNGGGEIVGYFVDKQLVGTNKWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGP 0	8289
ò	82	8	81
q	8590	PGETQPVTVAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELD 8	8649
ò	82		81
qq	8650	KDRVVIDNVGTKSELIIKDALRKDHGRYVITATNSCGSKFAAARVEVFDVPGPVLDLKPV 0	8709
ò	8		81
qq	8710	VTNRKWCLLNWSDPEDDGGSE1TGFIIERKDAKMHTWRQPIETERSKCDITGLLEGOEYK 6	8769
ò	82		81
g	8770	FRVIAKNKFGCGPPVEIGPILAVDPLGPPTSPERLTYTERQRSTITLDWKEPRSNCGSPI E	8829
ò	82		81
Ωp	8830	QGYIIEKRRHDKPDFERVNKRLCPTTSFLVENLDEHOMYEFRVKAVNEIGESEPSLPLNV (	8883
ò	82		81
엄	8890	VIQDDEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDAL (	8949
ò	82		81
QQ	8950	QITKEEVSRSEAKTELSIPKAVREDKGTYTVTASNRLGSVFRNVHVEVYDGAPSPPRNLAV	6006
ò	82		81
qq	9010	TDIKAESCYLTWDAPLDNGGSEITHYVIDKRDASRKKAEWEBVTNTAVEKRYGIWKLIPN	6906
ò	82		81
q	9070	GQYEFRVRAVNKYGI SDECKSDKVVI QDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNG	9129
ò	82		81
q	9130	GSPITGYWLEKREEGSPYWSRVSRAPITKVGLKGVEFNVPRLLEGVKYOFRAMAINAAGI	9189
ò	83	GW	83
qq	9190	GPPSEPSDPEVAGDPIFPPGPPSCPEVKDKTKSSISLGWKPPAKDGGSPIKGYIVEMQEE	9249
ò	84		83
q	9250	GTTDWKRVNEPDKLITTCECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIQE	9309
ò	84		83

10449	CKYCVVVENSTGSRKGFCOVNVVDHPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKITN	10390	Ĉ
	93 92		õ
10389	0 KLTIRVGEAFALTGRYSGKPKPKVSWFKDEADVLEDDRTHIKTTPATLALEKIKAKRSDS	1033	. <del>Q</del>
	3 92	σ.	õ
10329	TNDNLLSRKYTVKGLKEGDTYEYRVSAVNIVGQGKPSFCTKPITCKDELAPPTLHLDFRD	b 10270	g
	3	o	õ
10269	O ALVIREPITVPERPEDLEVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIGTEKFHKV	1021	g
	3 92	<b>о</b>	õ
505	0 PITNYVIEKRESDRRAWTPVTYTVTRQNATVQGLIQGKAYFFRIAAENSIGMGPFVETSE 102	5 10150	g
	3 92	, 93	δ
149	O RSHQGVYSLLAKWEAGERKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGS 101	06001	a
		89	õ
10089	DASVRDRIVVHAGGVIRIIAYVSGKPPPTVTWNWNERTLPQEATIETTAISSSMVIKNCQ	10030	g
	88	68 /	õ
10029	WEKGKDKEVRGTKLVVTGLKEGAFYKFRVSAVNIAGIGEPGEVTDVIEMKDRLVSPDLQL	9970	g
	88	68	õ
69	O SLPSDPATARDPIAPPGPPFPKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEE 996.	9910	Q
	88	. 89	ò
60	0 PVTGYWLEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPA 990:	9850	g
	88	89	ò
49	O YVFRIMAQNKYGIGEPLDSEPETARNLFSVPGAPDKPTVSSVTRNSMTVNWEEPEYDGGS 984	9790	g
	88SQTINB	84	ò
. 6846	ESVSADQMTLSWFPPKDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTIPKLLEGHE	9730	g
	4	84	õ
59	O DTHVNKLVVDDTCTLVIPQSRRSDTGLYTITAVNNLGTASKEMRLNVLGRPGPPVGPIKF 972	0670	g
	83	84	õ
69	) GPCDCQRPDMPPSIDLKEFMEVEEGTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLY 9669	9610	
	83	84	õ
60	) IVECLAMDPTGTKKEAMRQCNKRDVEELQFTVEDLVEGGEYEFRVKAVNAAGVSKPSATV 960	9550	8
	83	84	õ
49	AENRFGIGPPVETIQRTTARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHY 95	9490	a
	83	84	ठे
66	) SCRLSWKMPDDDGGDRIKGYVIEKRTIDGKAWTKVNPDCGSTTFVVPDLLSEQQYFFRVR <sup>.</sup> 948 <sup>.</sup>	9430	8
	83	84	ò
62	) LETAENSSVIIIPECKRSHTGKYSITAKNKAGQKTANCRVKVMDVPGPPKDLKVSDITRG 942	9370	g
	83	84	ò
69	EPEVFIDIGAQDCLVCKAGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQ 93	9310	요

ò	93	6	2
g	10450	YIIEKKEVGKDVWMPVTSASAKTTCKVSKLLEGKDYIFRIHAENLYGISDPLVSDSMKAK 1	10509
ò	93	6	92
g	10510	DRFRVPDAPDQPIVTEVTKDSALVTWNKPHDGGKPITNYILEKRETMSKRWARVTKDPIH 1	69501
ò	93	6	92
g	10570	PYTKPRVPDLLEGCQYBPRVSAENEIGIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTC 1	10629
ò	93	6	23
g	10630	NSVDLTWQPPRHDGGSKILGYIVEYQKVGDEEWRRANHTPESCPETKYKVTGLRDGQTYK 1	10689
ઠે	93	6	97
g	10690	FRVLAVNAAGESDPAHVPEPVLVKDRLEPPELILDANMAREQHIKVGDTLRLSAIIKGVP 1	10749
ò	98	6	97
g	10750	FPKVTWKKEDRDAPTKARIDVTPVGSKLEIRNAAHEDGGIYSLTVENPAGSKTVSVKVLV 1	10809
ò	98	6	97
q	10810	LDKPGPPRDLEVSEIRKDSCYLTWKEPLDDGGSVITNYVVERRDVASAQWSPLSATSKKK 1	10869
ò	98	6	9.1
g	10870	SHFAKHLNEGNQYLFRVAAENQYGRGPFVETPKPIKALDPLHPPGPPKDLHHVDVDKTEV 1	10929
ò	98	6	97
g	10930	SLVWNKPDRDGGSPITGYLVEYQEEGTQDWIKFKTVTNLECVVTGLQQGKTYRFRVKAEN 1	10989
ò	98	6	97
g	10990	IVGLGLPDTTIPIECQEKLVPPSVELDVKLIEGLVVKAGTTVRFPAIIRGVPVPTAKWTT 1	11049
ò	98	6	97
g	11050	DGSEIKTDEHYTVETDNFSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGP 1	11109
ò	98	6	97
g	11110	PTGPINILDVTPEHMTISWQPPKDDGGSPVINYIVEKODTRKDTWGVVSSGSSKTKLKIP 1	11169
ે	98	5	24
g	11170	HLQKGCEYVFRVRAENKIGVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAATVSWTL 1	11229
ò	98		76
qq	11230	PKSDGGSPITGYYMERREVTGKWVRVNKTPIADLKFRVTGLYEGNTYEFRVFAENLAGLS	11289
ò	86	ADDV	101
g	11290	KPSPSSDPIKACRPIKPGPPINPKLKDKSRETADLVWTKPLSDGGSPILGYVVECQKPG	11349
ò	102		101
g	11350	TAQWNRINKDELIRQCAFRVPGLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILHPP :	11409
ò	102		101
g	11410	EVELDVTCRDVITVRVGQTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVEL	11469
ò	102		101
qq	11470	QIKEAVRADHGKYIISAKNSSGHAQGSAIVNVLDRPGPCONLKVTNVTKENCTISWENPL	11529

ò	102	101		SNGBYGGT IVERTICE STOREGISTING TO SE
ź	600	PACCESTANDIVEVER PROXCMSIVE SOVITED ITANIFA VERVCAENKVGVGPTI 11589	01921 00	
3 (	71350		ογ	102
ò	102		Db 12670	10 YALNKAGSSPPSKPTEYVTARMPVDPPGK
g	11590	ETKTPILAINPIDRPGEPENLHIADKGKTFVYLKWRRPDYDGGSPNLSYHVERRLKGSDD 11649	, ,	102
ò	102	101	Db 12730	30 EACKLPGDKWVRCNTAPHQIPQEEYTATG
g	11650	WERVHKGSIKETHYMVDRCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQKPVLDLK_11709	ò	102
ò	102	101	Db 12790	90 LAENVPPRIDLSVAMKSLLTVKAGTNVCL
q	11710	LSGVLTVKAGDTIRLEAGVRGKRFFEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKA 11769		
ò	102	101	12	150 ORNLCTLELFSVNRKDSGDYTITAENSSG
q	11770	11770 KRSDGGKYVVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGC 11829		
ò	102	101		12910 LSWEPPLEDGGSEITNYIVDKRETSRPNW
g	11830	11830 EIQNYILEKCETKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESKP 11889	ò	102
ò	102	101		12970 KYGVGDPVFTEPAIAKNPYDPPGRCDPPV
Q	11890	11890 VIAKTKYDKPGRPDPPEVTKVSKEEMTVVWNPPEYDGGKSITGYFLEKKEKHSTRWVPVN 11949	ò	102
ò	102	101		13030 RETQAVNWTKVNRKPIIERTLKATGLOEC
g	11950	11950 KSAIPERRMKVQNLLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEPPGPPTNFRVV 12009	ò	102
ò	102	101	_	13090 YPPAPPAFPKVYDTTRSSVSLSWGKPAYI
q	12010	12010 DTTKHSITLGWGKPVYDGGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTS 12069	ò	102
ò	102	101		13150 TRFEVTGLMEDTQYQFRVYAVNKIGYSDE
QQ	12070	12070 LDENOEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRL 12129	ò	
ò	102		_	13210 AGVTMRLYVPVKGRPPPKITWSKPNVNL
ద	12130	FAIVRGRPAPKVTWRKVGIDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLVNPAGE 12189	ò	102
ò	102	101		13270 TLENSCGKKEYTIVVKVLDTPGPPINVT
q	12190	12190 KAVFVNVRVLDTPGPVSDLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWS 12249	ò	102
ò	102			13330 DAERKSWSTVTTECSKTSFRVPNLEEGK
q	12250	TVTPEVKKTSFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLE 12309	ò	102
ò	102			13390 VVDLKVRSVSKSSCSIGWKKPHSDGGSR
qq	12310	ATEMTKNSATLAWLPPLRDGGAKIDGYIISYREEEQPADRWTEYSVVKDLSLVVTGLKEG 12369	λ <sub>0</sub>	102
ò	102	101	Db 13	13450 EGKEYTFRVSAENENGEGTPSEITVVAR
Q	12370	12370 KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKILMPEQITIKAGKKLRIEAHVYGKP 12429		
ò	102		13	510 KGKPAPSVSWKKGEDPLATDTRVSVESS
g	12430	12430 HPTCKWKKGEDEVVTSSHLAVHKADSSSILIIKDVTRKDSGYYSLTAENSSGTDTQKIKV 12489	ò	102
ò	102	.101		13570 TISIKVVGKPGIPTGPIKFDEVTAEAMT
q	1249(	12490 VVMDAPGPPOPPFDISDIDADACSLSWHIPLEDGGSNITNYIVEKCDVSRGDWVTALASV 12549	ò	102
ò	102		Db 13	13630 ASAVQKTTFRVTRLHEGMEYTFRVSAEN
g	1255(	12550 TKTSCRVGKLIPGQEYIFRVRAENRFGISEPLTSPKMVAQFPFGVPSEPKMARVTKVNKD 12609	ò	102
ò	102	101		

ద	12610 C	CIFVAWDRPDSDGGSPIIGYLIERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFRI	12669
ò	102		101
පු	12670 }	YALNKAGSSPPSKPTEYVTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFV	12729
ò	102		101
g	12730 E	EACKL PGDKWVRCNTAPHQI PQEEYTATGLEEKAQYQFRA I ARTAVNI SPPSEPSDPVTI	12789
ò	102 .		101
qq	12790 I	LAENVPPRIDLSVAMKSLLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAM	12849
ò	102		101
q	12850 (	QRNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAM	12909
ò	102		101
Ωp	12910 1	LSWEPPLEDGGSEITNYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYOFRICAEN	12969
ò	102		101
qq	12970 1	KYGVGDPVFTEPAIAKNPYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEK	13029
ò	102		101
g	13030 1	RETQAVNWTKVNRKPI I ERTLKATGLQEGTEYEFRVTA I NKAGPGK PSDASKAA YARDPQ	13089
ò	102		101
g	13090	YPPAPPAFPKVYDTTRSSVSLSWGKPAYDGGSP11GYLVEVKRADSDNWVRCNLPONLOK	13149
ò	102		101
q	13150 '	TRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPDKHYPKDILI PPEGEHDADLRKTLILR	13209
ò	102		101
g	13210	AGVTMRLYVPVKGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYIL	13269
ò	102		101
g	13270	TLENSCGKKEYTIVVKVLDTPGPPINVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKR	13329
ò	102		101
đ	13330	DAERKSWSTVTTECSKTSPRVPNLEEGKSYPFRVPAENEYGIGDPGETRIAVKASQTPGP	13389
ò	102		101
. <u>අ</u>	13390	VVDLKVRSVSKSSCSIGWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLT	13449
ò	102		101
q	13450	EGKEYTFRVSAENENGEGTPSEITVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPI	13509
ò	102		101
q	13510	KGKPAPSVSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGKYTITLKNVAGTKEG	13569
ò	102		101
В	13570	TISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTC	13629
ò	102		101
g	13630	ASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEGLKSEPI VARHPFDVPDAPPPPNI VD	13689
ć	201		101

8	13690	VRHDSVSLTWTDPKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEY 13749	
≿	102	101	
g	13750	EFRVMAINLAGVGKPSLPSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLT 13809	
à	102	101	
ą	13810	GYIVEKRDLPSKSWMKANHVNVPECAFTVTDLVEGGKYEFRIRAKNTAGAISAPSESTET 13869	•
ò	102	101	
g	13870	IICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDIT 13929	
ò	102	101	
g	13930	OITSTPISSMLIIKYATRKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSA 13989	
ò	102	101	
QQ	13990	EKATLTWTPPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRV 14049	
ò	102	101	
e G	14050	SAVNHYGKGEPVQSEPVKMYDRFGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSEITGY 14109	
ò	102	101	
g	14110	HVERREKKSLRWVRAIKTPVSDLRCKVTGLQEGSTYEFRVSAENRAGIGPPSEASDSVLM 14169	
ò	102	101	
q	14170	KDAAYPPGPPSNPHVTDTTKKSASLAWGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGT 14229	
ò	102	-LYITRE	
qq	14230	:    ALRITQFVVPDLQTKEKYNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTL 14289	
ò	108	107	
q	14290	VVRAGLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFV 14349	
ò	108	101	
g	14350	MTIENPAGKKSGFVNVRVLDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEK 14409	
ò	108	107	
qq	14410	REATRKSYSTATTKCHKCTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASEAPS 14469	
ò	108	107	
g	14470	PPDSLNIMDITKSTVSLAWPKPKHDGGSKITGYVIEAQRKGSDQWTHITTVKGLECVVRN 14529	
ò	108	107	
g	14530	LTEGEEYTFQVMAVNSAGRSAPRESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE 14589	
ò	108	107	
g	14590	IPVLGRPKPTVTWKKGDQ1LKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGE 14649	
ò	108	107	
g	14650	VGDVITIQVHDIPGPPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTW 14709	
ò	108	107	
g	14710	) VELATTVIRTTYKATRLTTGLEYQFRVKAQNRYGVGPGITSAWIVANYPFKVPGPPGTPQ 14769	
ò	108	107	
ç	14770	VTAVTKDSMTTSWHEDISDGGSPILGYHVERKERNGILWOTVSKALVPGNIFKSSGLTDG 14829	

÷	801		,
g	14830	IAYEFRVIAENMAGKSKPSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGF	14667
ò	108		107
g	14890	KITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEP	14949
ò	108		107
ор	14950	SDAITCRDDVEAPKIKVDVKFKDTVIĽKAGEAFRLEADVSGRPPPTMEWSKDGKELEGTA	15009
à	108		107
qq	15010	KLEIKIADFSTNLVNKDSTRRDSGAYTLTATNPGGFAKHI FNVKVLDRPGPPEGPLAVTE	15069
ò	108		101
qq	15070	VTSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYI	15129
ò	108		107
g	15130	FRVMAVNKYGVGEPLESEPVLAVNPYGPPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEI	15189
ò	108		107
g	15190	INYIVERRDKAGGRWIKCNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPF	15249
ò	108		107
qq	15250	YKACDTVFKPGPPGNPRVLDTSRSSISIAWNKPIYDGGSEITGYMVEIALPEEDEWQIVT	15309
ò	108		107
QQ	15310	PPAGLKATSYTITGLTENQEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADL	15369
ò	108		107
셤	15370	RKVVIIRACCTLRLFVPIKGRPDPBVKWARDHGESLDKASIESASSYTLLIVGNVNRFDS	15429
ò	108		101
q	15430	GKYILTVENSSGSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTWDPPLLDGGSKIKNY	15489
ò	108		101
<u>a</u>	15490	IVEKRESTRKAYSTVATNCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKAS	15549
ò	108	3	107
g	15550	ERPLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEA	15609
ò	108		107
g	15610	TITGLIQGEEYSFRVSAQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLK	15669
ò	108		107
g	15670	VDVPFIGRPTPAVTWHKDNVPLKQTTRVNAESTENNSLLTIKDACREDVGHYVVKLTNSA	15729
ò	108		107
q	15730	GEAIETLNVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGGSSINNYIVEKRDTSTT	15789
ò	108		101
q	15790	TWQIVSATVARTTIKACRLKTGCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGT	-
ò	108		107
g	15850	PVVTLSSRDSMEVQWNEPISDGGSRVIGYHLERKERNSILWVKLNKTPIPQTKFKTTGLE	15909

ò	108	107		,
; ;		15969 1597 AMAINATAIN BEARDAGADAGA BARATIN TRANSVER TAN TRANSVER 15969	<u>а</u>	1699
2	01651		ò	11
ò	108		QO	1705
q	15970	GSKITGYIVEKKELPEGRWMKASFTNIIDTHFEVTGLVEDHRYEFRVIARNAAGVFSEPS 16029	ò	11
ò	108	107	i da	1711
q	16030	ESTGAITARDEVDPPRISMDPKYKDTIVVHAGESFKVDADIYGKPIPTIQWIKGDQELSN 16089		11
ò	108	107		1717
q	16090	TARLEIKSTDFATSLSVKDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVI 16149	8	11
ò	108	107	: E	1723
QQ	16150	SGVTAEKCTLAWKPPLQDGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNE 16209	. 8	12
ò	108	107	: E	1729
đ	16210	YTFRIMAVNKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGS 16269		12
ò	108	107	. A	1735
q	16270	EILGYVLEKRDKEGIRWTRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPS 16329	ò	12
ò	108	107	qq	1741
q	16330	AYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPIYDGGCEIQGYIVEKCDVNVGEWTM 16389	ò	13
ò	108	D1 109	<u>අ</u> ධ	1747
qq	16390	CTPPTGINKTNIEVEKLLEKHEYNFRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLDL 16449	8	13
ò	110	BL	; dd	1753
qq	16450	 ELRKIINIRAGGSLRLFVPIKGRPTPEVKWGKVDGEIRDAAIIDVTSSFTSLVLDNVNRY 16509	ò	13
ò	112	111	: qa	17
q	16510	DSGKYTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIK 16569	ò	
ò	112	111	: 6 	1.7
g	16570	NYIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIK 16629		
ò	112	111	φ <u>α</u>	17
g	16630	VAEVPQPPGKITVDDVTRNSVSLSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSL 16689		13
ò	112		- q0	17.7
q	16690	QAVITNLTQGEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDVKFAFSSYSVQVGQD 16749	\display="block" \displ	1
ò	112	111		17
qq	16750	LKMEVPISGRPKPTITWTKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN 16809	-	
ò	112	111		17
q	16810	VVGQKTASIEIVTLDKPDPPKGPVKFDDVSAESITLSWNPPLYTGGCQITNYIVQKRDTT 16869		
ò	112	111	· 8	17
g	16870	TTVWDVVSATVARTTLKVTKLKTGTEYQFRIFAENRYGQSFALESDPIVAQYPYKEPGPP 16929	ò	
ò	112	111	<b>q</b> 0	180
අ	16930	GTPFATAISKDSMVIQWHEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTQFKAQN 16989	<i>δ</i>	
ò	112	111		

q	16990	LEBGI EYEFRVYAENI VGVGKASKNSECYVARDPCDPPGTPEPIMVKRNEI TLØWTKPVY	17049
ò	112		111
q	17050	DGGSMITGYIVEKRDLPDGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISK	17109
ò	112		111
q	17110	PSDSTGPITAKDEVELPRISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEI	17169
ò	112	PDGNR 	116
QQ	17170	EESARCEIKNTDFKALLIVKDAIRIDGGQYILRASNVAGSKSFPVNVKVLDRPGPPEGPV	17229
ò	117	QVRGVTQLGG	126
g	17230		17289
ò	127		126
QQ	17290	NEYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDG	17349
ò	127		126
qq	17350	GSEIIGYIVEKRDRSGIRWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSP	17409
ò	127	ACSP	130
qq	17410		17469
ò	131		130
QQ	17470	QIVTPQTGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDL	17529
ò	131		133
Q	17530	DSELRKGIVVRAGGSARIHIPFKGRPMPEITWSREEGEFTDKVQIEKGVNYTQLSIDNCD	17589
ò	134		133
g	17590	RNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAK	17649
ò	134		133
g	17650	VKNYVI DKRESTRKAYANVSSKCSKTSFKVENLTEGA I YYFRVMAENEFGVGVPVETVDA	17709
ò	134		133
QQ	17710	VKAAEPPSPPGKVTLTDVSQTSASLMWEKPEHDGGSRVLGYVVEMQPKGTEKWSIVAESK	17769
ò	134		133
qq	17770	VCNAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAG	17829
ò	134		133
g	17830	EDLKIEIPVIGRPRPNISWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDFGKYTVTA	17889
ò	134		133
đ	17890	TNSAGTATENLSVIVLEKPGPPVGPVRFDEVSADFVVISWEPPAYTGGCQISNYIVEKRD	17949
ò	134		133
g	17950	TTTTTWHMVSATVARTTIKITKLKTGTEYQFRIFAENRYGKSAPLDSKAVIVQYPFKEPG	18009
ò	134		133
qq	18010	PPGTPFVTSISKDQMLVQWHEPVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIQDTKFKT	18069
ò	134		133

	19209	0 KVSGLDEGLMYEYRVYAENIAGIGKCSKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWS	19150	g
	133	b	13	ò
	19149	O PGPPGTPKVVHATKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQV	19090	셤
	133	4	13	ò
	19089	O KETTSTTWHIVSQAVARTSIKIVRLTTGSEYQFRVCAENRYGKSSYSESSAVVAEYPFSP	1903	g
	133	þ	13	ò
	19029	O LCVSNSAGSITVPITIIVLDRPGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIVEK	18970	g
	133	,	13,	ò
•	18969	O KAREQLKIDVPFKGRPQATVNWRKDGQTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYE	18910	å
	133	7	134	ò
	18909	O QVKTLEATISGLTAGEEYVFRVAAVNEKGRSDPRQLGVPVIARDIEIKPSVELPFHTFNV	18850	Q
	133		134	ò
	18849	O TEPVKVSEPPLPPGRVTLVDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEKWSTCT	18790	엄
	133		134	ò
	18789	) GAKITNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAET	18730	g
	133		134	ò
	18729	) NVTRFDSGRYNLTLENNSGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDG	18670	g
	133		134	ò
	18669	) IELDADLRKVVVLRASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEVTSSFTMLVID	18610	a
	133		134	ò
	18609	) DEWTTCTPPTGLOGKOFTVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPE	18550	a
	133		134	ò
	18549	) PSEPSVFYRACDALYPPGPPSNPKVTDTSRSSVSLAWSKPIYDGGAPVKGYVVEVKEAAA	18490	g
	133		134	ò
	18489	DDGGTE1EGY1LEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENAAGVGE	18430	g
	133		134	ò
	18429	LPGNEY1FRVMAVNKYG1GEPLESGPVTACNPYKPPGPPSTPEVSA1TKDSMVVTWARPV	18370	g
	133		134	ઠે
	18369	GPLKVTGVTAEKCYLAWNPPLQDGGANISHYIIEKRETSRLSWTQVSTEVOALNYKVTKL	18310	g
	133		134	ò
	18309	ELEETAARMEIKSTIQKTTLVVKDCIRTDGGQYILKLSNVGGTKSIPITVKVLDRPGSPE	18250	g
	133		134	ò
	18249	SEPSDSSGAITARDEIDAPNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGK	18190	g
	133		134	ò
	18189	AYDGGSKITGYIVEKKDLPDGRWMKASFTNVLETEFTVSGLVEDQRYEFRVIARNAAGNF	18130	g
	133		134	ઠે
	18129	TGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKP	18070	g

ò	134 -	133
qq	19210 F	KPHYDGGAKITGYIVERRELPDGRWLKCNYTNIQETYFEVTELTEDORYEFRVFARNAAD 19269
ò	134 -	133
qq	19270 8	SVSEPSESTGPIIVKDDVEPPRVAMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKD 19329
ò	134	133
q	19330 (	GIEIEERARTEIISTDNHTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPP 19389
ò	134	133
g	19390 4	AGPLEINGLTAEKCSLSWGRPQEDGGADIDYYHRKKRETSHLAWTICEGELOMTSCKVTK 19449
ò	134	133
qq	19450 1	LLKGNEYIFRVTGVNKYGVGEPLESVAIKALDPFTVPSPPTSLEITSVTKESMTLCWSRP 19509
ò	134	133
g	19510	ESDGGSEISGYIIERREKNSLRWVRVNKKPVYDLRVKSTGLREGCEYEYRVYAENAAGLS 19569
ò	134	133
q	19570 1	LPSETSPLIRAEDPVFLPSPPSKPKIVDSGKTTITIAMVKPLFDGGAPITGYTVEYKKSD 19629
ò	134	133,
QQ	19630	DTDWKTSIQSLRGTEYTISGLTTGAEYVFRVKSVNKVGASDPSDSSDPQIAKEREEEPLF 19689
ò	134	133
g	19690	DIDSEMRKTLIVKAGASFTMTVPFRGRPVPNVLMSKPDTDLRTRAYVDTTDSRTSLTIEN 19749
ò	134	133
qq	19750	ANRNDSGKYTLTIQNVLSAASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVPENDGG 19809
ò	134	133
qq	19810	APVKNYHIEKREASKKAWVSVTNNCNRLSYKVTNLOEGAIYYFRVSGENEFGVGIPAETK 19869
ò	134	133
g	19870	EGVKITEKPSPPEKLGVTSISKDSVSLTWLKPEHDGGSRIVHYVVEALEKGOKNWVKCAV 19929
ò	134	133
g	19930	AKSTHHVVSGLRENSEYFFRVFAENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTV 19989
ò	134	133
g	19990	YVRAGSNLKVDIPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGR 20049
ò	134	133
g	20050	YEITAANSSGTTKAFINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSQVTNYI 20109
δ	134	133
g	20110	LLKRETSTAVWTEVSATVARTWMKVMKLTTGEEYQFRIKAENRFGISDHIDSACVTVKLP 20169
ò	134	133
QQ	20170	YTTPGPPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWQKANKLVIRT 20229
ò	134	133
q	20230	THFKVTTISAGLIYEFRVYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSL 20289

ò	134	133	
Ωp	20290	SWQQPAFDGGSKITGYIVERRDLPDGRWTKASFTNVTETQFTISGLTQNSQYEFRVFARN 20349	
ò	134	133	
qq	20350	AVGSISNPSEVVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEW 20409	-
ò	134	133	
g	20410	YKDDKELÇTNALVCVENTTDLASILIKDADRLNSGCYELKLRNAMASASATIRVÇILDKP 20469	
ò	134		
gg	20470	GPPGGPIEFKTVTAEKITLLWRRPPADDGGAKITHYIVEKRETSRVVWSMVSEHLEECIIT 20529	
ò	138		
8	20530	TTKIIKGNEYIFRVRAVNKYGIGEPLESDSVVAKNAFVTPGPPGIPEVTKITKNSMTVVM 20589	
ò	138	137	
g	20590	SRPIADGGSDISGYFLEKRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAA 20649	
ò	138	137	
q	20650	GQGPFSEPSEFYKAADPIDPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIR 20709	
ò	138	137	
g	20710	QGEEEEWITVSTKGEVRTTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDIL 20769	
ò	138	137	
g	20770	EAPEIDLDVALRTSVIAKAGEDVQVLIPFKGRPPPTVTWRKDEKNLGSDARYSIENTDSS 20829	
ò	138	137	
q	20830	SLLTIPQVTRNDTGKYILTIENGVGEPKSSTVSVKVLDTPAACQKLQVKHVSRGTVTLLM 20889	
ò	138	137	
g	20890	DPPLIDGGSPIINYVIEKRDATKRTWSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENEIG 20949	
ò	138	137	
g	20950	) IGEPCETTEPVKAAEVPAPIRDLSMKDSTKTSVILSWTKPDFDGGSVITEYVVERKGKGE 21009	
ò	138	137	
qq	21010	) QTWSHAGISKTCEIEVSQLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELIITPEVDLS 21069	
ò	138	137	
q	21070	) DIPGAQVTVRIGHNVHLELPYKGKPKPSISWLKDGLPLKESEFVRFSKTENKITLSIKNA 21129	
ò	138	3	
q	21130	) KKEHGGKYTVILDNAVCRIAVPITVITLGPPSKPKGPIRFDEIKADSVILSWDVPEDNGG 21189	
ò	138	3	
q	21190	O GEITCYSIEKRETSQTNWKMYCSSVARTTFKVPNLVKDAEYQFRVRAENRYGVSQPLVSS 21249	
ò	138	137	
ద	21250	O IIVAKHOFRIPGPPGKPVIYNVTSDGMSLTWDAPVYDGGSEVTGFHVEKKERNSILWQKV 21309	
ò	138	8	
qq	21310	O NTSPISGREYRATGLVEGLDYQFRVYAENSAGLSSPSDPSKFTLAVSPVDPPGTPDYIDV 21369	
ò	138	8 137	_

g	21370	TRETITLK#NPPLRDGGSKIVGYSIEKRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEF	21429
ò	138		137
qq	21430	RIIARNAVGTISPPSQSSGIIMTRDENVPPIVEFGPEYFDGLIIKSGESLRIKALVQGRP	21489
ò	138		137
g	21490	VPRVTWFKDGVE1EKRMNME1TNVLGSTSLFVRDATRDHRGVYTVEAKNASGSAKAE1KV	21549
ò	138		137
q	21550	KVQDTPGKVVGPIRFTNITGEKMTLWWDAPLNDGCAPITHYIIEKRETSRLAWALIEDKC	21609
ò	138		137
qq	21610	EAQSYTAIKLINGNEYQFRVSAVNKFGVGRPLDSDPVVAQIQYTVPDAPGIPEPSNITGN	21669
ò	138		137
q	21670	SITLTWARPESDGGSEIQQYILERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEFH	21729
ò	138		137
đ	21730	VMAENAAGVGPASGISRLIKCREPVNPPGPPTVVKVTDTSKTTVSLEWSKPVFDGGMEII	21789
ò	138		137
q	21790	GYIIEMCKTDLGDWHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGAGKGDSCEVTGTI	21849
ò	138		137
QQ	21850	KAVDRLTAPELDIDANFKQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHT	21909
ò	138		137
qq	21910	TDSFSTLTVENCNRNDAGKYTLTVENNSGSKSITFTVKVLDTPGPPGPITFKDVTRGSAT	21969
ò	138		137
đ	21970	LMWDAPLLDGGARIHHYVVEKREASRRSWQVISEKCTRQIFKVNDLAEGVPYYFRVSAVN	22029
ò	138		137
đ	22030	EYGVGEPYEMPEPIVATEQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQ	22089
ò	138		137
g	22090	KGSDLWVEAGHTKQLTFTVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVÆLKEPQIEPT	22149
ò	138		137
g	22150	ADLIGITNQLITCKAGSPFTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLT	22209
ò	138		137
а	22210	, VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGPVTGPIEVSSVSAESCVLSWGEPK	22269
ò	138		137
qq	22270	) DGGGTEITNYIVEKRESGTTAMQLVNSSVKRTQIKVTHLTKYMEYSFRVSSENRFGVSKP	22329
ò	138		137
q	22330	) LESAPIIAEHPFVPPSAPTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTIL	22389
ò	138		137
셤	22390	) WVKENKVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPE	22449
ò	138		137

ò	142		141
g	23590	<b>TKIREYTLTHLPQGAEYRFRVLACNAGGPGEPAEVPGTVKVTEMLEYPDYELDERYOEGI</b>	23649
ò	142		141
q	23650	FVRQGGVIRLTIPIKGKPFPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYD	23709
ò	142		141
g	23710	LVLENKCGKKAVYIKVRVIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADILGYILE	23769
ò	142		141
QQ	23770	RREVPKAAWYTIDSRVRGTSLVVKGLKENVEYHFRVSAENQFGI 8KPLKSEEPVTPKTPL	23829
ò	142		141
g	23830	NPPEPPSNPPEVLDVTKSSVSLSWSRPKDDGGSRVTGYY1ERKETSTDKVVRHNKTQ1TT	23889
ò	142		141
g	23890	TMYTVTGLVPDAEYQFR11AQNDVGLSETSPASEPVVCKDPFDKPSQPGELE1LS1SKDS	23949
ò	142		141
qq	23950	VTLOWEKPECDGGKEILGY#VEYRQSGDSAWKKSNKERIKDKQFTIGGLLEATEYEFRVF	24009
ò	142		141
q	24010	AENETGLSRPRRTAMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKW	24069
ò	142		141
QC	24070	YRFGKELIQSRKYKMSSDGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATP	24129
ò	142		141
g	24130	QFHPGYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHL	24189
ò	142		141
g	24190	VMKNVQRKTHAGKYKVQLSNVFGTVDA1LDVE1QDKPDKPTGP1V1EALLKNSAVISWKP	24249
ò	142		141
Q	24250	PADDGGSWITNYVVEKCEAKEGAEWQLVSSAISVTTCRIVNLTENAGYYFRVSAQNTFGI	24309
ò	142		141
g	24310	SDPLEVSSVVIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDGGAKIRNYYLEKREK	24369
ò	142		141
පු	24370	KQNKWISVTTEEIRETVFSVKNLIEGLEYEFRVKCENLGGESEWSEISEPITPKSDVPIQ	24429
ò	142		141
g	24430	APHFKEELRNLNVRYQSNATLVCKVTGHPKPIVKWYRQGKEIIADGLKYRIQEFKGGYHQ	24489
ò	142		141
q	24490	LIIASVTDDDATVYQVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAVHALRGEVVS	3 24549
ઠે	142		. 141
g	24550	IKIPFSGKPDPVITWQKGQDLIDNNGHYQVIVTRSFTSLVFPNGVERKDAGFYVVCAKNR	24609
ò	142		. 141
g	24610	FGIDQKTVELDVADVPDPPRGVKVSDASRDSVNLTWTEPASDGGSKITNYIVEKCATTAE	24669

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Best Local Sim
Matches 101;
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PROSITE, E
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                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                   SMART;
SMART;
SMART;
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                                                                                                                                                                                                                                                                                                                          25090 YVCKIENYDQSTQVTWYFGVRQLENSEKYEITYEDGVAILYVKDITKLDDGTYRCKVVND 25149
                                                                                                                                                                                                                                                                                                                                                                   25150 YGEDSSYAELFVKGVREVYDYYCRRTMKKIKRRTDTMRLLERPPEFTLPLYNKTAYVGEN 25209
                                                                                                                                                  EIVSYVHQVCEALQFLHSHNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKPGDNFRL 24909
                                                                                                                                                                                             24969
                                                                                                        24790 TDQVLVKKEISILNIARHRNILHLHESFESMEELVMIFEFISGLDIFERINTSAFELNER 24849
                                                             24730 EVDETREVSMTKASHSSTKELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKG 24789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      titin
                                                                                                                              144
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  141
                                                                                                                                                                                                                                       24970 DEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIRTLKHRRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                             24910 LFTAPEYYAPEVHQHDVVSTATDMWSLGTLVYVLLSGINPFLAETNQQIIENIMNAEYTF
                     24670 RWLRVGQARETRYTVINLFGKTSYQFRVIAENKFGLSKPSEPSEPTITKEDKTRAMNYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20309627; PubMed=10850961;
Freiburg A., Trombitas K., Hell W., Cazorla O., Fougerousse F.,
Centner T., Kolmerer B., Witt C., Beckmann J.S., Gregorio C.C.,
Granzier H., Labeit S.;
Serias of exon-skipping events in the elastic spring region of
as the structural basis for myofibrillar elastic diversity.";
Circ. Res. 86:1114-1121(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-21573839; PubMed=11717165;
Bang M.L., Centner T., Fornoff F., Geach A.J., Gotthardt
McNabb M., Witt C.C., Labeit D., Gregorio C.C., Granzier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 26926 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, N2B-titin isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                              145 --- GVTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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      142
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610 EPREPGHLEESYAQQTTLEYGYKERISAAKVAEPPORPASEPHVVPKAVKPRVIQAPSET 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRTEERWEGRYGVQEQVTISGAAGAAASVSASAAAAAATGAKEVKQDADKSAAVATV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 VAAVDMARVREPVISAVEQTAQRTTTTAVHIQPAQEQVRKEAEKTAVTKVVVAADKAKEQ 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 VIQEAIMKETRKTVVPKVIVATPKVKEQDLVSRGREGITTKREQVQITQEKMRKEAEKTA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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310 AARISTSPIRSVRSPLLMRKTQASTVATGPEVPPWKQEGYVASSSEAEMRETTLTTSTQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 PHKTPHRIPPKPKSRSPTPPSIAAKAQLARQQSPSPIRHSPSPVRHVRAPTPSPVRSVSP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.2%; Score 272; DB 4; Length 26926; 0.4%; Pred. No. 10; ive 16; Mismatches 23; Indels 24887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TT; SM00408; IGC2; 93.

TT; SM00410; IG like; 3.

TY; SM00210; IG like; 1.

TY; SM00219; TYKC; 1.

TY; SM00219; TYKC; 1.

TYE; PS00931; FGGY KINASES 1; UNKNOWN 1.

STE; PS00209; IG MHC; UNKNOWN 1.

STE; PS00209; IG MHC; UNKNOWN 1.

STE; PS00201; PROTEIN KINASE DOW, 1.

STE; PS00109; PROTEIN KINASE DOW, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VAVGPDV------
Lead December 1 Buk pkinase.

Interpro; IPR001951; FOZ kin.

Interpro; IPR001952; HLH basic.

DR Interpro; IPR001559; 19.

DR Interpro; IPR001599; 19.

DR Interpro; IPR001509; 19.

INTERPRO; IPR00150; FOZ Like.

DR Interpro; IPR001506; FOZ Like.

DR Interpro; IPR00150; FOZ Like.

DR Interpro; IPR00150; FOZ Like.

DR Interpro; IPR00150; FOZ Like.

PR INTERPRO; IPR00150; FOZ LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00060; FN3; 132.
SMART; SM00409; IG; 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ELL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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28;

ò	39	38
Q	1870	NPEGVIEHKVKLEIQQREDFRSVLRRAPEPRPEFHVHEPGKLOFEVQKVDRPVDTTETKE 1929
ò	39	11   1   1   1   1   1   1   1   1   1
ор	1930	VVKLKRABERITHEKVPEESEELRSKFKRRTEEGYYEAITAVELKSRKKDESYEELLRKTK 1989
ò	43	42
ą	1990	DELLHWTKELTEEEKKALAEEGKITIPTFKPDKIELSPSMEAPKIFERIQSGTVGQGSDA 2049
ò	43	45
q	2050	
ò	46	45
QQ	2110	IAGETSSHAFLLVQAKQLITFTQELQDVVAKEKDTMATPECETSEPFVKVKWYKDGMEVH 2169
ò	46	45
qq	2170	EGDKYRMHSDRKVHFLSILTIDTSDAEDYSCVLVEDENVKTTAKLIVEGAVVEFVKELQD 2229
ò	4 6	45
සි	2230	IEVPESYSGELECIVSPENIEGKWYHNDVELKSNGKYTITSRRGRQNLTVKDVTKEDOGE 2289
. ò	46	45
q	2290	YSFVIDGKKTTCKLKMKPRPIAILQGLSDQKVCEGDIVQLEVKVSLESVEGVMMKDGQEV 2349
ò	46	45
qq	2350	QPSDRVHIVIDKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSGRVSVYSVDVITPLKDVN 2409
ò	46	45
셤	2410	VIEGTKAVLECKVSVPDVTSVKWYLNDEQIKPDDRVQAIVKGTKQRLVINRTHASDEGPY 2469
ò	46	45
엄	2470	KLIVGRVETNCNLSVEKIKIIRGLRDLTCTETQNVVFEVELSHSGIDVLWNFKDKEIKPS 2529
ò	46	45
අු	2530	SKYKIEAHGKIYKLTVLNMMKDDEGKYTFYAGENITSGKLTVAGGAISKPLTDOTVAESQ 2589
ò	. 4	45
ф	2590	EAVFECEVANPDSKGEMLRDGKHLPLTNNIRSESDGHKRRLIIAATKLDDIGEYTYKVAT 2649
ò	46	45
đ	2650	SKTSAKLKVEAVKIKKTLKNLTVTETQDAVFTVELTHPNVKGVQWIKNGVVLESNEKYAI 2709
ò	46	
qq	2710	SVKGTIYSLRIKNCAIVDESVYGFRLGRLGASARLHVETVKIIKKPKDVTALENATVAFE
ò	59	85
g	2770	>
ò	53	85
g	2830	KLFVETLHITKTMKNIEVPETKTASFECEVSHFNVPSMWLKNGVEIEMSEKFKIVVQGKL 2889
ò	59	. 85
ď	2890	HQLIIMNTSTEDSAEYTFVCGNDQVSATLTVTPIMITSMLKDINAEEKDTITFEVTVNYE 2949

ò		
g G	2950 GISYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGDAADYTFVAGKATSTATLYVEA	3009
ò	65	58
qq	3010 RHIEFRKHIKDIKVLEKKRAMFECEVSEPDITVQWMKDDQELQITDRIKIQKEKYVHRLL	3069
ò	59	58
q	3070 IPSTRMSDAGKYTVVAGGNVSTAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDV	3129
ò	29	58
g G	3130 DAHWYKDGIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYTFVAGRNRSSVTLYVNA	3189
ò	65	58
පු	3190 PEPPQVLQELQPVTVQSGKPARFCAVISGRPQPKISWYKEEQLLSTGFKCKFLHDGQEYT	3249
ò	65	58
g	3250 LLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEVPEVVSPDQEMPVYPPAIITPLQDTV	3309
ò	65	58
셤	3310 ISEGQPARFQCRVSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLEIAEAYPEDEGTYT	3369
ò	65	58
g	3370 FVASNAVGQVSSTANLSLEAPESILHERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLS	3429
ò	65	58
셤	3430 KINETLELLSESPVYSTKFDSEKEGTGPIFIKEVSNADISMGDVATLSVTVIGIPKPKIQ	3489
ò	65	58
g	3490 WFFNGVLLTPSADYKFVFDGDDHSLILLFTKLEDEGEYTCMASNDYGKTICSAYLKINSK	3549
ò	65	58
a	3550 GEGHKDTETESAVAKSLEKLGGPCPPHFLKELKPIRCAQGLPAIFEYTVVGEPAPTVTWF	3609
ò		58
q	3610 KENKQLCTSVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENMLGESTCAAELLVLLED	3669
ò	65	58
g	3670 TDMTDTPCKAKSTPEAPEDFPQTPLKGPAVEALDSEQEIATFVKDTILKAALITEENQOL	3729
ò	65	58
g G	3730 SYEHIAKANELSSQLPLGAQELQSILEQDKLTPESTREFLCINGSIHFQPLKEPSFNLQL	3789
ò	-53 -11TEPEG	65
Q	3790 QIVQSQKTFSKEGILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPLKTLLAEPÄĞN	3849
ò	99	65
Q	3850 YPQSSIEPPMHSYLTSVAEEVLSPKEKTVSDTNREQRVTLQKQEAQSALILSQSLAEGHV	3909
ò	99	65
g	3910 ESLOSPDVMISQVNYEPLVPSEHSCTEGGKILIESANPLENAGDSAVRIEEGKSLRFPL	3969
ò	99	59
qq	3970 ALEEKQVLLKEEHSDNVVMPPDQIIESKREPVAIKKVQEVQGRDLLSKESLLSGIPEEQR	4029
,		

g	4030 LNLKIQICRALQAAVASEQPGLFSEWLRNIEKVEVEAVNI	TQEPRHIMCMYLVTSAKSVT 4089
ò	,	59
g	Db 4090 EEVTIIIEDVDPQMANLKWELRDALCAIIYEEIDILTAEGPRIQGGAKTSLQEEMDSFSG	SLQEEMDSFSG 4149
ò	λδ ,	99 69
Q	Db 4150 SQKVEPITEPEVESKYLISPEEVSYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKP	SDEKQDESLKP 4209
ò	λδ	59
qq	Db 4210 SEEKEESSSESGTEEVATVKIQEAEGGFIKEDGPMIHTPLVDTVSEEGDIVHLTTSITNA	IVHLTTSITNA 4269
ò	λό	59 68
qq	Db 4270 KEVNWYFENKLVPSDEKFKCLQDQNTYTLVIDKVNTEDHQGEYVCEALNDSGKTATSAKL	DSGKTATSAKL 4329
ò	Oy 66	69
qq	Db 4330 TVVKRAAPVIKRKIEPLEVALGHLAKFTCEIQSAPNVFGWFKAGREIYESDKCSIRSSK	ESDKCSIRSSK 4389
ò	70	69
qq	Db 4390 YISSLEILRTQVVDCGEYTCKASNEYGSVSCTATLTVTVPGGEKKVRKLLPERKPEPKEE	LPERKPEPKEE 4449
ò	Ογ 70	69
Dp	Db 4450 VVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPPKPVEEVEVPTVTKRERKIPEPTK	KRERKIPEPTK 4509
ò	Ολ 70	69
qq	4510 VPEIKPAIPLPAPEPKPKPEAEVKTIKPPPVEPEPTPIAA	PVTVPVVGKKAEAKAPKEEA 4569
ò	Ογ 70	69
q	Db 4570 AKPKGPIKGVPKKTPSPIEAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDI	KEVKEIKDIIL 4629
ò	ογ 70	69
qq	Db 4630 TESEFVGSSAIFECLVSPSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAG	HIIDVQLSDAG 4689
ઠે	yo 70	69
g	4690 EYTCVLRLGNKEKTSTAKLVVEELPVRFVKTLEEEVTVVKGQPLYL	SCELNKERDVVWRK 4749
ò	Qy 70	69
g	4750 DGKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYTVTVENANNLEC	SSCVKVVEVIRD 4809
ò	ζλ 70	69
qq	Db 4810 WLVKPIRDQHVKPKGTAIFACDIAKDTPNIKWFKGYDEIPAEPNDKTEILRDGNHLYLKI	ILRDGNHLYLKI 4869
ò	Qy 70 07 KD	69
d	Db 4870 KNAMPEDIAEYAVEIEGKRYPAKLTLGEREVELLKPIEDVTIYEKESASFDA	SFDAEISEADIP 4929
ò	yo 70	69
đ	Db 4930 GQWKLKGELLRPSPTCEIKAEGGKRFLTLRKVKLDQAGEVLYQALNAITTAILTVKEIEL	TTAILTVKEIEL 4989
ò	Qy 70	69
đ	4990 DFAVPLKDVTVPERRQARFECVLTREANVIWSKGPDIIKSS	DKFDIIADGKKHILVINDS 5049
ò	yo yo	69
g	Db 5050 QFDDEGVYTAEVEGKKTSARLFVTGIRLKFMSPLEDQTVKEGETATFV	CELSHEKMHVVW 5
ò	Qy 70 Qy	69

i	:	169 יים עם אם אותי זהרים זם עוני את בסברה יחיום עעם דעוניה שבים הבי נייה החברני נייה החברני
2	5110	ň
ò	70	69
g G	5170	VKLHDKTAVEKDEITLKCEVSKDVPVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLK 5229
ò	7.0	69
g	5230	DKGEYVCDCGTDKTKANVTVEARLIKVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLK 5289
ò	70	69
q	5290	GQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIFITPL 5349
ò	7.0	69
g	5350	SDVKVFEKDEAKFECEVSREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDE 5409
ò	10	69
g	5410	AKYMFEAEDKHTSGKLIIEGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQ 5469
ò	70	69
g	5470	RLHTTRSVSMQDEGKTHSITFKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGKLQD 5529
ò	70	69
a	5530	YTGVEKDEVILQCEISKADAPVKWFKDGKEIKPSKNAVIKADGKKRMLILKKALKSDIGQ 5589
ò	70	69
g	5590	YTCDCGTDKTSGKLDIEDREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEAL 5649
ò	70	69
g	5650	LQTPDCEIKEEGKIHSLVLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVT 5709
ò	70	69
g	5710	VTAGETATFDCELSYEDIPVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVQ 5769
ò	70	69
q	5770	LTAKDFKTHANLFVKEPPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILK 5829
ò	70	69
g	5830	SKKYEIVADGRVRKLVIHDCTPEDIKTYTCDAKDFKTSCNLAVVPPHVEFLRPLTDLQVR 5889
ò	7.0	69
셤	5890	EKEMARFECELSRENAKVKWFKDGAEIKKGKKYDIISKGAVRILVINKCLLDDEAEYSCE 5949
ò	70	69
a	5950	VRTARTSGMLTVLEEEAVFTKNLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIETG 6009
ò	70	69
o G	6010	RYEILTEGRKRILVIQNAHLEDAGNYNCRLPSSRTDGKVKVHELAAEFISKPQNLEILEG 6069
ò	70	69
8	6070	EKAEFVCSISKESFPVQWKRDDKTLESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVG 6129
ò	70	69
g	6130	AARAAAHLTVIEKLRIVVPLKDTRVKEQQEVVFNCEVNTEGAKAKWFRNEEAIFDSSKYI 6189
ò	70	69
g	6190	ILQKDLVYTLRIRDAHLDDQANYNVSLTNHRGENVKSAANLIVEEEDLRIVEPLKDIETM 6249

ò	70	69 ************************************	_
QQ	6250 1	EKKSVTFWCKVNRLNVTLKWTKONGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDEGEYIVT 630	60
ò	70	69	_
qq	6310 4	AGQDKSVAELLIIEAPTEFVEHLEDQTVTEFDDAVFSCQLSREKANVKWYRNGREIKEGK 636	69
ò	70	69	_
qq	6370 1	KYKFEKDGSIHRLIIKDCRLDDECEYACGVEDRKSRARLFVEEIPVEIIRPPQDILEAPG 642	29
ò	. 07	69	_
q	6430 7	ADVVFLAELNKDKVEVQWLRNNMVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIAK 646	68
ò	70	69	_
q	6490 1	DKEARAKLELAAAPKIKTADQDLVVDVGKPLTMVVPYDAYPKAEAEWFKENEPLSTKTID 654	4 9
ò	70	69	_
q	6550	TTAEQTSFRILEAKKGDKGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNLEVTETFDGEV 660	609
ò	70	69	•
qq	6610	SLAWEEPLTDGGSKIIGYVVERRDIKRKTWVLATDRAESCEFTVTGLOKGGVEYLFRVSA 660	699
ò	70	69	•
qq	6670 1	RNRVGTGEPVETDNPVEARSKYDVPGPPLNVTITDVNRFGVSLTWEPPEYDGGAEITNYV 672	129
ò	70	69	_
qq	6730	IELRDKTSIRWDTAMTVRAEDLSATVTDVVEGQEYSFRVRAQNRIGVGKPSAATPFVKVA 67%	684
ò	70	76 TANLTSS 76 76 76 76 76 76	
qq	6790	DPIERPSPPVNLTSSDQTQSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLV 684	349
ò	77	92	
Q	6850	PELTYKVTGLEKGNKYLYRVSAENKAGVSDPSEILGPLTADDAFVEPTMDLSAFKDGLEV 690:	606
ò	77	94	
ΩP	6910	IVPNPITILVPSTGYPRPTATWCFGDKVLETGDRVKMKTLSAYAELVISPSERSDKGIYT 696	696
ò	77	96	w
g	6970	LKLENRVKTISGEIDVNVIARPSAPKELKFGDITKDSVHLTWEPPDDDGGSPLTGYVVEK 702	029
ò	77	LLSVC	
QQ	7030	REVSRKTWTKVMDFVTDLEFTVPDLVQGKEYLFKVCARNKCGPGEPAYVDEPVNMSTPAT 70	7089
ò	82	81	
g	7090	VPDPPENVKWRDRTANSIFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKM 71.	149
ò	82	81	-
qq	7150	EVTGLEEGKMYAYRVKALNRQGASKPSRPTEEIQAVDTQEAPEIFLDVKLLAGLTVKAGT 72	7209
ò	82	81	-
d G	7210	KIELPATVTGKPEPKITWTKADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYIIEAV 720	269
ò	82	81	-
В	7270	NVCGRATAVVEVNVLDKPGPPAAFDITDVTNESCLLTWNPPRDDGGSKITNYVVERRATD 73	7329

82		81
7330	SEVWHKLSSTVKDTNFKATKLIPNKEYIFRVAAENMYGVGEPVQASPITAKYQFDPPGPP	7389
82		81
7390	TRLEPSDITKDAVTLTWCEPDDDGGSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKG	7449
82		81
7450	LINKKKYRFRVLAENLAGPGKPSKSTEPILIKDPIDPPWPPGKPTVKDVGKTSVRLNWTK	7509
82		81
7510	PEHDGGAKI ESYVI EMLKTGTDEWVRVAEGVPTTQHLLPGLMEGQEYSFRVRAVNKAGES	7569
82		81
7570	<b>EPSEPSDPVLCREKLYPPSPPRWLEVINITKNTADLKWTVPEKDGGSPITNYIVEKRDVR</b>	7629
82		81
7630	RKGWQTVDTTVKDTKCTVTPLTEGSLYVFRVAAENAIGQSDYTEIEDSVLAKDTFTTPGP	7689
82		91
7690	PYALAVVDVTKRHVDLKWEPPKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNFRVT	7749
82		81
7750	DVIEGTEVOFQVRAENEAGVGHPSEPTEILSIEDPTSPPSPPLDLHVTDAGRKHIAIAWK	7809
82		81
7810	PPEKNGGSP11GYHVEMCPVGTEKWMRVNSRP1KDLKFKVEEGVVPDKEYVLRVRAVNA1	7869
82		81
7870	GVSEPSEISENVVAKDPDCKPTIDLETHDIIVIEGEKLSIPVPFRAVPVPTVSWHKDGKE	7929
82		81
7930	) VKASDRLTMKNDHISAHLEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDI	7989
82	2	81
7990	) KASDITKSSCKLTWEPPEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWTVKDLIPN	8049
82	2	81
8050	) GEYFFRVKAVNKVGGGEYIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYD	8109
82	2	81
8110	O GGSKIMGYIIEKIAKGEERWKRCNEHLVPILTYTAKGLEEGKEYQFRVRAENAAGISEPS	8169
82	2	81
8170	O RATPPTKAVDPIDAPKVILRTSLEVKRGDEIALDAŠISGSPYPTITWIKDENVIVPEEIK	8229
82	2	81
8230	O KRAAPLVRRRKGEVQEEEPFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVEND	8289
82	2	81
8290	0 HGIAKAPCTVSVLDTPGPPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKP	8349
82	2	81
8350	O DSEWIVVTSTLRHCKYSVTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAP	8409
. 82	2	81

g	8410	DKPIVEDVTSNSMLVKWNEPKDNGSPILGYWLEKREVNSTHWSRVNKSLLNALKANVDGL 8	8469
ઠે	82	8	81
g	8470	LEGLTYVFRVCAENAAGPGKFSPPSDPKTAHDPISPPGPPIPRVTDTSSTTIELEWEPPA 6	8529
ò	82	3	81
g	8530	FNGGGEIVGYFVDKQLVGTNEWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGP (	8589
ò	82		81
g	8590	PGETQPVTVAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELD (	8649
ò	82		81
g	8650	KDRVVIDNVGTKSELIIKDALRKDHGRYVITATNSCGSKFAAARVEVFDVPGPVLDLKPV	8709
ò	82		81
g	8710	VTNRKMCLLNWSDPEDDGGSEITGF1IERKDAKMHTWRQPIETERSKCDITGLLEGQEYK	8769
ò	82	:	81
g	8770	FRVIAKNKFGCGPPVEIGPILAVDPLGPPTSPERLTYTERTKSTITLDWKEPRSNGGSPI	8829
ò	82		91
q	8830	QGYIIEKRRHDKPDFERVNKRLCPTTSFLVENLDEHOMYEFRVKAVNEIGESEPSLPLNV	8889
ò	82		81
g	8890	VIQDDEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDAL	8949
ò	82		81
g	8950	QITKEEVSRSEAKTELSIPKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPPRNLAV	6006
ò	82		81
g	9010	TDIKAESCYLTWDAPLDNGGSEITHYVIDKRDASRKKAEWEEVTNTAVEKRYGIWKLIPN	6906
ò	82		81
g	9070	GQYEFRVRAVNKYGISDECKSDKVV1QDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNG	9129
ò	82		81
g	9130	GSPITGYWLEKREEGSPYWSRVSRAPITKVGLKGVEFNVPRLLEGVKYQ <b>GRA</b> MAINAAGI	9189
ò	82	MD	8 9
셤	9190	GPPSEPSDPEVAGDPIFPPGPPSCPEVKDKTKSSISLGWKPPAKDGGSPIKGYIVEMQEE	9249
ò	84		83
g	9250	GTIDWKRVNEPDKLITICECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIOE	9309
ò	84		83
g	9310	EPEVFIDIGAQDCLVCKAGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQ	9369
ò	84		83
q	9370	) LETAENSSVIIIPECKRSHTGKYSITAKNKAGQKTANCRVKVMDVPGPPKDLKVSDITRG	9429
ò	8		83
엄	9430	O SCRLSWKMPDDDGGDRIKGYVIEKRTIDGKAWTKVNPDCGSTTFVVPDLLSEQQYFFRVR	9489
ò	84		83

Db	9490 AENRFGIGPPVETIORTTARI	AENRFGIGPPVETIORTTARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHY	9549
ઠે	84		83
8	9550 IVECLAWDPTGTKKEAWRQC	IVECLAWDPTGTKKEAWRQCNKRDVEELQFTVEDLVEGGEYEFRVKAVNAAGVSKPSATV	6096
ò	84		83
g	9610 GPCDCQRPDMPPSIDLKEFM	GPCDCQRPDMPPSIDLKEFMEVEEGTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLY	6996
ò	84		83
g	9670 DTHVNKLVVDDTCTLVIPQS	DTHVNKLVVDDTCTLVIPQSRRSDTGLYTITAVNNLGTASKEMRLNVLGRPGPPVGPIKF	9729
ò	84		83
g	9730 ESVSADQMTLSWFPPKDDGG	ESVSADQMTLSWFPPKDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTIPKLLEGHE	9789
ò	84	SOTIN	. 88
g	9790 YVFRIMAQNKYGIGEPLDSE	YVFRIMAQNKYGIGEPLDSEPETARNLFSVPGAPDKPTVSSVTRNSMTVNWEEPEYDGGS	9849
ò	68		88
g	9850 PVTGYWLEMKDTTSKRWKRV	PVTGYWLEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPA	6066
ò	68		88
g	9910	SLPSDPATARDPIAPPGPPPRVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEE	6966
ò	68		88
q	9970	WEKGKDKEVRGTKLIVVTGLKEGAFYKFRVSAVNIAGIGEPGEVTDVIEMKDRLVSPDLOL	10029
ઠે	68		88
đ	10030	DASVRDRIVVHAGGVIRIIAYVSGKPPPTVTWNNNERTLPQEATIETTAISSSMVIKNCQ	10089
ò	68		92
ద	10090	RSHQGVYSLLAKNEAGERKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGS	10149
ઠે	66		92
6	10150	PITNYVIEKRESDRRAWTPVTYTVTRQNATVQGLIQGKAYFFRIAAENSIGMGPFVETSE	10209
ò			92
දු	10210	ALVIREPITVPERPEDLEVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIGTEKFHKV	10269
ò	93		. 26
g	10270	TNDNLLSRKYTVKGLKEGDŢVEYRVSAVNIVGQGKPSFCTKPITCKDELAPPTLHLDFRD	10329
ò	93		92
g	10330	KLTIRVGEAFALTGRYSGKPKPKVSWFKDEADVLEDDRTHIKTTPATLALEKIKAKRSDS	10389
ò			92
q	10390	GKYCVVVENSTGSRKGFCQVNVVDRPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKITN	10449
ò			92
g	10450	Y I I EKKEVGKDVWMPVTSASAKTTCKVSKLLEGKDY I FRIHAENLYGI SDPLVSDSMKAK	10509
ò			92
g	10510	DRFRVPDAPDQPIVTEVTKDSALVTWNKPHDGGKPITNYILEKRETMSKRWARVTKDPIH	10569
ઠે			92
ç	10570	PYTKFRVPDL1.EGCOYEFRVSAENEIGIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTC	10629

ò	93		92
g	10630	NSVDLTWQPPRHDGGSKILGYIVEYQKVGDEEWRRANHTPESCPETKYKVTGLRDGGTYK	10689
ò	93	TDDGHTDDGH	97
g	10690	:         FRVLAVNAAGESDPAHVPEPVLVKDRLEPPELILDANMAREOHIKVGDTLRLSAIIKGVP	10749
ò	98		97
q	10750	PPKVTWKKEDRDAPTKARIDVTPVGSKLEIRNAAHEDGGIYSLTVENPAGSKTVSVKVLV	10809
ò	86		97
q	10810	LDKPGPPRDLEVSEIRKDSCYLTWKEPLDDGGSVITNYVVERRDVASAQWSPLSATSKKK	10869
ò	86		76
q	10870	SHFAKHLNEGNQYLFRVAAENQYGRGPFVETPKPIKALDPLHPPGPPKDLHHVDVDKTEV	10929
ò	96		76
qq	10930	SLVWNKPDRDGGSPITGYLVEYQEEGTODWIKFKTVTNLECVVTGLQQGKTYRFRVKAEN	10989
ò	98		97
q	10990	IVGLGLPDTTIPIECQEKLVPPSVELDVKLIEGLVVKAGTTVRFPAIIRGVPVPTAKWTT	11049
ò	98		16
qq	11050	DGSEIKTDEHYTVETDNFSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGP	11109
ò	98		76
q	11110	PTGPINILDVTPEHMTISWQPPKDDGGSPVINYIVEKQDTRKDTWGVVSSGSSKTKLKIP	11169
ò	98		97
В	11170	HLQKGCEYVFRVRAENKIGVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAATVSWTL	11229
ò	98		97
g	11230	PKSDGGSP1TGYYMERREVTGKWVRVNKTP1ADLKFRVTGLYEGNTYEFRVFAENLAGLS	11289
ò	86	ADDV	101
qq	11290	KPSPSSDPIKACRPIKPPGPPINPKLKDKSRETADLVWTKPLSDGGSPILGYVVECQKPG	11349
ò	102	<b>7</b>	101
g	11350	TAQWNRINKDELIRQCAFRVPGLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILHPP	11409
ò	102		101
q	11410	EVELDVTCRDVITVRVGQTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVEL	11469
ò	102		101
đ	11470	QIKEAVRADHGKYIISAKNSSGHAQGSAIVNVLDRPGPCQNLKVTNVTKENCTISWENPL	11529
ò	102		101
q	11530	DNGGSEITNFIVEYRRPNQKGWSIVASDVTKRLIKANLLANNEYYFRVCAENKVGVGPTI	11589
ò	102		101
q	11590	ETKTPILAINPIDRPGEPENLHIADKGKTFVYLKWRRPDYDGGSPNLSYHVERRLKGSDD	11649
ò	102		101
g	11650	HERVHKGSIKETHYMVDRCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQKPVLDLK	11709

⋩	102		101
	11710	LSGVLTVKAGDTIRLEAGVRGKPFPEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKA	11769
?	102		101
· Q	11770	KRSDGGKYVVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGC	11829
à	102		101
g	11830	EIQNYILEKCETKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESKP	11889
ò	102		101
g	11890	VIAKTKYDKPGRPDPPEVTKVSKEEMTVVWNPPEYDGGKSITGYFLEKKEKHSTRWVPVN	11949
ò	102		101
q	11950	KSAIPERRMKVQNLLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEPPGPPTNFRVV	12009
ò	102		101
d D	12010	DTTKHSITLGWGKPVYDGGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTS	12069
ે	102		101
q	12070	LDENQEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRL	12129
ò	102		101
g	12130	PAIVRGRPAPKVTWRKVGIDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLVNPAGE	12189
ò	102		101
g	12190	KAVFVNVRVLDTPGPVSDLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWS	12249
ò	102		101
g	12250	TVTPEVKKTSFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLE	12309
ò	102		101
Q	12310	VTEMTKNSATLAWLPPLRDGGAKIDGYITSYREEEQPADRWTEYSVVKDLSLVVTGLKEG	12369
ઠે	102		101
g	12370	KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKILMPEQITIKAGKKLRIEAHVYGKP	12429
ò	102		101
a.	12430	HPTCKWKKGEDEVVTSSHLAVHKADSSSILIIKDVTRKDSGYYSLTAENSSGTDTQKIKV	12489
ò	102		101
g	12490	VVMDAPGPPPPPFDISDIDÅDACSLSWHIPLEDGGSNITNYIVEKCDVSRGDWVTALASV	12549
ò	102		101
qq	12550	TKTSCRVGKLIPGQEYIFRVRAENRFGISEPLTSPKMVAQFPFGVPSEPKNARVTKVNKD	12609
ò	102		101
g	12610	CIFVAWDRPDSDGGSP11GYL1ERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFR1	12669
ò	102		101
q	12670	) YALNKAGSSPPSKPTEYVTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFV	12729
ò	102		101
g	12730	) EACKLPGDKWVRCNTAPHQIPQEEYTATGLEEKAQYQFRAIARTAVNISPPSEPSDPVTI	12789
ò	102		. 101

	102	ò
,	13810 GYIVEKRDLPSKSMMKANHVNVPECAFTVTDLVEGGKYEFKIKAKNIAGAISAFSESIE:	QQ .
101		ò
13809	13750 EFRVMAINLAGVGKPSLPSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLT	g
101	102	ò
13749	13690 VRHDSVSLTWTDPKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEY	q
	102	ò
13689	13630 ASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPPNIVD	qq
101	102	ò
13629	13570 TISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTC	q
101	102	ò
13569	13510 KGKPAPSVSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGKYTITMANVAGTKEG	Q
101	102	ò
13509	13450 EGKEYTFRVSAENENGEGTPSEITVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPI	g
101	102	ò
13449	13390 VVDLKVRSVSKSSCSIGWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLT	q
101	102	ò
13389	13330 DAERKSWSTVTTECSKTSFRVANLEEGKSYFFRVFAENEYGIGDPGETRDAVKASQTPGP	ą d
101	102	ò
13329	13270 TLENSCGKKEYTIVVKVLDTPGPPVNVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKR	: A
101	102	ò
13269	13210 AGVTMRLYVPVKGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYIL	
101		
13209	13150 TRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPDKHYPKDILIPPEGELDADLRKTLILR	
101	102	ò
13149	13090 YPPAPPAFPKVYDTTRSSVSLSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPQNLQK	q
101	102	ò
13089	13030 RETQAVNWTKVNRKPIIERTLKATGLQEGTEYEFRVTAINKAGPGKPSDASKAAYARDPO	qq
101	102	ò
13029	12970 KYGVGDPVFTEPAIAKNPYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEK	q
101	102	ò
12969	12910 LSWEPPLEDGGSEITNYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYQFRICAEN	DP:
101	102	ò
12909	.2850 QRNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAM	Db 1
101	102	ò
2849	2790 LAENVPPRIDLSVAMKSLLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAM	요

윱	) 13870 IICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDI	T 13929
ò	, 102	- 101
a	) 13930 QITSTPTSSMLTIKYATRKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSA	A 13989
ò	, 102	- 101
q	) 13990 EKATLTWTPPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRV	V 14049
ò	, 102	- 101
q	14050 SAVNHYGKGEPVQSEPVKANDRFGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSE1TGY	Y 14109
ò	, 102	- 101
g	O 14110 HVERREKKSLRWVRAIKTPVSDLRCKVTGLQEGSTYEFRVSAENRAGIGPPSEASDSVLM	M 14169
ò	۲ 102	- 101
g	D 14170 KDAAYPPGPPSNPHVTDTTKKSASLAMGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGT	T 14229
ò	y 102 -LYITRF	- 107
셤	-  -     14230 ALRITQFVVPDLQTKEKYNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTL	L 14289
ò	у 108	- 107
g	b 14290 VVRAGLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFV	V 14349
ò	у 108	- 107
g	b 14350 MTIENPAGKKSGFVNVRVLDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEK	K 14409
ઠે	у 108	- 107
đ	D 14410 REATRKSYSTATTKCHKCTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASEAPS	S 14469
ò	у 108	107
đ	b 14470 PPDSLNIMDITKSTVSLAWPKPKHDGGSKITGYVIEAQRKGSDQWTHITTVKGLECVVRN	IN 14529
ò	у 108	107
8	b 14530 LTEGEEYTFOVMAVNSAGRSAPRESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE	Æ 14589
ò	у 108	107
q	b 14590 IPVLGRPKPTVTWKKGDQILKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGE	3E 14649
ò	γ 108	107
g	b 14650 VGDVITIQVHDIPGPPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTW	FW 14709
ò	y 108y	107
g	ND 14710 VELATTVIRTTYKATRLTTGLEYQFRVKAQNRYGVGPGITSACIVANYPFKVPGPPGTPQ	90 14769
ò	)y 108	107
g	)b 14770 VTAVTKDSMTISWHEPLSDGGSPILGYHVERKERNGILWQTVSKALVPGNIFKSSGLTDG	DG 14829
ò	)y 108	. 107 .
g	3b 14830 IAYEFRVIAENMAGKSKPSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGF	3F 14889
ò	Jy 108	107
g	3b 14890 KITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPFSEP	EP 14949
ò	λγ 108	107
5	35 14950 SDAITCRDDVEAPKIKVDVKFKDTVILKAGBAFRLEADVSGRPPPIMEWSKDGKELEGTA	TA 15009

		0	3
,01		1	3
15909	0 PVVTLSSRDSMEVQWNEPISDGGSRVIGYHLERKERNSILWVKLNKTPIPQTKFKTTGLE	15850	q
107	8	108	ò
15849	0 TWQIVSATVARTTIKACRLKTGCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGT	15790	q
107	8	108	ò
15789	O GEAIETLNVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGGSSINNYIVEKRDTSTT	15730	q
107	8	108	ò
15729	O VDVPFIGRPTPAVTWHKDNVPLKQTTRVNAESTENNSLLTIKDACREDVGHYVVKLTNSA	15670	ପ୍ର
107	8	108	ò
15669	O TITGLIQGEEYSFRVSAQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLK	15610	qq
107	80	108	ò
15609	0 ERPLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEA	15550	qa
101	80	108	ò
15549	0 IVEKRESTRKAYSTVATNCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKAS	15490	q
107	8	108	ò
15489	O GKYILTVENSSGSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTWDPPLLDGGSKIKNY	15430	q
107	6	108	ò
15429	) RKVVTIRACCTLRLFVPIKGRPAPEVKWARDHGESLDKASIESTSSYTLLIVGNVNRFDS	15370	qq
107	E	108	ò
15369	) PPAGLKATSYTITGLTENQEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADL	15310	g
107		108	ò
15309	) YKACDTVFKPGPPGNPRVLDTSRSSISIAWNKPIYDGGSEITGYMVEIALPEEDEWQIVT	15250	QQ
107		108	ò
15249	) INYIVERRDKAGQRWIKCNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPF	15190	qq
107		108	ò
15189	) FRVMAVNKYGVGEPLESEPVLAVNPYGPPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEI	15130	QQ
101		108	ò
15129	) UTSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYI	15070	QQ
107		108	ò
15069	KLEIKIADFSTNLVNKDSTRRDSGAYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTE	15010	qq
107		108	ò

			_
ò	108	101	
g	16090	TARLEIKSTDFATSLSVKDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVI 16149	
ò	108	107	
පු	16150	SGVTAEKCTLAWKPPLQDGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNE 16209	***
ò	108	107	
a	16210	YTFRIMAVNKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGS 16269	
È	108	107	
q	16270	EILGYVLEKRDKEGIRWTRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPS 16329	
ò	108	107	
සු	16330	AYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPIYDGGCEIQGYIVEKCDVSVGEWTM 16389	
ò	108		
đ	16390	CTPPTGINKTNIEVEKLLEKHEYNFRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLDL 16449	
ò	110	BL111	
g	16450	   ELRKIINIRAGGSLRLFVPIKGRPTPEVKMGKVDGEIRDAAIIDVTSSFTSLVLDNVNRY 16509	
ò	112	111	
g	16510	DSGKYTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIK 16569	
ઠે	112	111	
g	16570	HYIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIK 16629	
ò	112	111	
g	16630	) VAEVPQPPGKITVDDVTRNSVSLSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSL 16689	
ò	112	111	
g	16690	) QAVITNLTQGEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDVKPAFSSYSVQVGQD 16749	
ò	112	111	
g	16750	) LKIEVPISGRPKPTITWTKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN 16809	
ò	112	2	
g	16910	) VVGQKTASIEIVTLDKPDPPKGPVKFDDVSAESITLSWNPPLYTGGCQITNYIVQKRDTT 16869	
ò	112	2	
g	16870	O TTVWDVVSATVARTTLKVTKLKTGTEYQFRIFAENRYGQSFALESDPIVAQYPYKEPGPP 16929	
ò	112	2 111	
q	16930	0 GTPFATAISKDSMVIQWHEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTQFKAQN 16989	
ò	112	2	
g	16990	0 LEEGIEYEFRVYAENIVGVGKASKNSECYVARDPCDPPGTPEPIMVKRNEITLQWTKFVY 17049	
ò	112	2	
d	17050	O DGGSMITGYIVEKRDLPDGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISK 17109	
ò	112		
g	17110	PSDSTGPITAKDEVELPRISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEI	
ò	112	2PDGNR 116	-

1	134	ò
18249	) 18190 SEPSDSSGAITARDEIDAPNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGK	q
m		ò
18189	) 18130 AYDGGSKITGYIVEKKDLPDGRWMKASFTNVLETEFTVSGLVEDORYEFRVIARNAAGNF	đ
133	, 134	ò
18129	. 18070 TGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKP	qq
	134	ò
18069	. 18010 PPGTPFVTSISKDQMLVQWHEPVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIQDTKFKT	đ
	134	ò
18009	17950 TTTTTWHMVSATVARTTIKITKLKTGTEYQFRIFAENRYGKSAPLDSKAVIVQYPFKEPG	a
133	134	ò
17949	17890 TNSAGTATENLSVIVLEKPGPPVGPVRFDEVSADFVVISWEPPAYTGGCOLSNYIVEKRD	đ
133	134	ò
17889	17830 EDLKIEIPVIGRPRPNISWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDFGKYTVTA	a
133	134	ò
17829	17770 VCNAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAG	සි
133	134	ò
17769	17110 VKAAEPPSPPGKVTLTDVSQTSASLMWEKPEHDGGSRVLGYVVEMOPKGTEKWSIVAESK	g
133	134	ò
17709	17650 VKNYVIDKRESTRKAYANVSSKCSKTSFKVENLTEGAIYYFRVMAENEFGVGVPVETVDA	q
133	134	ò
17649	17590 RNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAK	g
133	134	ò
17589	17530 DSELRKGIVVRAGGSARIHIPFKGRPTPEITWSREEGEFTDKVQIEKGVNYTQLSIDNCD	a
133	131	ò
17529	17470 QIVTPQTGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDL	qq
130	131	ò
17469		q
130	127ACSP	ò
17409	17350 GSEIIGYIVEKRDRSGIRWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSP	qq
126		δ
17349	17290 NEYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDG :	g
126	127	ò
17289		: 음
126	DOUGHT TO THE PROPERTY OF THE	3 8
17229	:    17170 EESARCEIKNTDFKALLIVKDAIRIDGGQYILRASNVAGSKSFPVNVKVLDRPGPPEGPV	g

g	18250 E	ELEETAARMEIKSTIQKTTLVVKDCIRTDGGQYILKLSNVGGTKSIPITVKVLDRPGPPE	18309
ò	134		133
g	18310 C	GPLKVTGVTAEKCYLAWNPPLQDGGANISHY11EKRETSRLSWTQVSTEVQALNYKVTKL	18369
ò	134		133
g	18370 1	LPGNEY1FRVMAVNKYG1GEPLESGPVTACNPYKPPGPPSTPEVSA1TKDSMVVTWARPV	18429
ò	134 .		133
g	18430	DDGGTE1EGY1LEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENAAGVGE	18489
ò	134		133
q	18490 1	PSEPSVFYRACDALYPPGPPSNPKVTDTSRSSVSLAWSKPIYDGGAPVKGYVVEVKEAAA	18549
ò	134		133
g	18550 1	<b>DEWTTCTPPTGLQGKQFTVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPE</b>	18609
ò	134		133
g	18610	IELDADLRKVVVLRASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEVTSSFTMLVID	18669
ò	134		133
a	18670	NVTRFDSGRYNLTLENNSGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDG	18729
ò	134		133
g	18730	<b>GAKITNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAET</b>	18789
ò	134		133
g	18790	TEPVKVSEPPLPPGRVTLVDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEKWSTCT	18849
ò	134		133
g	18850	QVKTLEATISGLTAGEEYVFRVAAVNEKGRSDPROLGVPVIARDIEIKPSVELPFHTFNV	18909
ò	134		133
g	18910	KAREQLKIDVPFKGRPQATVNWRKDGQTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYE	18969
ò	134		133
g	18970	LCVSNSAGSITVPITIIVLDRPGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIVEK	19029
ò	134		133
q	19030	KETTSTTWHIVSQAVARTSIKIVRLTTGSEYQFRVCAENRYGKSSYSESSAVVAEYPFSP	19089
ò	134		133
g	19090	PGPPGTPKVVHATKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQM	19149
ò	134		133
g	19150	KVSGLDEGLMYEYRVYAENIAGIGKCSKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWS	19209
ò	134		133
qq	19210	KPHYDGGAKITGYIVERRELPDGRWLKCNYTNIQETYFEVTELTEDQRYEFRVFARNAAD	19269
ò	134		133
d	19270	SVSEPSESTGPIIVKDDVEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKD	19329
ò	134		. 133
q	19330	GIEIEERARTEIISTDNHTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPP	19389

ò	134	133	n
q	19390 7	AGPLEINGLTAEKCSLSWGRPQEDGGADIDYYIVEKRETSHLAWTICEGELQMTSCKVTK 1944	449
ò	134	133	m
g	19450 1	LLKGNEYIFRVTGVNKYGVGEPLESVAIKALDPFTVPSPPTSLEITSVTKESMTLCWSRP 1950	509
ò	134	133	9
පු	19510	ESDGGSEISGYIIERREKNSLRWVRVNKKPVYDLRVKSTGLREGCEYEYRVYAENAAGLS 1956	569
ò	134	133	m
වු	19570	LPSETSPLIRAEDPVFLPSPPSKPKIVDSGKTTITIAWVKPLFDGGAPITGYTVEYKKSD 1962	629
ઠે	134	133	m
qq	19630	DIDWKTSIQSLRGTEYTISGLTTGAEYVFRVKSVNKVGASDPSDSSDPQIAKEREEEPLF 1968	689
ò	134	133	м
q	19690	DIDSEMRKTLIVKAGASFTMTVPFRGRPVPNVLWSKPDTDLRTRAYVDTTDSRTSLTIEN 1974	749
ò	134	133	e
Q	19750	ANRNDSGKYTLTIQNVLSAASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVPENDGG 19809	608
ò	134	133	m,
g	19810	APVKNYHIEKREASKKAWVSVTNNCNRLSYKVTNLQEGAIYYFRVSGENEFGVGIPAETK 19869	698
ò	134		m m
g	19870	EGVKITEKPSPPEKLGVTSISKDSVSLTWLKPEHDGGSRIVHYVVEALEKGOKNWVKCAV 1999	19929
ò	134	133	Ē.
qq	19930	AKSTHHVVSGLRENSEYFFRVFAENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTV 1996	19989
ò	134	133	ũ
g	19990	YVRAGSNLKVDIPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGR 2004	049
ð	134	133	33
Q	20050	YEITAANSSGTTKAFINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSOVTNYI 2010	0109
ò	134	133	33
쉽	20110	LLKRETSTAVWTEVSATVARTMMKVWKLTTGEEYQFRIKAENRFGISDHIDSACVTVKLP 201	20169
ò	134	133	33
g	20170	YTTPGPPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWQKANKLVIRT	20229
ò	134	133	33
g	20230	THFKVTTISAGLIYEFRVYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSL 202	20289
ò	134	133	33
qq	20290	SWQQPAFDGGSKITGYIVERRDLPDGRWTKASFTNVTETQFIISGLTQNSQYEFRVFARN 203	0349
ò	134	133	33
q	20350	AVGSISNPSEVVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEW	20409
ò	134	133	33
g	20410	YKDDKELQTNALVCVENTTDLASILIKDADRLNSGCYELKLRNAMGSASATIRVQILDKP	20469

ò	134	TIO	137
gg	20470 GPPGGPIEFKTVTAEKITLLWRPPADDGGAKITHYIVEKRETSRVVWSMVSEHLEECIIT	IVEKRETSRVVWSMVSEHLEECIIT	20529
ò	138		137
a	20530 TTKIIKGNEYIFRVRAVNKYGIGEPLESDSVVAKNAFVTPGPPGIPEVTKITKNSMTVVW	AFVTPGPPGIPEVTKITKNSMTVVW	20589
ò	138		137
g	20590 SRPIADGGSDISGYFLEKRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAA	DTROKVTGLTENSDYQYRVCAVNAA	20649
ò	138		137
g	20650 GQGPFSEPSEFYKAADPIDPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIR	SITLGWSKPVYDGGSAVTGYVVEIR	20709
ò	138		137
qq	20110 GGEEEEWTTVSTKGEVRTTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDIL	VSAVNCAGQGEPIEMNEPVQAKDIL	20769
à	138		137
Q	20770 EAPEIDLDVALRTSVIAKAGEDVQVLIPFKGRPPPTVTWRKDEKNLGSDARYSIENTDSS	TVTWRKDEKNLGSDARYSIENTDSS	20829
ò	138		137
임	20830 SLLTIPQVTRNDTGKYILTIENGVGEPKSSTVSVKVLDTPAACQKLQVKHVSRGTVTLLM	VLDTPAACQKLQVKHVSRGTVTLLW	20889
ઠે	138		137
g	20890 DPPLIDGGSPIINYVIEKRDATKRTWSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENEIG	TSFKLIDLSEKTPFFFRVLAENEIG	20949
ò	138		137
g	20950 IGEPCETTEPVKAAEVPAPIRDLSMKDSTKTSVILSWTKPDFDGGSVITEYVVERKGKGE	SWTKPDFDGGSVITEYVVERKGKGE	21009
ò	138		137
g	21010 QTWSHAGISKTCEIEVSQLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELIITPEVDLS	GLSDPVTIGPITVKELIITPEVDLS	21069
ò	138		137
g	21070 DIPGAQVTVRIGHNVHLELPYKGKPKPSISWLKDGLPLKESEFVRFSKTENKITLSIKNA	LPLKESEFVRFSKTENKITLSIKNA	21129
ò	138		137
DP	21130 KKEHGGKYTVILDNAVCRIAVPITVITLGPPSKPKGPIRFDEIKADSVILSWDVPEDNGG	GPIRFDEIKADSVILSWDVPEDNGG	21189
ò	138		137
임	21190 GEITCYSIEKRETSQTNWKMVCSSVARTTFKVPNLVKDAEYQFRVRAENRYGVSQPLVSS	.VKDAEYQFRVRAENRYGVSQPLVSS	21249
ò	138		137
g	21250 IIVAKHQFRIPGPPGKPVIYNVTSDGMSLTWDAPVYDGGSEVTGFHVEKKERNSILWQKV	/YDGGSEVTGFHVEKKERNSILWQKV	21309
ò	138		137
g	21310 NTSPISGREYRATGLVEGLDYQFRVYAENSAGLSSPSDPSKFTLAVSPVDPPGTPDYIDV	SPSDPSKFTLAVSPVDPPGTPDYIDV	21369
ò	138		137
g	21370 TRETITLKWNPPLRDGGSKIVGYSIEKRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEF	/RCNFTDVSECQYTVTGLSPGDRYEF	21429
ઠે	138		137
q	. 21430 RIIARNAVGTISPPSQSSGIIMTRDENVPPIVEFGPEYFDGLIIKSGESLRIKALVQGRP	3PEYFDGLIIKSGESLRIKALVQGRP	21489
8	138		137
g	. 21490 VPRVTWFKDGVEIEKRMNMEITDVLGSTSLFVRDATRDHRGVYTVEAKNASGSAKAEIKV	ATRDHRGVYTVEAKNASGSAKAEIKV	21549
ઠે			137

g	21550 KVQ	KVQDTPGKVVGPIRFTNITGEKMTLWWDAPLNDGCAPITHYIIEKRETSRLAWALIEDKC 210	1609
ò	138	137	37
o C	21610 EA	EAQSYTAIKLINGNEYQFRVSAVNKFGVGRPLDSDPVVAQIQYTVPDAPGIPEPSNITGN 21(	21669
ò	138	13'	37
D	21670 SI	SITLIWARPESDGGSEIQQYILERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEFH 217	1729
ò	138	13.	37
Ωp	21730 VM	VMAENAAGVGPASGISRLIKCREPVNPPGPPTVVKVTDTSKTTVSLEWSKPVFDGGMEII 21°	21789
ò	138	137	37
qq	21790 GY	GYIIEMCKADLGDWHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGAGKGDSCEVTGTI 21	21849
ò	138	13.	37
තු	21850 KA	KAVDRLTAPELDIDANFKQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHT 21.	1909
ò	138	13.	37
g	21910 TD	TDSFSTLTVENCNRNDAGKYTLTVENNSGSKSITFTVKVLDTPGPPGPITFKDVTRGSAT 21	21969
ò	138	13	37
qq	21970 LM	LMWDAPLLDGGARIHHYVVEKREASRRSWQVISEKCTRQIFKVNDLAEGVPYYFRVSAVN 22	22029
ò	138	13	78
ф	22030 EY	EYGVGEPYEMPEPIVATEQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQ 22	22089
ò	138	13	137
Dβ	22090 KG	KGSDFWVEAGHTKQLTFTVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVIIKEPQIEPT 22	22149
ò	138	13	137
q	22150 AD	ADLIGITNQLITCKAGSPFTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLT 22	22209
ò	138	13	.37
qq	22210 VK	VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGPVTGPIEVSSVSAESCVLSWGEPK 22	22269
ò	138		137
đ	22270 DG	DGGGTEITNYIVEKRESGTTAWQLVNSSVKRTQIKVTHLTKYMEYSFRVSGENRFGVSKP 22	22329
ò	138		137
qq	22330 LE	LESAPIIAEHPFVPPSAPTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTIL 22	22389
ò	138	13	137
Q	22390 WV	WVKENKVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPE 22	22449
ò	138	13	137
В	22450 VT	VTDVTRSTVSLIWSAPAYDGGSKVVGYIIERKPVSEVGDGRWLKCNYTIVSDNFFTVTAL 22	22509
ò	138	13	137
đ	22510 SE	SEGDTYEFRVLAKNAAGVISKGSESTGPVTCRDEYAPPKAELDARLHGDLVTIRAGSDLV 22	22569
ò	138	27	137
g	22570 L	LDAAVGGKPEPKIIWTKGDKELDLCEKVSLQYTGKRATAVIKFCDRSDSGKYTLTVKNAS 2	22629
ò	138	13	137

셤	22630	GTKAVSVMVKVLDSPGPCGKLTVSRVTQEKCTLAWSLPQEDGGAEITHYIVERRETSRLN	22689
ò	138		137
qq	22690	WVIVEGECPTLSYVVTRLIKNNEYIFRVRAVNKYGPGVPVESEPIVARNSFTIPSPPGIP	22749
ò	138		137
g	22750	EEVGTGKEHIIIQWTKPESDGGNEISNYLVDKREKKSLRWTRVNKDYVVYDTRLKVTSLM	22809
ò	138		137
g	22810	EGCDYQFRVTAVNAAGNSEPSEASNFISCREPSYTPGPPSAPRVVDTTKHSISLAWTKPM	22869
ò	138		137
qq	22870	YDGGTDIVGYVLEMQEKDTDQWYRVHTNATIRNTEFTVPDLKMGQKYSFRVAAVNVKGMS	22929
ò	138		137
g	22930	EYSESIAEIEPVERIEIPDLELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQGID	22989
ò	138		137
g	22990	LASRAIIDTTESYSLLIVDKVNRYDAGKYTIEAENQSGKKSATVLVKVYDTPGPCPSVKV	23049
ò	138		137
g G	23050	KEVSRDSVTITWEIPTIDGGAPVNNYIVEKREAAMRAFKTVTTKCSKTLYRISGLVEGTM	23109
ò	138		137
q	23110	YY FRVL PENIYGIGE PCETSDAVLVS EVPLV PAKLEVVDVTKSTVTLAWEK PLYDGGSRL	23169
ò	138		137
g	23170	TGYVLEACKAGTERWMKVVTLKPTVLEHTVTSLNEGEQYLFRIRAQNEKGVSEPRETVTA	23229
ò	138		137
g	23230	VTVQDLRVLPT1DLSTMPQKT1HVPAGRPVELV1P1AGRPPPAASWFFAGSKLRESERVT	23289
ò	138	BDTG	141
g	23290		23349
ò	142		141
a	23350	TSITISWEPPELDGGAPLSGYVVEQRDAHRPGWLPVSESVTRSTFKFTRLTEGNEYVFRV	23409
ò	142		141
Q	23410	AATNRFGIGSYLQSEVIECRSSIRIPGPPETLQIFDVSRDGMTLTWYPPEDDGGSQVTGY	23469
ò	142		141
g	23470	IVERKEVRADRWVRVNKVPVTMTRYRSTGLTEGLEYEHRVTAINARGSGKPSRPSKPIVA	23529
ò	142		141
q	23530	) MDPIAPPGKPQNPRVTDTTRTSVSLAWSVPEDEGGSKVTGYLIEMQKVDQHEWTKCNTTP	23589
ò	142		141
qq	23590	) TKIREYTLTHLPQGAEYRFRVLACNAGGPGEPAEVPGTVKVTEMLEYPDYELDERYQEGI	23649
ò	142		141
a	23650	) FVRQGGVIRLTIPIKGKPFPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYD	23709
ò	142		141
£	23710	1.VLENKCGKKAVYIKVRVIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADILGYILE	23769

ò	142 -	141
g	23770 R	RREVPKAAMYTIDSRVRGTSLVVKGLKENVEYHFRVSAENQFGISKPLKSEEPVTPKTPL 23829
ò	142 -	141
qq	23830 N	NPPEPPSNPPEVLDVTKSSVSLSWSRPKDDGGSRVTGYYIERKETSTDKWVRHNKTQITT 23889
ò	142 -	141
g	23890 T	TMYTVTGLVPDAEYQFRIIAQNDVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKDS 23949
ò	142 -	141
g	23950 V	VTLQWEKPECDGGKEILGYWVEYRQSGDSAWKKSNKERIKDKOFTIGGLLEATEYEFRVF 24009
ò	142	141
Ωp	24010 A	AENETGLSRPRRTAMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKW 24069
ò	142 -	141
g	24070 1	YRFGKELIQSRKYKMSSDGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATP 24129
ò	142 -	141
g	24130	QFHPGYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHL 24189
ò	142	141
g	24190 \	VMKNVQRKTHAGKYKVQLSNVFGTVDAILDVEIQDKPDKPTGPIVIEALLKNSAVISWKP 24249
ò	142	141
a	24250	PADDGGSWITNYVVEKCEAKEGAEWQLVSSAISVTTCRIVNLTENAGYYFRVSAONTFGI 24309
ò	142	141
g	24310	SDPLEVSSVVIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDGGAKIRNYYLEKREK 24369
ò	142	141
qq	24370 1	KONKWISVTTEBIRETVFSVKNLIEGLEYEFRVKCENLGGESEWSBISEPITPKSDVPIO 24429
ò	142	141
g	24430	APHFKEELRNLAVRYQSNATLVCKVTGHPKPIVKWYRQGKEIIADGLKYRIQEFKGGYHQ 24489
ò	142	141
g	24490	LIIASVTDDDATVYQVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAVHALRGEVVS 24549
ò	142	141
g	24550	IKIPFSGKPDPVITWQKGQDLIDNNGHYQVIVTRSFTSLVFPNGVERKDAGFYVVCAKNR 24609
ò	142	141
g	24610	FGIDQKTVELDVADVPDPPRGVKVSDVSRDSVNLTWTEPASDGGSKITNYIVEKCATTAE 24669
ò	142	141
gg	24670	RWLRVGQARETRYTVINLFGKTSYQFRVIAENKFGLSKPSEPSEPTITKEDKTRAMNYDE 24729
ò	142	141
Q	24730	EVDETREVSMTKASHSSTKELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKG 24789
ò	142	141
g	24790	TDQVLVKKEISILNIARHRNILHLHESFESMEËLVMIFEFISGLDIFERINTSAFELNER 24849

28,

Oy 142FDLFDL		Query Match Best Local S Matches 98	.ch 1. Similarity 1.2%; Score 264; DB 2; Length 9507; 1. Similarity 1.2%; Pred. No. 1.1; 98; Conservative 19; Mismatches 30; Indels 7866; Gaps 28
145	144	Qy 2	AGGILH
Db 24910 LFTAPEYYAPEVHQHDVVSTATDMWSLGTLVYVLLSGINPFLAETNQQIIENIMNAEYTF	AETNOQIIENIMNAEYTF 24969	Dp 86	ERAGIDPAAVRGTRTGMFV
Qy 145	144	Oy 13	
Db 24970 DEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIRTLKHRRYY	(IERVSTKVIRTLKHRRYY 25029	Db 146	
Oy 145	144	Qy 17	
Db 25030 HTLIKKDLNMVVSAARISCGGA,RSQKGVSVAKVKVASIEIGPVSGQIMHAVGEEGGHVK	SPVSGQIMHAVGEEGGHVK 25089	Db 206	
Qy 145	144	0y 17	
Db 25090 YVCKIENYDQSTQVTWYFGVRQLENSEKYEITYEDGVAILYVKDITKLDDGTYRCKVVND	/KDITKLDDGTYRCKVVND 25149	Db 266	LERLSEARRNGHEILAVIRGSAVNQDGASNGLTAPNGPSQRRVIEQALVSARLSADEVDV 325
Oy 145	144	Qy 19	
Db 25150 YGEDSSYAELFVKGVREVYDYYCRRTMKKIKRRTDTMRLLERPPEFTLPLYNKTM	RPPEFTLPLYNKTAYVGEN 25209	Db 326	VEAHGTGTTLGDPVEAQALLATYGQGRDDDRPLLLGSVKSNLGHTQAAAGMAGVIKMVLA 385
Qy 145GVTI 148		0y 23	
Db 25210 VRFGVTI 25216		Db 386	MRHGVLPRTLHVDAPSSHVDWTQGAVRLLTEHVPWPQGEQPRRAGVSSFGLSGTNAHTIL 445
		0y 23	26
RESULT 5		Db 446	 Eeapaapspeaggedtapvaeplaagavpwlvsgrtrealragaarilehiltsrpglapl 505
OSEWA1 PRELIMINARY; PRT; 9507 AA.		0y 27	56
AC UJEWA1; DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	re)	w	DVAYSLATARSGLEHRAAFTAAGPDGARAALTALADGTPAPGLVQDTARTRSKLAFLFAG 565
01-JUN-2002 (TrEMBLrel. 21, Last annotation pimes protein	update)	Oy 27	26
		Db 566	QGSQRPGMGRELAARFPVFATALDEVLGHFDEGLERPLKDVLFAAEGTPEAALLDQTGYA 625
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	cteridae; aceae; Streptomyces.	0y 27	56
OX NCBI TaxID=68242;		Db 626	QPALFAIEVALYRLAESFGITPDFLAGHSIGEIAAAHVAGVFTLADAAALVLARGRLMQA 685
		Oy 27	56
RA Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martin RT "A complex militiensces R., Stem encoded by five polyketide	N., Martin J.F.; polyketide synthase	Db 686	LPEGGAMVSLEATEEEVLPLLEDRPDRLSIAAVNGPAAVVIAGEADDVTAVAEHFDALGR 745
	ŭ	0y 27	26
		Db 746	RIKRLRVSHAFHSPLMEPMLAEFRTAVSRLTPQAPVIPVVSGLTGTLATVEOLTSPDYWL 805
		0y 27	
InterPro; IPR002198; InterPro; IPR004410;		908 dd	DHARHAVRFADALRLARRARRHLPRMGPDGVLSAMAQSCCRGHGHRRRRRLRHARRVRP 865
InterPro; IPR001899; InterPro; IPR000794;		Qy 27	
InterPro; IF		998 40	GRPEAETLTAALAGLHTRGVAVQWEPYFQGTGARRADLPTYAFQRRRYWPKSLPATGGDV 925
Pfam; PF00698; Acyl		Qy 27	
		Db 926	RAAGLGAAHHPLLTAAVSVANSDGLLLTGRLSRRTHPWLADHAVRGTVLLPGTAFLELAV 985
Pfam; PF00550; pp TIGRFAMB; TIGR001		0y 27	56
PROSITE; PS50075; ACP_DOMAIN; 6. PROSITE; PS00606; B_KETOACYL_SYNTHASE; 6.		986 90	RAGDEAGCGRVEELTLAAPLVLPEEGGVQVQVWVGSPDASGRRAVSVHSRPDGPEELPWT 1045
PROSITE; PS00343; GRAM POS ANCHORING; PROSITE; PS00037; MYB_1; UNKNOWN 1.	· -	0y 27	
PROSITE; PS00012; PHOSPHOPANTETHE Phosphopantetheine.		Db 1046	QHAAGTLVAGEHHAGFDATVWPPADATPLDLDGFYARMADTGFGYGPLFGGLRAAWRSGD 1105
	B9F CRC64;	0y 27	26

ą	1106	DVYAEVALPDSDGAASTESSAAFGLHPALLDAALHAAAFVDLGEDARGGLPFSWQDVTLH 1165	
à	27	56	
ą	1166	ASGASTVRVKLTPDGDDAVALAVADTTGAPVASIGSLVLRTLPDEQIDAAHSLVRDALFE 1225	
⋩	27	56	
ą	1226	LRWSEARQTAHEAPASAAVLGPDLFGLERALAPTDLTVTAVPGPDAAPHAPDVVLAPVAG 1285	•
⋧	27	343434	
ą	1286	TTEDDVVTSVHARTAHVLERLRTWLTDERYAASRLVFVTRGALATDARQASDPVAAAVWG 1345	
ጵ	35	34	
ą	1346	LVRAAQSEHPGRFGLLDLDPGTTEPATEPLLRALALSSDEPQTAVRGTAVLTARLARAQA 1405	
à	35	34	
g	1406	PQAATEWDPEGTVVLTGATGGLGRVLARHLVAERGVRHLLLVSRRGADADGAGELMAELA 1465	
à	35	34	
q	1466	AHGAQVTLAACDLADRAAVRRLLSGVPAEHPVTAVVHSAGSLDDGVIASLTPERISAVLR 1525	
à	35	34	
g	1526	PKADAVWHLHEATRDLDLAAFVVFSSLSGTVGAAGQGNYAAANAFLDALAQLRRAQGLPG 1585	
à	35	34	
q	1586	LSLAWGPWAPTAGMTGGLTDDDLDRLARMGTPALTEEQGIALFDAATATDAAVLLPTRID 1645	
ò	35	34	
q	1646	LSVLRVQSEIPPLWRGLIRTPARRSVVSASETAVTLVQQLSRLAETDRREVVLDLVAGQV 1705	
ઠે	35	34	
g	1706	AAVLGHAGTADIDPRRPLRELGFDSLTAVELRNRLSAATGLRTAATVIFDHPTVDALAAH 1765	
ò	35	34	
g	1766	. LLDGLMGSEAAAAADAPRTAADDDPIVIVGMSCRYPGGVASPEDLWRLVSEGTDAISGLP 1825	
ò	35	34	
g	1826	TORGWDLDALYDPDPDRTGTSYSRFGGFLHTAADFDPAFFGMSPREALATDSQORLLLEA 1885	
à	35	34	
g G	1886	; SCEAVERAGIDPVSLRGSQTGVFAGVMYNDYATVLSGGQFEGHQGSGTAPSVASGRISYT 1945	
ò	35	34	
g	1946	: LGLEGPAVTVDTACSSSLVAMHWAWQALRAGECSLALAGGVTVMSTFGALIEFSRQRGLS 2005	
ò	35	34	
g	2006	; PDGRCKAFSDGADGVGWSEGVGVLVLERLSDARRNGHRVLAVVRGSAVNQDGASNGLTAP 2065	
ઠે	35	34	
QQ	2066	S NGPAQQRVIRQALSAAGLSATDIDAVEGHGTGTTLGDPIEAQALLAAYGQDREAGSPLLL 2125	
ò	35	3 NIG 37	
qq	2126	GSVKSNIGHTQAAAGVAGVIKMVMAMRHGVLPRTLHADEPSSHVEWDSGAVRLLTEETPW	
ò	38	37	

g	2186 PQADRPRRAAVSSFGF	SCTNAHLIVEEPAAVAERREEPALTPAVVPWTLSGKSRAALRDQ 2245
ò	38	42
QQ	2246 AARLRSFLEERPALDPADVALSLATTRSA	ADVALSLATTRSAFDQRAVVTGDRDELLRALADLAADRPGPALT 2305
ò	43	46
qq	2306 EGEVGGAGKLAVVFSC	EGEVGGAGKLAVVFSGQGSQRPGAGRELAARFPVFAQALDEVTAALDPHLDRPLKDILFA 2365
ò	47	46
qq	2366 PEGSPEAALLDRTEW1	PEGSPEAALLDRTEWTQPALFAIGVALHRLLGTWGIRPDVLLGHSIGEITAAHVAGVLSL 2425
ò	47	94
qq	2426 PDAARLVIARGRLMQA	PDAARLVIARGRLMQALPAGGAMISLEATEDETAPLLAGRDHEVSLAAVNGPRSVVVAGE 2485
ò	47	46
g	2486 LAAAEEIAAHFADRGF	IAAHFADRGRKTKRLTVSHAFHSPLMEPALDGLREAAAELTYHAPDVTVISGLT 2545
ò	47	46
g	2546 GRPATEAELRSADYW	GRPATEAELRSADYWVAHARGAVRFADTLRAAHDCGAGTFLELGPDSVLSAAAQDALGDD 2605
ò	47	94 46
qq	2606 AEAHIVPLLRHGRGE	AEAHIVPLLRHGRGEERCAATALARLHVRGTTADWPGYLAGTGARTIDLPTYAFQHERYW 2665
ò	47	46
q	2666 PEQAPARLAQGAADPI	PEQAPARLAQGAADPADAELWGAVERGDATELAALLGLRDEQHASLYALLPALSSWRQHR 2725
ò	47	GAOF 50
q	2726 QEKALLDSTRYRVAWI	QEKALLDSTRYRVAWRPVQATAAPVLDGTWLLVTADGIDSDEILDALRGHGAQFETLVLD 2785
ò	51RVHL	54
QQ	1     2786 DACRDRAHLAGRLAAVRDQDRPLTGVL	VRDQDRPLTGVLSLLPLADRSGAEAGAEAGAETGAQPSTGLALSL 2845
ò	25	54
q	2846 VLIQALADTGLAAPL	VLIQALADTGLAAPLWTLTRGAVTTGADDPLTHPLQAAVWGLGRVAALEHPQLWSGLIDL 2905
ò	25	54
q	2906	PAALDAPATQHLVSALAAEGGEDQIAVRATGAFGRRLVRHPQAELPPADAFTARGTVLIT 2965
ò	55	54
qq	2966	GGTGALGAEAARWLARSGAEHLLLTSRRGPEAPGAAELAAEIEELGARVTLAACDTADRA 3025
ò	. 55	
QQ	3026	ALAALLDSLPDEHPLTGVVHAAGVGQAAALADTPLADAAQAMAAKLLGAAHLDSLLDGHD 3085
ò	55	54
qq	3086	LDFFVLVSSIAGVWGSAGQSAYSAANAYLDALAEHRAARGLPATSVAWGPWAEAGWATHE 3145
ò		75
ପ୍ର	3146	AVTDELHKRGLRFLAPATALAELRRAVVHRDVTVTVADIDWERYHPVPTSTRPSALFDEL 3205
ò	55	89
g	3206	aevqalirpedesaapefaarlrgldqdgqerllgdlvraeaaialghdsadaiaerraf 3265
ò		
d	3266	RDAGFDSLTAVELRKRLAALTGLALPATLVFDYPTPVALARHÜREQLLGTAQESAAPVAV 3325

25 26 27 28 29 29 29 29 29 29 29 29 29 29 29 29 29	75 -	4406 D	75 -	4466 A	- 27	4526 0	75 -	4586 7	75	4646 E	75 -	4706 7	. 57	4766 1	75	4826	75	4886	75	4946	75	2006	83	9905	83	5126	83	5186	, 83	5246	7 97	5306	, 103	5366	106	5426	111
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	٥ -	qa	ò	q <sub>Q</sub>	δ 	<u>ස</u>	ò	<u>අ</u>	ò	ි අ <u>පි</u>	ò	සි	, o	qa	λο	<u>გ</u>	ò	<del>අ</del>	ò	<b>q</b> a	ò	qa	8	<b>q</b> 0	<i>ک</i> 	QQ	<i>&amp;</i> 	<b>q</b> 0	λο —	ф 	ò	<b>q</b> a	ò	ପ୍ର	δ	ପ୍ର 	
FPDEPIAIVGMSCRFPGGURSPROLMDLYSEGVDAISDFYNRGWNTGLFHPD  (STOGGFLHDAGEFDASFFGISPREALSMDPOORLLLETTWEAFEHAGIDPTT  TEIGSTYGESGLAUDGSAGHLYTGTSPSVLSGRLAYLFGLEGPAVTVDTAGS  LACOSLRNGESSLALAGGATVMTNPNPFVAFSRQRALAGDGRCKAFSEGADGW  VLVLERLSDAORNGHEILAVYRGSAINQDGASNGLSAPNGPSGQRYTRQALAN  TLLEEARPHEATPAGPVPPAGDAIPWVLSARTPGALRAQAAQLAAHLDGEAA  TLLEEARPPHEATPAGPVPPAGDAIPWVLSARTPGALRAQAAQLAAHLDGEAA  TLLEEARPPHEATPAGGATVATAGGSARAALDALATGGSAPGIVQGTADTDGRTVFT  TLVAARTLEPDHRAVVVGTDDASRRAALDALATGGSAPGIVQGTADTDGRTVFT  TLVAARTLEPDHRAVVVGTDDASRRAALDALATGGSAPGIVQGTADTDGRTVFT  WASCAALMTSHGITPDAVVGTBGSRRAALDALATGGSAPGIVQGTADTDGRTVFT  WASCAALMTSHGITPDAVVGTBGTAAAAVAGALSLEDAARVALRSQAIAA  WASCAALMTSHGITPDAVVGTBGTAAAAVAGALSLEDAARVALRSGAIAA  WASCAALMAGAGTGARRVPLPWRTYAFQREHLWAIPERSPDRFBADBA  AGAFVRGADADWSAVFAGTGARRVPLPWTYAFQREHLWAIPERSPDRRFBADBA  AGAFVRGADADWSAVFAGTGARRVPLPALSHWRKRRRELSTVDSWRYRATWRPLT  GGTWLVVAPEGADTDTLTGVLAAHGAGTRTLVLDDSCADRATTARALTGLDGANGTGLDGANGTGLTGCANYSTGRAD				54					356	54		54													4045	67										74	RLTRP 4405
			DEPIAIVGMSCRFPGGVRSPRQLWDLVSEGVDAISDFPVNRGWNTGLFHP!		toggflhdagefdasffgisprealsmdpqqrlllettweafehagidpt'		IGSTYQEYGLGVEDGSAGHLVTGTSPSVLSGRLAYLFGLEGPAVTVDTAC:		COSLRNGESSLALAGGATÚMTNPNPFVAFSRORALAGDGRCKAFSEGADG		VLERLSDAQRNGHEILAVVRGSAINQDGASNGLSAPNGPSQQRVIRQALA		)AVEAHGTGTALGDP1EAQALLATYGPGRDPDSPLLLGSVKSN1GHTOSAA		alrngolprtlhadtpsshidwtpgtvslíteptdwpegerprrcavssf		lebaprpheatpagpvppagdaipwvlsartpgalraqaaqlaahldgea		VAARTLFDHRAVVVGTDDASRRAALDALATGGSAPGIVQGTADTDGRTVF	BG9b	AGMGARLLEESPVFAARLTECATALSEFVDWSLLDVLRQADGAPTLDRVDV		/SLAALWTSHGITPDAVVGHSQGBIAAAAVAGALSLEDAARVVALRSQAIA		LSVPLPAADVEORLAAYEDLSIAAVNGPRSTVVSGATAPLDALQAELVGEL		YASHSAQVERVRDELRTVLEPVRPRPAQVPFFSTVTGDWLDTTVMDAEYWF		QPAIGELLAQGHHFFIEVSSHPVLSMGIQATAEEAGAAAAVLGTLRRDTG#		EAFVRGADADWSAVFAGTGARRVPLPTYAFQREHLWAI PERSPDRPEADP!		EEDVEALASRLRLDRTSLAPVLPALSHWRKRRRELSTVDSWRYRATWKPL!	NITANLT	TWLVVAPEGADTDTLTGVLAAHGAGTRTLVLDDSCADRATLTARLTGLDG;		ooonnaacathptLSRAVTLTVALVQALGDAGIDAPLWCLTQGAVSTGRA
		ò	рр	ò	g	ò	q	ò	q	ò	g	ò	qq	ò	දු	ò	g	ò	g	ò	q	ò	q	ò	q	ò	g	ò	g	ò	g	ò	g	ò	qq	ò	Ę

ò	75	74
q	4406 DQAQILGLGWTAALEHPQRCGAGLVDLPEELDRRAGERLAAVLTGRSGEDQLAVRSSGVF 4	4465
ò		74
Q	4466 ARRVVRAAPADPAPARPWTPRGTTLVTGGTGTLAPHLARWLAQQGAEHIVLTSRRGPAAP	4525
ò		74
qq	4526 GAAELVQELAELGCQAEAVACDLTDRDAVAQMLAALRAEGRTVRTVVHTAVTIELAPLDE	4585
ò		74
qq	4586 TTLDDFAKVMDAKVIGARHLDELLGDDLDAFVLYSSTAGMWGSGAHAAYVAGNAYLNALA	4645
ò	75	74
qq	4646 EHRRARGARATAVSWGIWADDLKLGRVDPGQIRRSGLVFMDPQLALTGLRQALDDEETHL	4705
ò		74
qq	4706 AVADVDWGRYYPVFTAARPTRLFEDLPEVRQLAQESAEVTDSGSEFATRLDGLAAVEQDR	4765
ò	75	74
QQ	4766 LLLDLVRTEAATALGHASPDVLSEQRAFRDVGFDSLTAVDLRNRIASVTGLALPSTMVFD	4825
ò	75	74
đ	4826 YPNPLALVAFLRESLAGSATGTAATTTHTAAADEPIAIIGMSCRYPGGVGSPEDLWRLVT	4885
ò	75	74
đ	4886 EGGDATGEFPADRGWDAEGLYDPDPARGHTYSTRGGFLHDAADFDASFFGISPREALAM	4945
ò	75	74
g	4946 DPQQRLLLETSWEAMERAGIDPATLRGSSTGTFIGASYQDYRAFGAGPDGAEGHLITGTI	5005
ò	75 SSLLSVCGVCG	82
qq	:     5006 SSVLSGRLSYTYGFEGPAVSLDTACSSSLVALHLACQSLRNGESSLALAGGVSIMSTPGA	5065
ò	83	82
q	5066 FVGFSRQRAMAADGRCKAYSDQADGMSLAEGVGLVLVERLSDARRNGHQVLAVIRGSAVN	5125
ò	83	82
qq	5126 ODGASNGLTAPNGPSQQRVIRQALANAEVDPDGIDVIDGHGTGTALGDPIEAQALLATYG	5185
ò	83	83
g	5186 QGRDPEHPLLLGSVKSNIGHTQMASGVASVIKMVMAMRHAAVPRSLHIDRPSSHVDWSSG	5245
ò	B3BDDTDBGBDDTDBG	96
g	5246 AIQLLTEPLPWPATGHPRRAGVSSFGLSGTNVHTILEQAPEDRTËEDTDTAPARPADPTP	5305
ò	76	102
q	5306 VPVTLSGRTEAGLRAQAGRLLTHLADHPELPLTDLAFSLATSRAALEHRAAVVTDDPDTL	5365
ò	103YIT	105
QQ	5366 TRALTALRDATPDGGLLTGRPDRGRLAFLFTGQGSQRPGMGRELYDRHPVYAEALDAVLA	5425
ò	106	110
g	5426 RFDLELDRPLREILFADPGTPEAELLDDTGYTQPALFALEVALFRLAESWGLRPDYVAGH	5485
ò	111	114

DR PROSITE; PSS0075; ACP_DOMAIN; 11.  DR PROSITE; PS000125; AMPEDNOANTETHEINE; UNKNOWN 9.  ENGINE PS000105; PHOSPHOPANTETHEINE; UNKNOWN 9.  I JG 9800105; PHOSPHOPANTETHEINE; UNKNOWN 9.  KW Ligase; Antibiotic biosynthesis; PhosphopanteTheine; Repeat;  KW MILITIANCTIONAL BIOSYNCHE 13 x 3 AA APPROXIMATE REPEATS.  DOMAIN 1 15179 12585 DOMAIN 2.  FT REPEAT 1087 2586 DOMAIN 3.  FT REPEAT 5565 7061 DOMAIN 3.  FT REPEAT 9617 10113 DOMAIN 5.  FT REPEAT 9617 11113 DOMAIN 9.  FT REPEAT 10114 12185 DOMAIN 9.  FT REPEAT 10114 12185 DOMAIN 10.  FT REPEAT 10160 1060 PHOSPHOPANTETHEINE (POTENTIAL).  FT REPEAT 1060 1060 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 2558 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1060 1060 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1060 1060 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1060 1060 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1058 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1058 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1058 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1058 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1058 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDING 1056 1056 PHOSPHOPANTETHEINE (POTENTIAL).  FT BINDI	Duery Match  34.24; Score 264; DB 3; Best Local Similarity 0.084; Pred 102, Conservative 24; Mismatches 21; AdGGIL 2098 AdGHULEIGTGTGMVLFNLGQAGLKSYIGLEPSQSAVQFVNKA 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
0y         141         140           Db         7706         LAAHLRANGLPPMDPARALTALARSLGTDTPSVTVADVRWDEFAPAFTRRHSALFAELP         7765           0y         141         140           Db         7766         EAREALAESDGSAPGTADAASGLRAELAARPDAERTEHLLALVRDRVAAVLGFADADAV         7825           0y         141         140           0y         141         144           0y         141         144           0y         141         144           0y         145         141           0y         145         144           0y         145         145           0y         145         145           0y         145         145           0y	RESULT 6  909164  PRELIMINARY; PRT; 15281 AA.  009164  CON 1000-1996 (TrEMBLE-1 01, Created)  DT 01-NOV-1996 (TrEMBLE-1 20, Last sequence update)  O1-NOV-1996 (TrEMBLE-1 20, Last sequence update)  DT 01-NOV-1996 (TrEMBLE-1 20, Last sequence update)  CYCLOSPOCIATION INTRIBUTED.

32;

⋩	12	11
ą	2698	EESTIQKILEKEQTTPFNLASEPGFRLALLKTGEDEHILSTVMHHAISDGWSVDIFQQEI 2757
≿	12	
ą	2758 (	GQFYSAILRGHDPLAQIAPLSIQYRDFATWQRQIFQVAEHRRQLAYWTKQLADNKPAELL 2817
⋩	12	11
ą	2818	TDFKRPPMLSGRAGEIPVVVDGLIYEKLQDFCRIRQVTAFTVLLAAFRAAHYRWTGTEDA 2877
⋩	12	11
ą	2878	TIGTPIANRNRPELEGLIGFFVNTQCMRITVDVEDSFETLVHQVRETTLAAHANQDVPFE 2937
<b>À</b>	12	
ą	2938	QIVSNILPGSSDTSRNPLVQLMFALHSQQNLGKVRLEGIEEEIISIAETTRFDIEFHLVQ 2997
ጵ	12	
ရွ	2998	EAERLNGSIVYAADLFVPETIQSVITIFQGILQKGLGEPDMPVASMALDGGLESLRSTGL 3057
ጵ	12	18 VAVGPDV
. ද	3058	 LHPQQTDYPCDASVVQIFKQQVAVNPDVIAVRDESTRLSYADLDRKSDQVACWLSRRGIA 3117
à	19	. 18
g	3118	PETFVAILAPRSCETIVAILGVLKANLAYLPLDVNVPASRLEAILSEVSGSMLVLVGAET 3177
à	19	18
g	3178	PIPEGMAEAETIRITEILADAKTDDINGLAASQPTAASLAYVIFTSGSTGRPKGVMVEHR 3237
à	19	18
g	3238	GIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLLESTAL 3297
ò	19	18
QQ	3298	EKVFFDQRVNVALLPPALLKQCLDNSPALVKTLSVLYIGGDRLDASDAAKARGLVQTQAF 3357
ઠે	19	18
g	3358	NAYGPTENTVMSTIYPIAEDPFINGVPIGHAVSNSGAFVMDQNQQITPPGAMGELIVTGD 3417
ò	19	18
g	3418	GLARGYTTSSLNTGRFINVDIDGEQVRAYRTGDRVRYRPKDLQIEFFGRIDHQVKIRGHR 3477
ò	19	18
Q	3478	IEPAEVEYALLSHDLVTDAAVVTHSQENQDLEMVGFVAARVADVREDESSNQVQEWQTHF 3537
ò	19	18
ପ୍ର	3538	DSIAYADITTIDQQSLGRDFMSWTSMYDGSLIKKSQMQEWLDDTMRSLLDSQPPGHVLEV 3597
ò	19	18
op Op	3598	GTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGLEDRIRVEVGTATDIDRL 3657
ò	19	18
q	3658	GDDLHAGLVVVNSVAQYFPSQDYLAQLVRDLTKVPGVERIFFGDMRSHAINRDFLVARAV 3717
ò	19	18
셤	3718	HALGDKATKAEIQREVVRMEESEDELLVDPAFFTSLTTQVENIKHVEILPKRMRATNELS 3777

ò	19	18	18
Q	3778 SYRYAAVLHUNDLAKP	SYRYAAVLHVNDLAKPAHKVSPGAWVDFAATKMDRDALIRLLRGTKISDHIAIANIPNSK 36	3837
ò	19	16	18
QQ	3838 TIVERTICESVYDLGG	TIVERTICESVYDLGGDAKDSNDRVSWLSAARSNAVKVASLSAIDLVDIAQEAGFRVEIS 36	3897
ò	19	16	18
q	3898 CARQWSQNGALDAVFH	CARQWSQNGALDAVFHHLGPSPQSSHVLIDFLTDHQGRPEEALTNHPLHRAQSRRVERQI 3	3957
ò	19	10	18
qq	3958 RERLQTLLPAYMIPAC	rerlotlepaymipaqimvldklplnangkvdrkqltqraqtvpkakqvsapvaprteie 4(	4017
ò	19	1	18
g	4018 RVLCQEFSDVLGVDIG	RVLCQEFSDVLGVDIGIMENPFDLGGHSLMATKLAARISRRLETHVSVKEIFDHPRVCDL 40	4077
ò	19	18	18
q	4078 VLIVOQGSAPHDPIVS	VLIVQQGSAPHDDIVSTKYTGPVPQSFAQGRLWFLDQLNFGATWYLMPLAVRLRGAMNVH 4)	4137
ò	19	16	18
q	4138 ALTAALLALERRHELI	ALTAALLALERRHELLRTTFYEQNGVGMQKVNPVVTETLRIIDLSNGDGDYLPTLKKEQT 41	4197
ò	19	16	18
q	4198 APFHLETEPGWRVALI	APFHLETEPGWRVALLRLGPGDYILSVVMHHIISDGWSVDVLFQELGQFYSTAVKGHDPL 4:	4257
ò	19	18	18
q	4258 SQTTPLPIHYRDFALM	SQTTPLPIHYRDFALWQKKPTQESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGOAG 4.	4317
ò	19	10	18
q	4318 EMSVTIEGALYKNLEE	EMSVTIEGALYKNLEEFCRVHRVTSFVVLLAALRAAHYRLTGSEDATIGTPIANRNRPEL 4	4377
ò	19	]	18
g	4378 EQIIGFFUNTQCIRIT	EQIIGFFVNTQCIRITVNEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDAS 4	4437
ò	19		18
q	4438 RNPLVQLMFAVHSQK	RNPLVQLMFAVHSQKNLGELKLENAHSEVVPTEITTRFDLBFHLFQQDDKLEGSILYSTD 4	4497
ò	19	1	18
qq	4498 LFEAVSVQSLLSVFQ	LFEAVSVOSLLSVFQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSV 4	4557
ò	19	1	18
엄	4558 VDVFHEQVSINPDSI	VDVFHEQVSINPDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCE 4	4617
ò	19	1	18
엄	4618 TIIAFLGILKANLAYI	TIIAFLGILKANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVP 4	4677
ò		1	18
qq	4678 IRDTFTTLTDGTLQD	IRDTFTTLTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMVQHRNIVRLVKNSNVV 4	4737
ò	19		23
qq	4738 AKOPAAARIAHISNL	akopaaariahisnlafdassweiyaplinggaivcadyfttidpqalqetfqeheirga 4	4797
ò	24		23
g	4798 MLPPSLLKQCLVQAP	MLPPSLLKQCLVQAPDMISRLDILFAAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILS 4	4857
ò	24	2	23

ą	4858	TIYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDGLARGYMDPKL	4917
≿	24		23
۾	4918	DADRFIQLTVNGSEQVRAYRTGDRVRYRPRDFGIEFFGRMDQQIKIRGHRIEPAEVEQAF	4977
⋧	24		23.
g	4978	LNDGFVEDVALVIRTPENQEPEMVAFVTAKGDNSAREEEATTQIEGWEAHFEGGAYANIE	5037
≿	24	DDT	
ð	5038	EIESEALGYDFMGWTSMYDGTEIDKDEMREWLNDTMRSLLDGKPAGRVLEVGTGTGMIMF	5097
≿	27		30
ą	5098	:   NLGRSQGLERYIGLEPAPSAAEFVNNAAKSFPGLAGRAEVHVGTAADVGTLQGLTSDMAV	5157
⋧	31		30
ą	5158	INSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAMNRDFAAARAAYSLADNASKD	5217
À	31		30
ą	5218	RVRQKMMELEEKEEELLVDPAFFTALASQLQDRIQHVEILPKRMKATNELSSYRYAAVLH	5277
ጵ	31		30
ą	5278	ISDEPLP1YKIDPEAWINFEGSRLTREALAQVLKENENAESVAISNIPYSKTVVERHIVR	5337
à	31		30
g	5338	SLDQEDANAPEESMDGSDWISAVRTRAQQCHTLSASDLFDIAEDAGFRVEVSWARQHSQH	5397
à	31	NITI	33
g	5398	GALDAVFHHLKPATEDSRVLIKPPTDHQGRPLKSLTNQPLLPAQSRRAELLIREGLQTLL	5457
à	34		33
g	5458	PPYMIPSQITLIDRMPLNANGKVDRRELARRAKITQKSKPVEDIVPPRNSVEATVCKGFT	5517
ò	34		33
요	5518	DVLGVEVGITDNFFNLGGHSLMATKLAARLGRQLNTRISVRDVFDQPVVADLAAVIQRNS	5577
ò	34		38
g G	5578	APHEPIKPADYTGPVPQSFAQGRLWFLDQLNVGATWYLMPLGIRLHGSLRVDALATAISA	5637
ò	39		38
QQ	5638	LEQRHEPLRTTFHEEDGVGVQVVQDHRPKDLRIIDLSTQPKDAYLAVLKHEQTTLFDLAT	5697
à	39		38
g	569B	EPGWRVALIRLGEEEHILSIVWHHIISDGWSVEVLFDEWHRFYSSALRQODPMEQILPLP	5757
ò	39		38
셤	5758	I IQYRDFAAWQKTEEQVAEHQRQLDYWTEHLADSTPAELLTDLPRPSILSGRANELPLTIE	5817
<u>ج</u>	9		38
g	5818	§ GRLHDKLRAFCRVHQATPFVILLAALRAAHYRLTGAEDATLGTPIANRNRPELENMIGFF	5877
ò	39		38
gg	5878	3 VNTQCMRIAIEENDNFESLVRRVRSTATSAFANQDVPFESIVSSLLPGSRDASRNPLVQV	5937
ò	39		38

g	5938 ILAVHSQQDLGKLTLEGLRDEAVDSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLKTI 59	
ò	36	
q	5998 ESVVSVFLETLRRALDQPLTPLAVLPLTDGVGEIASKGLLDVPRTDYPRDANIVEVFQQH 605	157
ò	39 38	æ
Op	6058 VRATPDAIAVKDATSILTYAQLDQQSDRLAIWLSRRHMMPETLVGVLAPRSCETIIAMFG 611	117
ò	39 38	80
QQ	6118 IMKANLAYLPLDINSPAARLRSILSAVDGNKLVLLGSGVTAPEQENPEVEAVGIQEILAG 61	6177
ò	39 38	80
qq	6178 TGLDKTQGSNARPSATSLAYVIFTSGSTGKPKGVMVEHRSVTRLAKPSNVISKLPQGARV 62	6237
ò	39 38	<b>6</b> 0
q	6238 AHLANIAFDASIWEIATTLLNGATLVCLDYHTVLDCRTLKEVFERESITVVTLMPALLKQ 62	6297
ò	39 38	89
q	6298 CVAEIPETLAHLDLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTVISTIYEVDADE 63	6357
ò	39 38	80
g	6358 MFVNGVPIGKTVSNSGAYVMDRNQQLVPSGVVGELVVTGDGLARGYTDPSLNKNRFIYIT 64	6417
ò	39 38	60
QΩ	6418 VNGESIRAYRTGDRVRYRPHDLQIEFFGRMDQOVKIRGHRIEPGEVESALLSHNSVQDAA 64	6477
ò	363	80
qq	6478 VVICAPADQDSGAEMVAFVAARNTEDEDTQEEEAVDQVQGWETHFETAAYSEVKDIRQSE 65	537
ò	3636	8
qq	6538 VGNDFMGWTSMYDGSEIDKTDMHEWLNDTWRMILDAREPGHVLEIGTGTGMVMFNLAKCP 65:	597
ò	39 38	8
q	6598 GLQGYVGFEPSKSAAQFVNDAAQSFPALKDGRSIVHVGTATDINKAGPIQPRLVVINSVA 66	6657
ò	36 36	38
qq	6658 QYFPTPEYLFRVVEALVQIPSVERIVFGDMRTNAINRDFVASRALHTLGEKANKRLVRQM 6	6717
ò		5
q	- 6718 IYELEANEEELLTDPAFFTSLRTRLGEKIKHVEILPKTMKATNELSKYRYAAVLHVRGSR 6'	6777
ò	4 6	45
С	6778 EQSTIHQVSPNAWIDFAADGLDRQTLINLLKEHKDAGTVAJGNIPYSKTIVERFVNKSLS 6	6837
ò	4	5
qq	6838 EDDMEEGGNSLDGSAWVAAVRMAAQSCPSLDAMDVKEIAQEAGYQVEVSWARQWSQNGAL 6	6897
ò	46	6
g	6898 DAIFHHFEPPKEGARTLIEFPTDYEGRNVNTLINRPLNSIOSRRLGTGREKLOTLLPPY 6	6957
ò		<b>4</b> .
q	6958 MIPSRIMVLDQMPVNNNGKIDRKELVRRAIVAPKPRSAATRVAPRNEIEAILRDEFEDVL 7	7017
ò		<u>د</u> م
đ	7018 GTEVSVLDNFFDLGGHSLMATKLAARVSRRLDAHISIKDVFDQPVLADLAASIQRESAPH 7	7077

>	20		49
Ω	7078	EPI PQRPYTGPAEQSFAQGRLWFLDQLNLGATWYLMPLAIRIRGQLRVAALSAALFALER	7137
>	20		4.9
Д	7138	RHETLRTTFEESDGVGVQIVGEARNSDLRVHDVSTGDDGEYLEVLRREQTVPFDLSSEPG	7197
>	20	FRVHLVK	
Ω	7198	wrvclyktgeedhylsivmhhiiydgwsvdilrgelgqfysaalrgqdflhanplpiqy	7257
>	57		99
Д	7258	RDFAAWQREAKQVEEHQRQLGYW\$KQLVDSTPAELLTDLPRPSILSGRAGSVDVTIEGSV	7317
٠.	57	MVILT	61
۵	7318	YGALQSFCRTRSVTTFVVLLTVFRIAHFRLTAVDDATIGTPIANRNRPELETLVGCFVNT	7377
≽	62		61
ڡۣ	7378	OCMRISIADDDNFEGLVRQVRNVATAAYANQDVPFERIVSALVPGSRNTSRNPLVQLMFA	7437
<u>&gt;</u>	62		61
٩	7438	VQSVEDYDQVRLEGLESVMMPGEASTRFDMEFHLVPGDQKLTGSVLYSSDLFEQGTIQNF	7497
≽	62		61
۵	7498	VDIFQECLRSVLDQPLTPISVLPFSNAISNLESLDLLEMPTSDYPRDRTVVDLFREQAAI	7557
<u>≻</u>	62		61
õ	7558	CPDSIAVKDSSSQLTYAQLDEQSDRVAAWLHERHMPAESLVGVLSPRSCETIIAYFGIMK	7617
≿	62		61
ą	7618	ANLAYLPLDVYAPDARLAAILDTVEGERLLLLGAGVPQPGIQIPRLSTAYIAEALSHATT	7677
≿	62	DBG	65
ą	7678	VDVTSIPQPSATSLAYVIFTSGSTGKPKGVMIEHRGIVRLVRDTNVNVFPESGSALPVSH	7737
⋩	99		59
ą	7738	FSNLAWDAATWEIYTAVLNGGTVVCIDRDTMLDIAALNSTFRKENVRAAFFTPAFLKQCL	7977
ጵ	99	APNITANL	73
ą	7798	AETPELVANLEILHTAGDRLDPGDANLAGKTAKGGIFNVLGHTENTAYSTFYPVVGEETF	7857
۶	74		73
ą	7858	VNGVPVGRGISNSHAYIIDRHQKLVPAGVMGELILTGDGVARGYTDSALNKDRFVYIDIN	7917
ጵ	74		73
ą	7918	. GKSTWSYRTGDKARYRPRDGQLEFFGRMDQMVKIRGVRIEPGEVELTLLDHKSVLAATVV	7977
à	74		73
g	7978	VRRPPNGDPEMIAFITIDAEDDVQTHKAIYKHLQGILPAYMIPSHLVILDQMPVTDNGKV	8037
à	74		73
g	8038	: DRKDLALRAQTVQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEVGITDGFFDLGGHSLLA	8097
à	74		73
8	8608	3 TKLAARLSRQLNTRVSVKDVFDQPILADLARIIRRGSHRHDPIPATPYTGPVEQSFAQGR	8157

à	74	73
д	B158 LWFI	LWFLEQLNLGASWYLMPFAIRMRGPLQTKALAVALNALVHRHEALRTTFEDHDGVGVQVI 8217
ò	74	73
qq	8218 QPKS	QPKSSQDLRIIDLSDAVDDTAYLAALKREQTTAFDLTSEPGWRVSLLRLGDDDYILSIVM 8277
ò	74	73
q	8278 HHI	HHIISDGWTVDVLRQELGGFYSAAIRGGEPLSQAKSLPIOYRDFAVWQRQENQIKEOAKO 8337
ò	74	73
qq	8338 LKY	LKYWSQQLADSTPCEFLTDLPRPSILSGEADAVPMVIDGTVYQLLTDFCRTHQVTSFSVL 8397
ò	74	73
q	8398 LAAI	LAAFRTAHYRLTGTLDATVGTPIANRNRPELEGLIGFFVNTQCMRMAISETETFESLVQQ 8457
ò	74	73
g	8458 VRL	VRLTTTEAFANQDVPFEQIVSTLLPGSRDTSRNPLVQVMFALQSQQDLGRIQLEGMTDEA 8517
ò	. 74	73
qq	8518 LET	LETPLSTRLDLEVHLFQEVGKLSGSLLYSTDLFEVETIRGIVDVFLEILRRGLEQPKQRL 8577
ò	74	73
q	8578 MAM	MAMPITDGITKLRDQGLLTVAKPAYPRESSVIDLFRQQVAAAPDAIAVWDSSSTLTYADL 8637
ò	74	73
q	8638 DGQ	DGQSNKLAHWLCQRNMAPETLVAVFAPRSCLTIVAFLGVLKANLAYLPLDVNAPAARIEA 8697
ઠે	74	73
q	8698 ILS	ILSAVPGHKLVLVQAHGPELGLTMADTELVQIDEALASSSSGDHEQIHASGPTATSLAYV 8757
ò	74	73
Q	8758 MFT	MFTSGSTGKPKGVMIDHRSIIRLVKNSDVVATLPTPVRMANVSNLAFDISVOEIYTALLN 8817
ò	74	73
qq	8818 GGT	GGTLVCLDYLTLLDSKILYNVFVEAQVNAAMFTPVLLKQCLGNMPAIISRLSVLFNVGDR 8877
ò	74	73
QQ	8878 LDA	LDAHDAVAASGLIQDAVYNAYGPTENGMOSTMYKVDVNEPFVNGVPIGRSITNSGAYVMD 8937
ò	74	73
q	8938 GNQ	GNQQLVSPGVMGEIVVTGDGLARGYTDSALDEDRFVHVTIDGEENIKAYRTGDRVRYRPK 8997
ò	74	73
q	8998 DFE	DFEIEFFGRMDOQVKIRGHRIEPAEVEHALLGHDLVHDAAVVLRKPANQEPEMIAFITSQ 9057
ò	74	73
q	9058 EDE	EDETIEQHESNKQVQGWGEHFDVSRYADIKDLDTSTFGHDFLGWTSMYDGVDIPVNEMKE 9117
ò	74	78 7
g	9118 WLD	:     WLDETTASLLDNRPPGHILEIGAGTGMILSNLGKVDGLQKYVGLDPAPSAAIFVNEAVKS 9177
ò	62	18
g	9178 LPS	LPSLAGKARVLVGTALDIGSLDKNEIQPELVVINSVAQYFPTSEYLIKVVKAVVEVPSVK 9237
ò	62	78

9297	9357	81	9417	81	9477	81	9537	81	9597	81	9657	81	9717	81	7776	84	9837	84	9897	84	9957	84	10017	88	10077	88	10137	06	10197	06	10257	06	10317	06
8 RVFFGDIRSQALNRDFLAARAVRALGDNASKEQIREKIAELEESEEELLVDPAFFVSLRS	9. OLPNIKHVEVLPKLMKATNELSSYRYAAVLHISHNEEEQLLIQDIDPTAMVDFAATOKDS	DAS 64	18 QGLRNLLQQGRDDVMIAVGNIPYSKTIVERHIMNSLDQDHVNSLDGTSWISDARSAAAIC	82	.8 TSFDAPALTQLAKEEGFRVELSWARQRSQNGALDAVFHRLATDANCERSRVLVHFPTDHQ	82	18 GROLRTLTNRPLORAQSRRIESGVFEALQTALPAYMIPSRIIVLPQMPTNANGKVDRKQL	82	18 ARRAQVVAKRKAVSARVAPRNDTEIVLCEEYADILGTEVGITDNFFDMGGHSLMATKLAA	82	98 RLSRRLDTRVTVKEVFDKPVLADLAASIEQGSTPHLPIASSVYSGPVEQSYAQGRLWFLD	82	8 OFNLNATWYHMSLAMRLLGPLNMDALDVALRALEQRHETLRTTFEAQKDIGVQVVHEAGM	82	(8 KRLKVLDLSDKNEKEHMAVLENEQMRPFTLASEPGWKGHLARLGPTEYILSLVMHHMFSD	82 GWS	  8 GWSVDILRQELGQFYSAALRGRDPLSQVKPLPIQYRDFAAWQKEAAQVAEHERQLAYWEN	58	38 QLADSTPGELLTDFPRPQFLSGKAGVIPVTIEGPVYEKLLKFSKERQVTLFSVLLTAFRA	SE	38 THFRLTGAEDATIGTPIANRNRPELEHIIGFFVNTQCMRLLLDTGSTFESLVQHVRSVAT	38	58 DAYSNODIPFERIVSALLPGSRDASRSPLIQLMFALHSQPDLGNITLEGLEHERLPTSVA	58	:    18 TRFDMEFHLFQEPNKLSGSILFADELFQPETINSVVTVFQEILRRGLDQPQVSISTMPLT		78 DGLIDLEKLGLLEIESSNFPRDYSVVDVFRQQVAANPNAPAVVDSETSMSYTSLDQKSEQ	68	 38 IAAWLHAQGLRPESLICVMAPRSFETIVSLFGILKAGYAYLPLDVNSPAARIQPILSEVE	91	98 GKRLVLLGSGIDMPQSDRMDVETARIQDILTNTKVERSDPMSRPSATSLAYVIFTSGSTG	91	58 RPKGVMIEHRNILRLVKQSNVTSQLPQDLRMAHISNLAFDASIWEIFTAILNGGALICID	
9238	9298	7	9358	80	9418	σ,	9478	60	9538	ω	959	Φ.	9658	œ	9718	80	9778	80	9838	æ	9888	æ	9958	60	10018	60	10078	σ.	10138	o,	10198	υ,	10258	٥,
a 8	9	ò	qq	ò	q	ò	g	ò	පු	ò	g	ò	g	ò	g	ò	g	ò	g	ò	g	ò	g	ò	a	ò	g	ò	ద	ò	q	ò	đ	ò

g	10318	YFTLLDSQALRTTFEKARVNATLFAPALLKECLNHAPTLFEDLKVLY1GGDRLDATDAAK	10377
ò	91		06
β	10378	IQALVKGTVYNAYGPTENTVMSTIYRLTDGESYANGVPIGNAVSSSGAYIMDQKQRLVPP	10437
ò	91		90
g	10438	GVMGELVVSGDGLARGYTNSTLNADRFVDIVINDQKARAYRTGDRTRYRPKDGSIEFFGR	10497
ò	91		90
qq	10498	MDQQVKIRGHRVEPAEVEQAMLGNKAIHDAAVVVQAVDGQETEMIGFVSMASDRFSEGEE	10557
ò	. 16	TDG	93
q	10558	EITNOVOEWEDHFESTAYAGIEAIDOATLGRDFTSWTSMYNGNLIDKAEMEEWLDDTMOS	10617
ò	94		93
g	10618	LLDKEDARPCAEIGTGTGMVLFNLPKNDGLESYVGIEPSRSAALFVDKAAQDFPGLQGKT	10677
ò	94		93
Q	10678	<b>QILVGTAEDIKLVKDFHPDVVVINSVAQYFPSRSYLVQIASELIHMTSVKTIFFGDMRSW</b>	10737
ò	94	DP	95
Q	10738	ATNRDFLVSRALYTLGDKATKDQIRQEVARLEENEDELLVDPAFFTSLTSQWPGKVKHVE	10797
ò	96		95
q	10798	ILPKRMRTSNELSSYRYAAVLHICRDGEGRNRYGRRVHSVEENAWIDFASSGMDRHALVQ	10857
ò	96		95
q	10858	MLDERRDAKTVAIGNI PHSNTINERHFTTSLDTEGEGIAQDSLDGSAWQSATKAMAARCP	10917
ò	96		95
qq	10918	CLSVTELVEIGQAAGFRVEVSWARQRSQHGALDVVFHHLEDDRVGRVLINFPTDFERLPP	10977
ò	96		95
đ	10978	STGLTSRPLQRIQNRRFESQIREQLQTLLPPYMVPSRIVVLERMPLNANSKVDRKELARK	11037
ò	96	GH	97
g	11038	ARTLQTIKPSATRVAPRNDIEAVLCDEFQAVLGVTVGVMDNFFELGGHSLMATKLAARLS	11097
ò	86		101
q	11098	RRLDTRVSVKDIFNQPILQDLADVVQTGSAPHEAIPSTPYSGPVEQSFSQGRLWFLDQLN	11157
ò	102		101
đ	11158	LNASWYHMPLASRLRGPLRIEALQSALATIEARHESLRTTFEEQDGVPVQIVRAARNKOL	11217
ò	102		101
g	11218	RIIDVSGTEDAYLAALKQEQDAAFDLTAEPGWRVALLRLGPDDHVLSIVMHHIISDGWSV	11277
ò	102	,t,	103
q	11278	  DILRQELGQLYSNASSQPAPLPIQYRDFAIWQKQDSQIAEHQKQLNYWKRQLVNSKPAEL	11337
ò	104		103
<del>Q</del>	11338	LADFTRPKALSGDADVIPIEIDDQVYQNLRSFCRARHVTSFVALLAAFRAAHYRLTGAED	11397
ò	104		103
g	11398	<b>ATIGSPIANRNRPELEGLIGCFVNTQCLRIPVKSEDTFDTLVKQARETATEAQDNODVPF</b>	11457

ò	104	
; A	11458	FRIVSSMVASSEDTSENDI MANAGOUR CATAL BOLLONG CATAL
ò	112	TOTAL TOTAL
g	11518	EDOGMLGGNVVFSKDLFESETIRSVVAVFORTI RRGI ANDHANI ATT DI TROTTO DEI DOTO 1000 1000 1000 1000 1000 1000 1000 1
ò	112	
Q	11578	
ò	114	
q	11638	GSDT
ઠે	119	
qq	11698	
ò	120	GVT 122
g	11758	:   GITRLVKNSNVVAKQPAAAIAHLSNIAFDASSWEIYAPLLNGGTVVCIDYYTTIDIKAL 11817
ò	123	122
g	11818	EAVFKQHHIRGAMLPPALLKQCLVSAPTMISSLEILFAAGDRLSSQDAILARRAVGSGVY 11877
ò	123	122
q	11878	NAYGPTENTVLSTIHNIGENEAFSNGVPIGNAVSNSGAFVMDQNQQLVSAGVIGELVVTG 11937
ò	123	122
q	11938	DGLARGYTDSKLRVDRFIYITLDGNRVRAYRTGDRVRHRPKDGQIEFFGRMDQQIKIRGH 11997
ò	123	122
qq	11998	RIEPAEVEQALARDPAISDSAVITOLTDEEEPELVAFFSLKGNANGTNGVNGVSDQEKID 12057
ò	123	
ପ୍ଧ	12058	GDEQHALLMENKIRHNLQALLPTYMIPSRIIHVDQLPVNANGKIDRNELAVRAQATPRTS 12117
ò	123	122
g	12118	SVSTYVAPRNDIETIICKEFADILSVRVGITDNFFDLGGHSLIATKLAARLSRRLDTRVS 12177
ò	123	122
g	12178 \	VRDVFDTFVVGQLAASIQQGSTPHEAIPALSHSGPVQQSFAQGRLWFLDRFNLNAAWYIM 12237
ò	123	122
qq	12238	PFGVRLRGPLRVDALQTALRALEERHELLRTTFEEQDGVGMQIVHSPRMRDICVVDISGA 12297
ò	123 .	122
Q	12298 N	NEDLAKLKEEQQAPFNLSTEVAMRVALFKAGENHHILSIVMHHIISDGWSVDIFQQELAQ 12357
ò	123	122
q	12358 F	FYSVAVRGHDPLSQVKPLPIHYRDFAVWQRQDKQVAVHESQLQYWIEQLADSTPAEILSD 12417
ò	123 -	
g	12418 F	FNRPEVLSGEAGTVPIVIEDEVYEKLSLFCRNHQVTSFVVLLAAFRVAHYRLTGAEDATI 12477
ò	123 -	122
đ	12478 G	12478 GTPIANRNRPELEDLIGFFVNTQCMRIALEEHDNFLSVVRRVRSTAASAFENQDVPFERL 12537

ò	, 123	122
qa	12538	VSALLPGSRDASRNPLVQLMFVVHSQRNLGKLQLEGLEGEPTPYTATTRFDVEFHLFEQD 12597
ò	, 123	122
d d	12598	KGLAGNVVFAADLFEAATIRSVVEVFHEILRRGLDQPDIAISTWPLVDGLAALNSRNLPA 12657
ò	, 123	122
qq	12658	VEDIEPDFATEASVVDVFQTQVVANPDALAVTDTSTKLTYAELDQQSDHVAAWLSKQKLP 12717
ò	, 123	122
qq	12718	AESIVVVLAPRSSETIVACIGILKANLAYLPMDSNVPEARRQAILSEIPGEKFVLLGAGV 12777
ò	, 123	122
qa	12778	PIPDNKTADVRMVF1SDIVASKTDKSYSPGTRPSASSLAYVIFTSGSTGRPKGVMVEHRG 12837
٥٧	123	122
qq	12838	VISLVKQNASRIPQSLRMAHVSNLAFDASVWEIFTTLLNGGTLFCISYFTVLDSKALSAA 12897
ò	123	122
qq	12898	PSDHRINITLLPPALLKQCLADAPSVLSSLESLYIGGDRLDGADATKVKDLVKGKAYNAY 12957
ò	123	122
đ	12958	GPTENSVMSTIYTIEHETFANGVPIGTSLGPKSKAYIMDQDQQLVPAGVMGELVVAGDGL 13017
ò	123	122
qq	13018	ARGYTDPSLNTGRFIHITIDGKQVQAYRTGDRVRYRPRDYQIEFFGRLDQQIKIRGHRIE 13077
ò	123	122
qu	13078	PAEVEQALLSDSSINDAVVVSAQNKEGLEMVGYITTQAAQSVDKEEASNKVQEWEAHFDS 13137
ò	123	122
qa	13138	TAYANIGGIDRDALGQDFLSWTSMYDGSLIPREEMQEWLNDTMRSLLDNOPPGKVLEIGT 13197
ò	123	122
qa	13198	GTGMVLFNLGKVEGLQSYAGLEPSRSVTAWVNKAIETFPSLAGSARVHVGTAEDISSIDG 13257
ò	123	122
qq	13258	LRSDLVVINSVAQYFPSREYLAELTANLIRLPGVKRIFFGDMRTYATNKDFLVARAVHTL 13317
ò	123	122
ΩD	13318	GSNASKAMVRQQVAKLEDDEEELLVDPAFFTSLSDQFPDEIKHVEILPKRMAATNELSSY 13377
δ	123	122
qq	13378	RYAAVIHVGGHQMPNGEDEDKQWAVKDINPKAWVDFAGTRMDRQALLQLLQDRQRGDDVV 13437
ò	123	122
QO	13438	AVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAWISRTQSRAKECPALSVADLIEIGKG 13497
<b>6</b>	123	122
QQ	13498	IGFEVEASWARQHSQRGGLDAVFHRFEPPRHSGHVMFRFPTEHKGRSSSSLTNRPLHLLQ 13557
ò	123	122
qq	13558	SRRLEAKVRERLQSLLPPYMIPSRITLLDQMPLTSNGKVDRKKLARQARVIPRSAASTLD 13617
ò	123	35 C

Db 14698 NETEAAICDEFETILGVKVGIT 14719	RESULT 7	33NW6 PRELIMINARY;		01-JUN-2002 (TrEMBLrel. 21, Last annotati. AmphC.				RP SEQUENCE FROM N.A. RA Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., Oliynyk M.;		Submitted (MAR. EMBL; AF357202						Pfam, PF00 TIGREAMS:	PROSITE; PSS0075; ACP DOMAIN; 6. PROSITE: PS00059; ADH ZINC; UNKNOWN 1.	DR PROSITE; PS00606; B KETOACYL SYNTHASE; UNKNOWN 6. DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN 5.	Phosphopan SEQUENCE	Query Match 31.4%; Score 243;	ocal Similarity 1.1%; Pred	Oy 1 AAG3	Db 384 AAGVIKMIMAIQHGVLPRSLHAERPTSNVDWTAGAVELLDRAVDWPETGRARRAGVSSFG 443	Oy 4	Db 444 ISGTNAHLILEQAPTAPERPAPDPAARPALVPWTLSGRTAAALDAQRERLAAHLESHPGA 503	Qy 43	Db 504 DPLDIGFALADGRATFEHRAVLLCAGTDASAATEIAHGSVDDGASAVLFSGQGSQRLGMG 563	Oy 43	DD 564 RELHARFPVFAEAFDEIAALLDRHIDRPLREVVWGSDAELLNETGWTQPALFAVEVALYR 623	6 4 6дтипъ	:      D 624 LVSSLGVTPDYVGGHSIGEĮAAAHVAGVLSLEDACALVAARARLMQELPRGGAMLAVRAT 683	9 109	Db 684 EEEVAPHLTERVSIASVNGPSSVVVAGDEDEVAAIAAHFEAQDRKTTRLRVSHAFHSPLM 743	9 TO TO TO TO TO TO TO TO TO TO TO TO TO	Db 744 DPMLEEFRRVARGLTYHEPRIPVVSNLTGAIADPADLCTADYWVRHVREAVRFADGVTTL 803	
:    DD 13618 FVAPRTEIEVVLCEEFTDLLGVKVGITDNFFELGGHSLLATKLSARLSRRLDAGITVKQV 13677	Oy 127 126	Db 11678 FDQPVLADLAASILQGSSRHRSIPSLPYEGPVEQSFAQGRLWFLDQFNIDALWYLIPFAL 13737	Qy 127 126	Db 13738 RMRGPLQVDALAAALVALEERHESLRTTFEERDGVGIQVVQPLRTTKDIRIIDVSGMRDD 13797	Oy 127ACSPTW	Db 13798 DAYLEPLQKEQQTPFDLASEPGWRVALLKLGKDDHILSIVWHHIISDGWSTEVLQRELGQ 13857	Oy 133 132	Db 13858 FYLAAKSGKAPLSQVAPLPIQYRDFAVWQRQEEQVAESQRQLDYWKKQLADSSPAELLAD 13917	Qy 133 132	Db 13918 YTRPNVLSGEAGSVSFVINDSVYKSLVSFCRSRQVTTFTTLLAAFRAAHYRMTGSDDATI 13977	Qy 133 SÇLI 136	Db 13978 GTPIANRNRPELENLIGCFVNTQCMRITIGDDETFESLVQQVRSTTATAFENQDVPFERI 14037	Qy 137 TEDTGFDL 144	Db 14038 VSTLSAGSRDTSRNPLVQLLFAVHSQQGLGRIQLDGVVDEPVLSTVSTRFDLEFHAFQEA 14097	Oy 145 144	Db 14098 DRLNGSVMFATDLFQPETIQGFVAVVEEVLQRGLEQPQSPIATMPLAEGIAQLRDAGALQ 14157	Qy 145 144	Db 14158 MPKSDYPRNASLVDVFQQQAMASPSTVAVTDSTSKLTYAELDRLSDQAASYLRRQOLPAE 14217	Ογ 145 144	Db 14218 TMVAVLAPRSCETIIAFLAILKANLAYMPLDVNTPSARMEAIISSVPGRRLILVGSGVRH 14277	Qy 145 144	Db 14278 ADINVPNAKTMLISDTVTGTDAIGTPEPLVVRPSATSLAYVIFTSGSTGKPKGVMVEHRA 14337	Qy 145 144	Db 14338 IMRLVKDSNVVTHMPPATRMAHVTNIAFDVSLFEMCATLLNGGTLVCIDYLTLLDSTMLR 14397	Qy 145 144	Db 14398 ETFEREGVRAAIFPPALLRQCLVNMPDAIGMLEAVYVACDRFHSRDARATQALAGPRVYN 14457	- 144	Db 14458 AYGPTENAILSTIYNIDKHDPYVNGVPIGSAVSNSGAYVMDRNQQLLPPGVMGELVVTGE 14517	Qy 145 144	Db 14518 GVARGYTDASLDTDRFVTVTIDGQRQRAYRTGDRVRYRPKGFQIEFFGRLDQQAKIRGHR 14577	Oy 145 144	Db 14578 VELGEVEHALLSENSYTDAAVVLRTMEEEDPQLVAFVTTDHEYRSGSSNEEEDPYATQAA 14637	:	Db 14638 GDMRKRLRSLLPYYMVPSRVTILRQMPLNANGKVDRKDLARRAQMTPTASSSGPVHVAPR 14697	Oy 145	

ò	10	17	
g	804	:       AGRGVTTLLEVGPDGVLSAMAQESLPEGTTGVPLLRKDRPEEESALTGLARVHVRGLTVR 863	
ò	18	17	
g	864	WARLFDSAGAGRADLFTYPFQNQRVWPAAGRSARTSPAAGLGSADHPLLGAAVELADGEG 923	
ò	18	17	
g	924	FLFTSRLSVHSHPWLADHGVQAAPCVPGTAFVELAIRAGDEAGCDRVEELTLAAPLVLPE 983	
ò	18	17	
q	984	RGAVQLQVRVGAPDPAGRRTLGIFSRVEDGFDLPWSQHATGVLTTGAGAPDAAFDATVWP 1043	
ò	18	17	
g	1044	PAGAEQVDLDGCYERLAGLGFDYGPAFRALRAAWRRGTEVFAEVALSENAGTDPADFGLH 1103	
ò	18		
g	1104	PALLDAAQHAAAYNDLGAISRGGLPFAWEGVHLAASGATTVRARITSVGEDTVSIAVYDT 1163	
ò	18	VPQ	
g	1164	   AGGTVLSVDSLVSRAVPKDIPGTARAVHRDSLFQVDWTPLRSQSGQLPETVALVGADPAG 1223	
ò	21	- 20	
a	1224	LADTLRTGGVQVTVHPDLAALAADPAPVPGTVLTALPGDQDTPAADAAHTTAAAVLGLAQ 1283	
ò	21	34	
g	1284	HWLTEDRFADARLVLVTRDATAGGDLAAAAAGGLIRTARTENPGRFVLLDLATGTPAAPA 1343	
ò	35	. 34	
g	1344	ALVAALAAAYDEPDLAVRGSDVLTARLARVPAPDAGADWNPDGTVLITGGTGGLGGVLAR 1403	
ò	35	34	
g	1404	HLVTERGVRRLLLASRRGPAADGAPALVDELTALGASVDVAACDVTDREALAALLARVPA 1463	
ò	35	34	
g	1464	AHPLSAVVHTAGVVDDGVIGSLTAERLDTVLRPKADAAWHLHELTRDLDLDAFVLFSSVA 1523	
ò	35	34	
셤	1524	ATLGSPGQGNYAAGNAFLDALAAHRHALGLPATSLAWGPWTQSVGMTGTLSDIDVERIAR 1583	
ò	35	34	
g	1584	SGMPPLTVEQGVALFDAALATGGPALLPVRLDLAVLRTQGEIAPLLRGLIRTTVRRAAAQ 1643	
ò	35	96	
g	1644	VSVTADGLAQQLAGLDAAARREALLGLVRTQIAQVLGHADAGQVEAARQFQDLGFDSLTA 1703	
ò	35	34	
a	1704	VELRNĞLNSATGLRLPATMVFDYPTPNALADHLSDELLGTGDNIPLPTPAGALPATTDDP 1763	
ઠે	35	34	
g	1764	IVIVGMACRYPGGVTSPEDLWRLVSEGADATGPFPVNRGWDVDNLYDPDPDRPGHTYVRA 1823	
à	35	34	
qq	1824	GGFLHDAGSFDADFFGMSPREALSTDSQQRLLLELSWEAVERAGIDPHSLRGSRTGVFAG 1883	

ò	35		34
đ	1884	VMYNDYGTILTGEEYEAFRGNGSAPSVASGRVSYTLGLEGPAVTVDTACSSSLVGMHLAA	1943
ò	35		34
ପ୍ର	1944	QALRTGECTLALAGGVTVMSTPSTFVDFSRQRGLAADGRSKAFAEAADGVAWSEGVGMLL	2003
ò	35		34
đ	2004	LERRSDAIRNGHEILAVLRGSAVNQDGASNGLTAPNGPSQQRVIRQALASGGLSPEDVDV	2063
ò	35	DIN	37
g	2064	 VEAHGTGTTLGDPIEAQALIATYGRDREPERPLWLGSVKSNIGHTQAAAGVAGVIKMIMS	2123
ò	38		37
g	2124	MRHGLLPQTLHVDAPSSHVDWDAGAVELLTEQTEWPENDRVRRAAVSSFGISGTNAHVII	2183
ò	38	ABLURD	43
셤	2184	EQPAAGPAPAAPSGPAEELPAAPWPLSAKTPEALRDQAARLLAHVEAHPETRPADIAYSL	2243
ò	44		43
đ	2244	LTSRSVFDHRAAVLGADRTEALRALAALAAGTDDSALLTGTARGGRTAFLFSGQGSQRLG	2303
ò	44		43
d d	2304	MGRELYGRVPVFTEALDAVLAVLDGELEGSLREVMWGEDADLLNETGWTQPALFAVEVAL	2363
ò	4		43
<b>අ</b>	2364	YRLVESWGVKPDFVAGHSIGEIAAAHIAGVLTLADACRLVAARAALMQALPEGGAMIAVE	2423
ò	44		43
g	2424	ATEDEVLPLLTGDVSIAAVNGPSSVVVSGAEAAALAVAGHFTEQGRRTSRLRVSHAFHSP	2483
ò	44		43
q	2484	LMDPMLDEFRSVAEGLSYSAPAI PVVSNLTGTLADPADLCSADYWVRHVRDAVRFADCVG	2543
ò	44		43
g	2544	TLGEHGVTTFVELGPDGVLSAMAQOSVTEGAVTVPVLRKDRSEEQALVTALCRLYVLGID	2603
ò	4		43
셤	2604	ADWTSALTVGGAARVDLPTYAFQHRWFWPAARAAHPHDMRAAGLGSASHPLLGAAVELPG	2663
ò	4		43
qq	2664	GEGVLLTGRLSLQSHPWLADHAVHGTVLLPGTALLDLAIRAGDEAGCGHLEDLTLAAPLT	2723
ò	44		43
Q	2724	LPQDGAVLLQVRVGAADDAGRRTVTVHARPEDATDGVWTLHATGTLSDTAATGTALDTTV	2783
ò	44	-PSLGAQFR	51
g	2784	   PPRGAQALDTEGCYQRFAAHGFAYGPLFQGLTAAWKAGEALYAEIALPEEGHDDAAGFA	2843
ે જે	52	HA	53
q	2844	 VHPALLDAALHPALLTDDDGGLPFSWENVSLHASGATALRVRLAPAGANALSVTAADPAG	2903
ò	54		53
qq	2904	RPVVSIARLLARPVEADQLTGDAGHLRDALFRLEWTPVPLPDGTPTESLALLGPDTDDLA	2963
ò	54		53

ą	2964	<b>EALGEGAVRYATLADLLAADAPVPGAVLVPLTAGSDTDDTPGAVHTRTAAALTLLQEWLA</b>	3023
à	54		53
ą	3024	EDRFNGSRLVLVTRGAVATDDAPVTDLAAAALVGLVRSAQTENPGVFGFMDLDADGASDS	3083
à	54		53
ą	3084	ALTRALGLDEPQLALRGGRALAARLTRATADSTARVAWSSEGTVLVTGGTGGLGGLVARH	3143
à	54		53
g	3144	LVMERGVRRLLLTSRSGLGAAGAGDLVAELEGLGAEVSVAACDVADRDAVTALVAAVPAE	3203
à	54		53
a	3204	HPLVAVVHTAGVLDDGVLDSLTEERLATVLRPKVDGAWNLHEATRHLDLDAFVVFSSVAG	3263
ò	54		53
q	3264	VFGGAGQANYAAANAFLDALTAHRHALGLPAVSLAWGPWQQGAGMTAGLDERDIRRAAES	3323
ò	54		53
셤	3324	GMPLITVEQGLALFDAALTTDEAALVTSRLDLAAFRGRPEIPALLRGLIRTPVRRAAATG	3383
ò	54		53
g	3384	AADGADAGLVQRLAGLDREQRHEVLLDLVRTSAALVLGHAAGSDIDADRAFRDLGFDSLT	3443
ò	54		53
g	3444	AVELRNRLRTATGLRLSATMVFDHPTLSALADHLLTELFGAEAETLTPVTLLPPTDDDPI	3503
ò	54		53
ρp	3504	VIVGWACRFPGDVTSPEDLWRLVSEGTDAISDFPANRGWDVDSLYHPDPEHSGTSYTRSG	3563
·\$	54		53
q	3564	I GFLHDAGDFDPPFFGMSPREALATDSQQRLLLETSWEAIERAGIDPLSLRDSRTGVFAGV	3623
ò	54		53
q	3624	I MYHDYGSLLGGKEFEGFQGGSAGSVASGRVSYTFGFEGPAVTVDTACSSSLVALHWAAQ	3683
ò	54		53
QQ	3684	ALRSGECSLALAGGVTVMSTPSTFIEFSRQQGLSADGRSKAFAESADGVGWSEGVGMLLL	3743
ò	54		53
q	3744	1 ERQSDAIRNGHEILAVVRGSAVNQDGASNGLTAPNGPSQQRVIRQALASGGLSTGDVDAV	3803
ò	Ω 4.	DXXM	57
g	3804	4 EAHGTGTTLGDP1EAQALIATYGQNRTDEQPLWLGSLKSNIGHTQAAAGVAGVIKWVSM	3863
ò	58	T11A	61
g	3864	4 RHGVLPCTLHVDAPSSHVDWTEGAVELLTEQTEWPETDRVRRAAVSSFGISGTNAHVILE	3923
ò	62	2 BPEGAP	67
g	3924		
ò	68		67
g	3984	4 TSRSAFDHRAVVLATGREDALRALTALADDEANSAAVTGRTRSGRRAALFSGQGSQRLGM	1 4043
ò	68	6	67

qq	4044 GF	GRELYGRFPVFAEALDAVLAVLDGELEGSLREVMWGEDAGLLNETGWTOPALFAVEVALY 4103
ò	. 89	
g	4104 RI	rlveswgvrpdfvaghsigeiaaahiagvfsledaarlvaargrlmoalpaggamvavOa 4163
ò	- 89	29
qq	4164 T)	TEDEVIPYLSDEVSIAALNGPASVVVSGAEGAVLEVAARFEAEGRKATMLRVSHAFHSPL 4223
ò	89	
qq	4224 M	MDLMLDEFRAVAETLSFAAPVIPVVSNILTGSLATAEELCSPEYWVRHVREAVRFADGVSA 4283
ò	- 87	
Ор	4284 L	LEAOGVTTFLELGPDGVLSAMAQESLTGDEAVTVALLRKDRDEETAALTALAALHTAGVR 4343
ò	78 -	77
g	4344 L	LDWNAFFAGTGATRVDLPTYAFQHTTYWPSGTHSAADAAAVGLTAAGHPLLNGSVQLAEG 4403
ò	78 -	
g	4404 E	EGVLFTGRLSLQSHPWLADHAVHGTVLLPGTALLDLAFRAGDEVGCDRVEELTLAAPLVL 4463
ò	78 -	
đ	4464 P	PERGAVQTQVRVGVADDTGRRTVTVHSRPEDATDVSWTQHATGTLMPGGTARDTGFDATV 4523
ò	- 84	77
g	4524 W	WPPTGAEALDTEGCYERFTALGFGYGPVFQGLKAAWRSGDVLYAEVVLQEAGAADDEAGF 4583
ò	78 -	10.71
q	4584 G	GLHPALLDAALHASLVAHEGEEGNGGLPFAWEGAVLHATGATALRVRLTPTDEARQSVAI 4643
ò	79 8	SVÇ
- <u>6</u>	4644 P	:   avcdtag@pvasidrllvravtgdQlneaagiardalfalG#tplpQdgdipaavalvGP 4703
ò	84	83
q	4704	DITGLAADLIAAGAAVTAHQDLAALAADGTDIPGTVVVTVDGTAAPVAEAAHTVAAEALA 4763
ò	84 -	83
<u>8</u>	4764 I	LAORWTAEDRFAGARLVFATCGAVEAGGSQVTDVAAAAVWGLVRSAQSESPDTFVLVDRE 4823
ò	84	83
g	4824 7	aadaagdaaergslflaalgsgepqlalrddvvlagrlarfdaagawtlpaerawhldst 4883
ò	. 84	
q	4884	TPGSINGLALTPHPEALEPLTGHQARIEVRAAGLNPRDVLKALGMYPGDAGRYGHEAAGV 4943
ò	84	83
đ	4944	VVEVGPDVTHIAPGDRVMGMVSGSFASFAVTDARRLTHLPEQCTWEIGASLPLVFLTAYH 5003
ò	84	
g	5004	ALKELGGLTAGEKVLIHAGAGGVGWAAIQIARHFGAEVFATASEAKMDVLRSLGVADDHI 5063
ò	84	
q	5064	ASSRILDFEAAFAAVAGENGLDVVLNSLAGEFVDASMRLLGTGGRFLEMGKTDIREDDSV 5123
ò	88	8
q	5124	PDGITYQSFDLAFVDPEVIGAMGRELTELFAAGDLHPLPVRAWDIRHATDAFRHMSMARH 5183

>-	88	8	
Д	5184	IGKIVLTVPRAMSSEGTVLVTGGTGGLGGLVARHLVMERGVRRLLLTSRSGLDAAGAREL 5243	
>-	88	8.1	
۵	5244	VAELENLGAEVSVAACDVADRDAVDTLIAGIPAEHPLRAVVHTAGVLDDGVLGSLTEERL 5303	
≽	88	8	
۵	5304	ATVLRPKVDGAWNLHEATRRLDLDAFVVFSSVAGVFGGAGQANYAAGNAFLDALTAHRQS 5363	
<u>≯</u>	88	8.	
ā	5364	LGLPGLSLAMGAWAQGAGMTAGLDERDIRRAAESGMPLITVEQGLALLDTALTTGSAALV 5423	
≿	88		
ā	5424	PVRLDLAVLRARGTVAPLMRGLVRAPARRAAATAATGDTALVDRLTRLQRTERRDALLTL 5483	
≿	88	87	
ą	5484	VREQAALVLGHSGGGGIDPSRAFRDLGFDSLTAVELRNRLGAATGVRLSATAVFDYPTVV 5543	
≿	88	91	
۾	5544	ALVDHLLTELLGPDAESDAEEAAPAEALLDDDPIVIVGMACRFPGGITSPEDLWRLLGEG 5603	
≿	92	98	
Ď	5604	SDVISDFPVNRGWDVDSLYDPDPAHTGTSYTRSGGFLHNAADFDADFFGMSPREAMATDS 5663	
≿	6	86	
ą	5664	QQRLLLESTWEAIERAGIDPVTLRGSRTGVFAGVMYSGYGTALDGDEFEGFQGQGSALSV 5723	
≿	66	86	
ą	5724	ASGRVSYTFGFEGPAMTIDTACSSALVAMHLAAQALRSGECSLALAGGVTVMSIPDTFVE 5783	
≿	66	86	
ą	5784	FSRQRGLSPDGRCKPFSESADGVGWSEGVGMLLLERQSDAIRNGHRVLAVVRGSAVNQDG 5843	
à	66	86	
ą	5844	ASNGLTAPNGPSQQRVIRQALASGGLSTGDVDAVEAHGTGTTLGDPIEAQALLATYGQNR 5903	
≿	66	86	
ą	5904	PEDRPLLLGSVKSNIGHTQAAAGAAGVIKMVMAMQHGVLPRSLNISEPSSHVDWSAGAVE 5963	
⋩	66	86	
ą	5964	LLTEQTEWPETDRVRRAGVSSFGISGTNAHVILEQPAKVIQGTVVAASAAPGPDVVEPAV 6023	
ጵ	6 6	86	
g	6024	VPWVLSGKTPEALRDQAARLLATVTEEPAPRPVDVALSLATQRSQFAHRGVVLAGEHEET 6083	
à	66	86	
q	6084	VRALAALADGEPHSSVTTGTVSSGRRAALFSGQGSQRLGMGRELYGRFPVFAEALDAVLA 6143	
à	66	86	
ą	6144	VLDGELGGSLREVMWGEDAGLLNETGWTQPALFAVEVALYRLVESWGVRPDFVAGHSIGE 6203	
ò	66	86	
a	6204	IAAAHIAGVFSLEDAARLVAARGRLMQALPAGGAMVAVQATEDEVVPHLSDGVSIAALNG 6263	

ò	STATEMENT TO THE PROPERTY OF T
q	6264 PTSVVVSGVEDAVLEVAARFEAEGRKTTRLRVSHAFHSPLMDPMLDEFRAVAEGLSFAAP 6323
ò	111
Q	6324 VIPVVSNLTGSLATAEELCSPEYWVRHVREAVRFADGVAALEAOGVTTFLELGPDGVLSA 6383
ò	111
q	6384 MAQESLTGDETVTIPLLRKDRDEETAALTALGRLHATGTRVDWAGFLAPAGARTVDLPTY 6443
ò	111
đ.	6444 AFQHRPFWPSGKRGATDVNSVGITAAAHPLLNAVVELAEGEGLVFTGRLSLNSHTWLADH 6503
ò	111
q	6504 AVMGTVLLPGTALLELALRAGDEVGCDHVEELTLAAPLVLTEQGAVRTQVRVGAEDAAGR 6563
ò	111 110
g	6564 RTVIIHSRPERSTDAPWTQHATGVLATGLPTAAAPFDATVWPPADAEPVDLTGFYEAREA 6623
ò	111 114
QQ	6624 EGFAYGQAFQGLKAAWRRGDEVFAEITLPDGTQKEAESFGLHPALLDAGLHAAWLAAPTG 6683
ò	115 114
g	6684 DGTTGSVPFSWNGVSLVASGASSVRVRLGRDTDGTLTLAVADTTGAPVAAVQALTMRAVS 6743
ò	115 114
g	6744 AEALSSAAALVRDSLFRLDWTPVTPAGSAEPTAALVGEDPFGLVRSLREAGTEIGRRASL 6803
ò	115118118
g	6804 TDDAELPDLLLLPVTAEEHEEAADTPAVTHALTRQVLELVRARLEDERHAATRRVFVTRG 6863
ò	119 118
q	6864 ATTGHDLAAAAVWGLVRSAQSENPGCFGLIDLDPETTRPLPLTALLGDEPQLRLQDDDLR 6923
ò	119 124
QQ	6924 AARLVRRPAPATDAVSAFGGEGAVLVTGGTGGLGAVLARHLVAEHGVRELVLVSRRGGAA 6983
ò	125
Ω	6984 AGAAELVAELAESGARATVVACDVTDRAAVAELVAAHPVSAVVHSAGVLDDGLIASLTPE 7043
ò	125 124
đ	7044 RLSGVLRPKVDAAMNLHEATRDLDLDAFVVFSSVAGVFGNAGQANYAAGNAFLDALMEHR 7103
ò	125 124
셤	7104 RAAGLPGLSLAWGPWEQTGTGGMTGTLSDAELERLASSGVPPLAVEQGLALFDAALSTED 7163
ò	125 124
Q	7164 AALVPVRLDLPALRGQGEVPPLLRSLIRARSRRAAVAGSATATGLRDRLAVLDAVERREV 7223
·ờ	125 124
g	7224 LVDLVRGQVALVLGHADATAVHPTRAFRDLGFDSLTSVELRNRLNAVTGLRLPATMVFDY 7283
ò	125 124
q	7284 PTVEVLVDFILDELLGTEVEAEVVQRGTAAVADDPIVIVGMACRYPGGVASPEDLWRLVT 7343
ò	125 124

s qid\_1\_15fused.rspt

		Db 8424 ADGGTAGLPFSWTDVSLHASGATVLRVRLTPTGDRTLSLSAVDPSGTPVVSVGSLVTRSV 8483
q	7344 EGTDAVSAFPVNRGWDVENLYHPDPDNIGTSYTRSGGFLHEAGEFDPGFFGMSPREALST 7403	
ò	125 124	ω.
q	7404 DSQQRLLLETSWEAIERAGIDPVGLRGSATGVFAGVMYSDYSAMLASPEFEGFQGGGSSP 7463	136
ò	125 124	ω
අ	7464 SVASGRVSYTFGFEGPAVTVDTACSSSLVAMHWAMQALRSGEISLALAGGVTVMSTPGVF 7523	09 136 135
ò	125 124	Db 8604 RLVFVTRGAVDTRDLGAAAVQGLVRSAQTENPGALGLVDLDGTPESAAALAAALGSAEPQ 8663
qq	7524 VDFARQRGLSPDGRCKAFSDSADGVGWSEGVGMLVLERQSDAIRNGHEILAVVRGSAVNQ 7583	Qy 136 135
ò	125 124	Db 8664 LALRDGRPHAARLARLARPADTAAPTAWQSDGTVLVTGGTGGLGAQFARHLVDAYGVRNL 8723
qq	7584 DGASNGLTAPNGPSQQRVIRQALASGGLSAQEIDVVEAHGTGTTLGDPIEAQALLATYGR 7643	Ογ 136 135
ò	125 124	Db 8724 LLVSRRGGDAPGTTELVAELIAHGAEVTVQACDVADPDAVTALVAGIPAEHPLTAVVHTA 8783
qq	7644 DRDPEQPLWLGSVKSNIGHTQAAAGVAGVIKMVMSMRHGVLPRTLHVDAPSSHVDWTEGA 7703	Ογ 136 135
ò	125 124	DD 8784 GVLDDGVIGSLTGERLARVLRPKADAAWNLHQATRGLDLDAFIVFSSVAGVFGGAGOANY 8843
qq	7104 VELLTEQTEWPETEHVRRAGVSSFGISGTNAHVILEQPAKVIQGTVIGGSTPESGVVEPS 7763	Qy 136 138 138
ò	125 124	DD 8844 AAGNAFLDALMEHRRAAGLPGLSLAWGPWDQAGGMTETLSDAEAERLARAGMPPLAAEQG 8903
g	7764 VVPWVLSGKTPEALRSQAAKLLASVEAELDRPLVDVGSSLVAARSLFEHRAVVLATDADT 7823	ον 139 138
ò	125 124	Db 8904 FALFDAALAAGNGTGTGSEDTTGTALVVPVRLDLAALAAQGEVPAVLRGLVRTRRTVA 8963
q	7824 AARALAALAVGEPDPAAVSGPARTGRSAALFSGQGSQRLGMGRELYGRFPVFAEALDAVL 7883	Qy 139
ò	125 124	Db 8964 GGTVTADGLVARLTALTAEERREALLGLVRTQAALVLGHADAASVDAAAQFRDVGFÖSLT 9023
g	7884 AVLDGELDGSLREVMWGEDAGLLNETGWTQPALFAVEVALHRLVESFGVTPDFVAGHSIG 7943	ον 145 144
ò	125 127	Db 9024 AVELRNRLSAATGLRLTATLVFDYPNAATLASHLHDELFGAETESALALFVKQLPATTDD 9083
g	7944 EIAAAHIAGVESLEDAARLVAARGRLMQALPAGGAMVAVQATEDEVIPYLSDEVSIAALN 8003	Ογ 145
ò	128 127	Db 9084 PIVIVGMACRYPGGVASPEDLWRLLLEGTDAITEFPVNRGWDIESVYHPDPEHLGTSYTR 9143
qq	8004 GPASVVVSGAEGAVLEVAARFEAEGRKATMLRVSHAFHSPLMDPMLDEFRAVAEGLSFAA 8063	09 145
ò	128 130	9144 SGGFLHEAGEFDPGFFGMSPREALATDSQQRLLLESSWEAIERAGIDPVC
Q	8064 PVIPVVSNLTGSLATAEELCSPEYWVRHVREAVRFADGVTTLEEGGVTTFLELGPDGVLS 8123	Oy 145 144
ò	131 135	Db 9204 GVMYSDYGSILGGKEFEGLQGGSAGSVASGRVSYTFGFEGPAVTVDTACSSSLVAMHLA 9263
q	8124 AMAQESLIGDEAVTVPLLRKNIAEEAATVAALARLHIGGLRIDMSALFAGTGARRVELPT 8183	Qy 145GVTI 148
ò	136 135	Db 9264 AQALRTGECSLALACGVTV 9282
g	8184 YAFQHQWFWPAAPLGGGDVRAAGLGSAEHPLLGAAVELAAGEGVLFTGRLALHSHPWLAD 8243	
ò	136 135	SULT 8
q	8244 HTVDGTVLLPGTALLELAIRAGDEVGSDQVEELTITAPLVLPERGAVQVQVAVEAPDAAG 8303	D93NX9 PRELIMINARY;
ò	136 135	01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence up
g	8304 RRVVGVYARPEGTGDTAWSQHAAGVLAPAGSRPAPAFDTAVWPPEGAQAVDADGCYEEF 8363	01-JUN-2002 (TrEMBLrel. 21, Last Amphl.
ò		
g	8364 AAAGFGYGPLFQGLRAAWRRGDEWFAEVALPEGTENTAAGFGLHPALFDSALHALLLTPA 8423	OC Bacteria; Firmicutes; Actinobacteria, Actinobacteria; Streptomyces.
ò	136	

RA E	SEQUENCE FROM N.A. Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., Ollynyk M.; Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., Ollynyk M.; "The amphotenticin blosynchetic gene cluster from Streptomyces	a &
RT	osus."; mitted (MAR-2001) to the EMBL/GenBank/DDBJ dat	qa —
888	EMBL; AF357202; AAK73501.1; InterPro; IPR001227; Ac Transferase. InterPro: IPR002198; ADH short.	ò
888	IPR004410; Fabb. IPR001899; Gram po	a :
R G		÷ =
2 2	Pro; IPR003880; Ppantne PF00698; Acyl_transf;	3 8
2 2 2	Pfam; PF00106; adh short; 1. Pfam; PF00109; ketoacyl-synt; 6. neo neo-con; ketoacyl-synt; 6.	<b>a</b>
2 2 2	2801; Xeccacy1-8ync-c, 0550; pp-binding; 6. TIGR00128; fabD; 6.	ò
88	PSS0075; ACP DOMAIN; 6. PS00606; B KETOACYL SYNTHASE;	qa
888	GRAM POS ANCHORING; UNKNOWN MYB 1; UNKNOWN 1 PHOSPHOPANTETHEINE; UNKNOWN	ે દ
S &	Phosphopantetheine. SEQUENCE 9510 Aa; 992817 MW; 1A8E003A1SD478CF CRC64;	8 8
ÓΜ̈́	ry Match 31.2%; Score 241; DB 2; Length 9510; t Local Similarity 1.0%; Pred. No. 18;	8 8
Σ	95; Conservative 18; Mismatches 31; inders 310; daps	ò
දි දි		a 8
ò	4.	; A
qq	148 AMAQDYRVGPADGAEGFQLTGNTGSVLSGRISYTFGTVGPAVTVDTACSSSLVAVHLATQ 207	i ò
ò	6	qq
q	208 ALRAGECTLALAGGVTVVMSGPGTFIEMGRQGGLSVDGRCRSFGDTADGTGWAEGVGILVL 267	ò
ò		qq
g	268 ERLSDAIRNGREILAVVRGTAVNQDGASNGLTAFNGPSQQAVIEQALVNARLSAGDIDVV 327	λŏ
ò	L	qq
q	328 EAHGTGTTLGDPVEAQALLATYGQQRDEDKPLLLGSVKSNISHTQAAAGVAGVIKMVMAM 387	ò
ò		qa
g	388 RHGVLPRTLLADEPTRHVDWSQGAVRVLTENTEWPATGAPRRAAVSSFGISGTNAHTIVE 447	٥٥
ò	2	qa
q	448 QAPEPEPADPEDDAPSTPAAVTGVLPVLLSGRSPEVLRAQAAALLTTLGTGTPPAPADLA 507	ò
ò	L	q
q	508 YSLATTRTAFEHRAVLLASDLPELTGRLTAIAEGTDPAVLADTVTGTARTETRLAVLFTG 567	ò
ò		q <sub>Q</sub>
đ	568 QGAQRLGAGRELAARFPVFAAALDAALDAFTPHLDVPLRKVLWGEDADRLDRTEYAQPAL 627	ò
ò		q
g	628 FAVEVALYRLLESPEVKPDHLAGHSVGEIAAAHVAGVFSLDDAATLVAARGRLMQALPEG 687	ò
ò	2	<b>q</b> 0

qq	688 GAMVAVQASEDEVAPLLAGHEDLVSLAAVNGPSAVVLSGDETTVTELAARLAADGRKTSR 7	747
ò	80	,
d	748 LRVSHAFHSPLMAPMLDEFRNVVEGLTLHSPLLPVVSDVTGEPATVAQLTSPDYWVDHVR	807
ò	8	4
g	808 QAVRFADGIDWLARHDVTAFLELGPDSVLSAMAQNCLDAAGSDALTVPALREGRPEDHTF (	867
ò	80	4
qq	868 TAALAALHTQGTALHWDACFTGTGARRTDLPTYTFQRRRYWPRAVQGGAADLRSVGLGAA	927
ò	8	12
q	928 HHPLLSAAVSLADSEGALLTGRISLLSHPWLADHTVRGATLLPGTAFLELAVRAGDEVGC	987
ò	13	12
οg	988 DRVDELTLAAPLVLPEQGGVQVQLWIGNPDASGRRSVTVYGRPDADEDAPWTSHATGVLS	1047
ò	13	12
q	1048 ASRTTSDFDATVWPPADAETLPVDGLYERLAEGGFGYGPLFQGLRAAWRRGDEVFAEVVL	1107
ò		12
g	1108 PESGHTDAESFGLHPALLDSALHAASFVDLDERAAGGLPFSWEGVSLHASGATTLRVRLA	1167
ò	13	12
qq	1168 PAAGDAVAIAVADDSGQLVLSADSLILRAVAAREIDAAAALVRDALFRLDWVPVTAVAAS	1227
ò	13	12
q	1228 GTAAALVGEDPFGLRALPQFGDLAVHPDLADLAAAADGAVPDTVLLPLTGTGPDADPVTAA	1287
ò	13	12
qq	1288 HRAATEALAAVRTWLEQDERFAASRLALVTRGATTGHDPAAAAVWGLVRSAQSENPGRFL	1347
ò	13	12
qq	1348 LVDLDADQDTPALPAAALTSEEPQLAVRGEELRAARLVRRPASTAEAVPAFGGEGAVLVT	1407
ò	13	12
g	1408 GGTGGLGAVLARHLVAEHGVRELVLVSRRGGAAAGAAELVAELAESGARATVVACDVTDR	1467
ò	13	12
q	1468 AAVAELVAAHPVSAVVHSAGVLDDGMVGTLTPERLTTVLRPKVDAAMNLHEATRDLDLKA	1527
ò	13AVGP	16
qq	1528 FVLFSSVAGVLGSPGQANYAAGNAFLDALAAHRRAAGLPGLSLÄWGPWEQTGGMTGGISE	1587
ò	17	16
qq	1588 DDLRRMARAGTPALIVEQGLALLDAALDGDDAALAPVRLDLSVLRAQGEVPPLLRSLIRG	1647
ò	17	16
qq	1648 RSRRAAVAGSATAGGLAQRLARLDAESRDELVLDLVRGQVALVLGHATGAEIDAGRAFRE	1707
ò	17	16
g	1708 LGFDSLTAVELRNRLNTVTGLRLPATLVFDYPTVSHLASYVLDELLGTEVEAEVVQRGTA	1767
ò	17	16
qq	1768 AVADDPIVIVGMACRYPGGVTSPEDLWRLVTEGTDAVSGFPVNRGWDVENLYHPDPDHPG	1827

ò	17	
a	1828	TAYTRSGGFLHEAGEFDPGFFGMSPREALATDSQQRLLLEASWEAIERAGIDPVGLRGSA 1887
ò	17	16
QQ	1888	TGVFAGVMYSDYSAMLGSPEFEGFQGSGSSPSLASGRVSYTLGLEGPAVTVDTACSSSLV 1947
ò	17	
Op	1948	AMHWAMQALRSGEISLALAGGUTVMSTPAVFVDFARQRGLSPDGRCKAFSDSADGVGWSE 2007
ò	11	16
g	2008	GVGMLVLERQSDAIRNGHQILAÅVRGSAVNQDGASNGLTAPNGPSQQRVIRQALASGGLS 2067
ò	17	DVFQAH 22
g	2068	AGDVDVVEAHGTGTTLGDP1EAQALLATYGRDRDPEQPLLLGSVKSNIGHTQAAAGVAGV 2127
ò	23	
임	2128	IKMVMSMRHGVLPRTLHVDAPSSHVDWTEGAVELLTEQTAWPETGRPRRAAVSSFGISGT 2187
ò	23	22
QQ	2188	NVHTVLEQAPGTTVPAPAAPERTAGAVPLLLSGRTRDALRAQAARLLTHLQNHPEPSLAD 2247
ò	23	
g	2248	LGHSLATTRSRFERRAAVIAQDREGLLASLGSLAAGRPDPAVVEGEAAGRARVAVMFSGQ 2307
ò	23	22
g	2308	GSQRAAMGRELYETQPRFAAAFDEVCAALDPLLDRPLREVVFAAEGSEEAALLDRTGWTQ 2367
ò	23	22
පු	2368	PALFAVEVALYRLVESWGVRADFVTGHSIGEIAAAHIAGVFTLQDAARLVAARATLMEAL 2427
ò	23	22
g	2428	PSGGAMVAVQATEEEVAPLLGEGLSVAAVNGPTSVVVSGDEDPAVELAAEFSGRGRRTKR 2487
ò	23	. 22
qq	2488	LRVSHAFHSPHMDAMLDAFRTVAETLSYAAPRIPLVSDLTGRRADDAEVRTADYWVRHVR 2547
ò	23	OEDT
q	2548	EAVRFADCVRTLRDAGATLFLELGPDGLLTAMAEDTLGDERYDHNTALVPLLRADRPEES 2607
ò	30	
8	2608	AAATAAARLQIHGVDLDWTAYLAGTGARRVDLPTYAFQHAHYWPQLPSAAPSPAGDPADQ 2667
ò	30	29
qq	2668	KLWAAVERGDAAELAAVLGLDEDSLTPLDSLLPALSSWRRGNQEKALLDTLRYRVEWTRL 2727
ò	30	29
ద	2728	SKPAAPVLDGTWLLVSSDATADDETELLDGLAEALGAHGARVRRLVLDADCADRAVLGAR 2787
ò	30	
g G	2788	LADTENADNTAQVLSVLPLDERPTDGPAGFTQGLALTIALVQALADTGAHGRLWTATRGA 2847
ò	30	
g	2848	VSTGPADPVTHPAQATAWGMGRGVALEHPRLWGGLVDLPADFDRGAGQRLAEVLAVKDAP 2907

ò	30	53
В	2908	DGEDQVALRATGVHGRRLVRHIVDELPSADQFTASGSVLITGGTGGLGAETARWLARSGA 2967
ò	30	29
QC	2968	AHLVLTSRRGPDAPGAAELRAELEQSGASVSIVACDVADRDALAAVLDGLSADQPLTGVV 3027
ò	30	29
q	3028	HTAGVGHYGPLDALTPAEFAGLTAAKLAGAAHLDNLLGDRELDFFILFGSIAGVWGSGDQ 3087
ò	30	56
đ	3088	SAYGAANAYLDALALARRARGLAATSIAWGPWGGTGMAADDAVSGTLRRQGLGLLDPAPA 3147
ò	30	
đ	3148	LTEMRRAVVRQDVTVTVADVDWTRYAPLFTSARPSALISDLPEVRALAAENTPADTGDAS 3207
ò	. 30	34
q	3208	EIVORVRSLSEPEQLRLLTDLVRTEAATVLGHSSAGAVPEDRAFRBIGFDSLTAVELRKH 3267
ò	35	34
g	3268	LGAATGLSLPSTWVFDYPTPLELAQYLRAEWVGSVLEVAGPVATGGTDDEPIAIIGMSCR 3327
ò	35	34
a	3328	YPGGVSSPEQLWDLVLSGTDAITDFPVNRGWNTAGLYDPDPDHPGTTYSTQGGFLHEADE 3387
ò	35	34
q	3388	FDPMFFGISPREALVMDPQQRLLLETTWEAFERAGLTPDTLRGSLTGTFIGSSYQEYGMG 3447
ò	35	34
qq	3448	AGDGAEGHLVTGTSPSVLSGRLAYVFGLEGPAVTVDTACSSSLVALHLACQALRNGESNL 3507
ò	35	34
đ	3508	AVAGGATVMTTPNAFVAFSRQRALAQDGRCKAFSESADGMTLAEGVGIVLVERLSDARRN 3567
ò	35	34
q	3568	GHPVLAVIRGSAINQDGASNGLSAPNGPSQORVIRQALANARVAPGEIDLLEAHGTGTPL 3627
ò	35	37
qq	3628	GDP1EAQALFATYGRTRTPETALLLGSVKSNIGHSQSAAGVAS11KMVMALRHGVMPQTL
ò	38	37
g	3688	HADEPSSHVDWSPGTVRLLGENTDWPQTGRPRRAAVSSFGISGTNAHVILEQETEAPAAE 3747
ò	38	•
අු	3748	DEQLAPAPLPVAAGVVPWLLSARGAAALREQADRLLTHLVTADPAARPIDIGLSLATSRA 3807
ò	38	37
qq	3808	LFEHRAVVVPPAGTDPLEALRAVAADGPSGVVARGVADVAGRTVFVFPGQGSQWAGMGAQ 3867
ò	38	37
q	3868	LLDESPVFAERIAECAAALAEFTDWNLIDVLRGAEGAPTLERVDVVQPASFAVMVSLAAV
ò	38	
q	3928	wraqgvepdavvghsqgeiaaavvsgalslrdgarvvtiraqaigrslagrggmmsvalp
ò	38	37

54		55	ò
5067	) VSYLFGLEGPAVTLDTACSSSLVAIĤĽACQSLRNGESTLALAGGASIMSTPMSFIGFSRQ	5008	අ
54	- NHL	52	ò
5007	LETAMEVFENAGLDPVAQRGSRTGTFIGASYQDYGAAVPGSEGSEGHMITGSLPSVLSGR	4948	8
51	LGAQFR	46	ò
4947	VFPADRGWDAEALYDPDPDASGRTYSVQGGFLRDVADFDPGFFGISPREALSMDPQQRLL	4888	a
45	1 1 1 1	38	ò
4887	GFLHSELADVHSAGAVAVTAGAPVDDDP1AIVGMSCRYPGGITSAEQLWRVSLEEVDAVS	4828	g
37		38	ò
4827	EAASVLGLSSAEDLTDQRAFRDVGFDSLTAVGLRNRLASVTGLTLPSTWVFDYPNPAALA	4768	g
37		38	ઠે
4767	HPVYTSARPTPLFDEVPEVQRLTAAAEQSAGDPARGEFAAALLALPAAEQHRKLLETVRT	4708	g
37		38	ò
4707	LSLSWGIWADDLQLGRVDPQMIRRSGLEFMDPQLALSGLKRALDDDEQVIAVADVDWETY	4648	g
37		38	ò
4647	AKVTGAQILDELLDDEELDDFVLYSSTAGMWGSGAHAAYVAGNAYLAALAEHRRARGLTA	4588	g
37		38	ò
4587	RGTETTLAACDITDRDAVAALLESLKAEGRTVRTVVHTAATIELHTLDATTLDDFÖRVLA	4528	g
37		38	ò
4527	DGSARDWKPRGTTLVTGGSGTLAPHLARWLAEQGAEHLVLVSRRGPEAPGAAELRAELAE	4468	Q
37		38	ò
4467	AALECPGRWGGVVDLPETLDARAGQRLAAVLAGALGDDDQIALRSSGVFTRRIVRADAAP	4408	6
37		38	ò
4407	AVPGTGLVLGVALTVALVQALGDAGIDTPLWALTRGAVSTGRSDKVTAPVQAQVTGIGWT	4348	g
37		38	ò
4347	SADGVDDTDVAEALETGGAEVRRLVLDESCTDRAVLRERLTDADGLTGIVSVLAGAERTG	4288	g
37		38	ò
4287	ALTAALGIDEDSVAAVLPALSSWRRARKERSTVDSWRYRPTWKPVTKLPQRTLDGTWLLV	4228	g
37		38	ò
4227	GVQVDWAAVFEGTGASRVDLPTYAFQHENLWAMAAAPEAVTAADPEDAAFWTAVEDGDVS	4168	8
37		38	ò
4167	DLIAADHRAFIEVSSHPVLAMSVQDMIDDAGVAGVASGTLRRDNGGLDRFLLSAAEVFVR	4108	a
37		38	Ś
4107	PHVEDLHDEILELLAEVAPRTSEIPFFSTVTGDWLDTTVMDAGYWYRSLRGRVLFADAVR	4048	a
37		38	ò
4047	VAEVEARLEAFEGRVSVAAENGPRSSVVAGEPEALDELHAQLTAEEIRARRVAVDYASHS	3988	g

q	5068	RALAEDGRCKAYAEGADGMTLAEGVGLILLERLSDARRNGHEVLAVIRGSAVNQDGASNG 5127
ò	55	95
g	5128	LTAPNGPSQQRVIRQALANAGVEANDIDVLEGHGTGTALGDPIEAQALFATYGKDRDPER 5187
ò	55	VXMV
QQ	5188	PVLLGSVKSNIGHTQMASGVASIIKLVHALREGVAPKSLHIDQPSTHVDWSSGTIQLLTE 5247
ò	63	9
QQ	5248	RTEWPETGRPRRAAVSSFGLSGTNVHTVLEQAPAADAPAAEDTPAPRDALVPVLVSGRGE 5107
ò	63	62
q	5308	AALRAQAGALLDLLAERPGIHPTDLAFSLATSRAALEHRAAVVADDHEALVRGLTALRDG 5367
ò	63	62
q	5368	LPGAGLVQGRTGRGRTAFLFTGQGSQRLGMGRELYERHPVFADALDAVLARIDGTTBRPL 5427
ò	63	62
QQ	5428	RDVLFAAEGSQDAALLHRTGYAQPALFALEVALFRLLESWGVTPDYLAGHSVGBIAAAHV 5487
ò	63	65 65G 65
g	5488	AGVLDLDDACTLVAARGRLMQALPEGGAMVALEAAEDEVLPHLEGLADQVSVAAVNGPRS 5547
ò	99	69 - IN48
QQ	5548	VVVAGEEEPVLALAAHFAEGGRRTKRLRVSHAFHSPLMDPMLDDFAAVARALTYHÄPSIP 5607
ò	7.0	69
qq	5608	FVSNVTGTLAAPEQVCTADYWVSHVRSAVRFADGIGWLSTQGGVQTFLELGPDGVLSGWA 5667
ò	70	69
Q	5668	RESLTDASRTALLPTLRGDRPEEQALVTAVAAAHAHGFDVDWTAWFGGSGARRVALPTYA 5727
ò	70	77 77 77 77 77
q	5728	FQRERYWPDTTAAGITAPAPGSALDAEFWAAVEHADVÄSLTASLGLDDATVTAMVPALTA 5787
ò	78	77
q	5788	WRORRGEGSALDSWRYRVTWKPRGGAPGAAPTGRWLVLVPAEHRDEATAAWAADVEAALA 5847
ò	78	14
qq	5848	TATVRVEVTGTDRAALAARLTEAADGDTFQGVLSLLALAPGDAGHPGAPAALTLTATALO 5907
ઠે	78	77
qq	5908	ALGDARIDAPLWNITRGAVAVGRSEQVTAPEQAAVWGLFRAAALELPARVGGSVDLPEDL 5967
ò	78	77
qq	5968	DTQAARRLRGILAAADGEDAVAVRASGVFLRRLAHSPAADTVGSAFDPAAGTVLITGGTG 6027
ò	78	77
QQ	6028	GIGGHLARRLARDGAAHLLLTSRRGPDAPGAGELRAELEESGARVTIAACDAADRDALAA 6087
ò	78	77
qq	6088	LLATVPEDAPLTAVFHTAGVVDDHVVDELTPESFATVLHAKTVAARHLHDLTAGHDLAAF 6147
ò	78	77
පු	6148	VLFSSTAGLIGAAGQGNYAAANSQLDALAEQRRAQGLPALSVAMGPWAGSGMVADAAEIA 6207

				ò	_
ò	78			q <sub>0</sub>	72(
qq	6208	ARVRRGGFEPLDPASGVAALLRAVDNGDTSVAVADIDWERFLRAFASARPLPLVADLPET	6267	ò	-
ò	78		77	; A	73
q	6268	AGANAPAAAGTGSGLREQLAGLPAEERHAHVLDLLRTQVAAVLGHSDARTVDDDLAFRD	6327	6	
ò	78		7.7	: E	74
a	6328	LGFDSLTVLELRNALNALTGLSLPASLVYDHPTPREMADFLLAELLGSLPESTRHAVATR	6387	i è	
ò	78		7.7	; £	74
g	6388	AVDEDPIAVVGLACRFPGGVSTPEELWQLLAEGRDGITGFPDDRNWDIAALGAGASDTLH	6447	3 8	
ò	7.8		77	;	7.5
g	6448	GGFLAQVADFDARFFGISPREALAMDPQQRLLLETTWEALERAGIDPAALRGSTTGVFVG	6507	è	1
ò	78		77	G G	75
g	6508	TNGQDYPNLLRRSTSDVSGYVATGNTASVMSGRLSYALGLEGPAVTIDTACSSSLVALHW	6567	ò	
ઠે	78		77	연	76
q	6268	AGHALSAGECDLVVAGGVSVMSTPDSFVEFSTQGGLAPDGHCKPFSDDADGTAWSEGVG1	6627	ò	
ò	78		77	: A	77
g	6628	LVLERLSDAIRNGHEVRGIIRGTAVNQDGASNGLTAPNGPSQQRVIRQALADARLAPSEI	6687	łè	•
ò	78		77	; A	77
g	6688	DAVEAHGTGTTLGDP1EAQALLNTYGPGRDTDQPLLLGTVKSNIGHTQAAAGVAGV1KML	6747	8	
ò	78			: A	78
a	6748	6748 LAMQHGTLPRTLHVTSPTSHVDWSSGAVSLLTEERDWPETGRPRRAGVSAFGVSGTNAHV	6807	}	-
ò	78		77	7 6	7.8
Q	6808	IVEGAPIDEPVVEPTEEPAPAAEVTTVPWIVSGRSREALQDQVDRLTAYAAARPELSPLD	6867	ò	-
ò	78		77	đ	79
QQ	6868	VGRSLATDRTLFPHRAVLLAGPDGVREAARSVASRTRGRTAFLFSGQGAQRALMGRELYE	6927	ò	-
ò	78	Oswidow	85	i . É	ā
g	6928	:     :   :   :     :	6987	3 8	3 -
ò	86		85	; £	ι α
q	6988	I VESWGLTPDQVAGHSIGEIAAAHVAGVFSLEDACALVAARASLMQELPRGGAMLAVRATE	7047	ò	3 -
ò	86		85	: q	83
q	7048	BEVAPHLTERVSVAAVNGPSAVVVAGDEAEVAAIAAHFEAQDRKTTRLRVSHAFHSPLMD	7107	è	-
ò	98		85	3 8	. 6
g	7108	3 PMLTAFARVAESLTYHEPVIPLVSTVTGVPAGAELLTPGYWVRHVRETVRFADGVRALRE	7167	ò	-
ò	86		85		ά
q	7168	DGVTTFVEIGPDGQLTAAAQQTLDASGDEAPATVVALQRRDRSEETTLLEGLATLHTQGA	7227	} &	5 "
ò	96		85	- AC	80
g	7228	3 GPDWTAWFAGTGGHRVELPTYAFQRERYWPEPAAPGATGVQDPVDAAFWAAVEREDLESL	7287	δ 	

ò	98		85
g	7288	TASLGLDGDTVTTMVPALSAWRRRTDARSTARDWRYHESWTALGTPAHSAGAGRVLALVP	7347
ò	86		85
qq	7348	AEHAGTDWAETLVAALGADPLVVDGTSGSLARELADLVPQQATFAPSRRPARTLAAPAES '	7407
ò	98		85
g	7408	PSTSSTGTSGRHTESTHRTPLLDGQTSPAGTLDPAGWTVVVSLLAAGTGTLPAPDAAPAA	7467
ò	98		8.5
g	7468	VLEALEAAGVDAPLWCVTRGAVSVAGEAPAAVGQAALWGMGRVAALEHPERFGGLADLAP	7527
ò	98		85
g	7528	DADAATAALLAAHLAEPGGEDQIAVRATGLFGRRLVRTAVAPGDSGWRPHGTVLVVGGTR	7587
ò	98	TINDEDD	92
g	7588	AMGARAARWLAREGAARLVLTTSPADSATDTEELRAELGRLGAEVTVAPYDGGDRDAARA	7647
ò	93		93
g	7648	LLDGLTGLTAVVYADDTPADGPAALAPVDTLAEAATGRSLDAFVLFGSVAGVWGVRGHT	7107
ò	93	TDB	25
q	7708	DEAAEGAYVDALARALRAEGTPALAVSWNAWAELTDESTTRHLRMNGLPVMDADAALTAL	7767
ò	96		95
g	7768	AGAVADGSAAVTVADVRWDTFAPAHHETRPTALFDGLPEARTALAGAARDRAEGATASDG	7827
ò	96	GHADLVLYITRPDL	109
g	7828	YGRWILEQPAADRDDIILLALVSEKAALVIĞHADTTLVEPDLPFRDLGFDSLTAVDLRNQL	7887
ò	110	11	111
g	7888	TAATGITLEPATLVFDHPNPAALAAHLRTELLGGATDTAAPVAAPAATGDDPIVIVGMACR	7947
ò	112		111
8	7948	FPGGVNSPEDLWQLVLDEVDAVGDFPADRGWDLDALAGDGRGRSATDQGGFLYDATDFDP	8007
ò	112	3	111
q	8008	GLFGVSPREAMVMDPQQRILLEASWEALERAGIDPGTLRGSGTTGVFVGGGSGDYRPPAE	8067
ò	112		111
g	8908	YGGWQTAQSASLLSGRLAYTFGIQGPTVSVDTACSSSLVALHLAAQALRSGECSIALAGG	8127
ò	112		115
q	8128	VTVMATPVGFVEFSAQGALSPDGRCRAFSEDANGTGWSEGVGMLVVERLSDARRNGHRVL	8187
ò	116		115
c C	8188	AVLRGSAINQDGASNGLTAPSGPAQQRVIRQALANARLEAADVDAVEAHGTGTKLGDPIE	8247
ò	116		115
g	8248	AQALLATYGQDRERPVLVGSLKANIGHTQAASGVGGVIKMVLAMQHGLLPRSLYTENPSS	8307
ò	116		115
8	8308	HVDWTAGNARLLTELTPWPESERVRRAAVSSFGASGTNAHLILEQPEPVRQPVEGARPAE	8367
ò	116		115

116
DOBATARA DEGITA DA CELA DA CONTROLA DE CONTROLA DE CONTROLA DE CONTROLA CONTROLA DE CONTRO
POLIS PAY VILS GRESCHALRAGARKLIAH VACHEET VADLART LATTRAVEEHAANTAAD  RAALIAGITAAVAEGTTAAHIYEHQVERTGKHAVLFSGGGSGOLGMGRDLYERFBAFAEAF  BAVLARLDGHLGASLRDVWHGDOETLNETGHTQPALFAFEVALYRLVESMGYTPBFVAG  HSVGEIAAAHVAGVLSLDDACRLVAARARLMODLPRGGAMVAVEATEGEVAARLTEAVSI  AAVNGPTS VULAGAEDAUGALAVAARARLMODLPRGGAMVAVEATEGEVAARLTEAVSI  AAVNGPTS VULAGAEDAUGABURCHLVAARARLMODLPRGGAMVAVEATEGEVAARLTEAVSI  AAVNGPTS VULAGAEDAGABELCDADYWARHST SRLKVSHAFHSVLMDPWLAEFRKVAESL  RYBARRIAVVSNYTGOVAGADELCDADYWARHST SRLKVSHAFHSVLMDPWLAEFRKVAESL  PTYAFORGR FMPDTLPTAPOGCATAGEADGTDSAFWDANAGEBGGYLACGGEDPWVT  TALDALGTR VVRAEVGADGREAMAATLREAAGEGTRFGGVYSLLALRETVHGDVPEGVAL  TGTLLOALGDAGIEAPLMCVTRSAVSANRSDR PRRPLQAAVMGLGRVALLENDTBVTGTVLJT  EDTGF  GGTGATGAHVARRLANDGVQHLVLLSRRGAEAPGATALRDELQTLGAGVTLAACDASBRG  GLAAVLDAI PDDRRLTAAVLHAAGVLDDGVIDRLTFERYQKVFRAKVTSALLLDELTRDLD  LAAFVLFSSSASSAVGNPGQANYAAANANLDALAERRRYQRLGAATSSAFGGARPSALLREF  GGDGATGATGAHVARRLANDGVQHLVLLSRRGAEAPGATALRDELQTLGAGVTLAACDASBRG  GABDAARRAGVAAMDPDLAVESLLRLYTGKEPTAVVAEVDLURFRAAGGGARPSALLREF  PGYRETVAAAAAAAABASPEGTLADRLAGWARRRLDTVVDLVATRRAAGVLGYPDIDAVGAERS  -DLGV 146  FRILGV 3933

RESULT 9

27; Litin.
S OR D-TITIN OR CG1915.
S OR D-TITIN OR CG1915.
Arbitopheric fly).
Arsyoca; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Arthropoda; Tracheata; Hexapoda; Insecta;
Aryoca; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Nydroidea; Drosophilidae; Drosophila. Match 31.2%; Score 241; DB 5; Length 16215; ocal Similarity 0.6%; Pred. No. 90; s 90; Conservative 29; Mismatches 29; Indels 15640; Gaps 9 YTCTARNQYGEAICSVYIQPEGAPMPALQPIQNLEKNIYSNGYSYTSIEEGERVDTFEYR 218 9 LLREVSFREAITRRSGYEQDSQLSQELDRNQGPAQAPQISQKPRSSKLIEGSDAVFTARV 278 9 GSNPKPRLTWFHNGQRLVASQKYEISYSSGVATLRVKNATARDGGHYTLLAENLQGCVVS 338 9 SAVLAVEPAAETAYEPKPVDVMAEQLEAGKALPPAFVKAFGDREITEGRMTRFDCRVTGN 398 PYPEVFWLINGROVRDDASHKILVNESGSHSLMITNVTRLDAGAVQCLARNKAGEVAIEA 458 9 QLAVLEKEQVVAPQFVQRFSTMTVREGEPITMSANAIGTPQPRITWQKDGVQISSTAERF 518 9 ÁQGGNALFEGRLRGNPKPFVTWTRKGAPLLESQKFRMSYNEATGDVSLLINQIGPGDEGE 158 Zhang Y.O., Broadie K.S.;
Zhang Y.O., Broadie K.S.;
Zhang Y.O., Broadie K.S.;
Chang Y.O., Broadie K.S.;
Chang Y.O., Broadie K.S.;
Chang Y.O., Broadie K.S.;
Chang X.O., Broadie K.S.;
Submitted (FBE-2000) to the EMBL/GenBank/DDBJ databases.
I.- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
HSSP; PSG-76; JTLK.
HSSP; PSG-76; JTLK.
INCEPPO; IPRO03106; AARNA\_ligaseII.
InterPro; IPRO03106; AARNA\_ligaseII.
InterPro; IPRO03508; FN III.
InterPro; IPRO0360; Ig\_like.
InterPro; IPRO0360; Ig\_like.
InterPro; IPRO03006; Ig\_NHC.
InterPro; IPRO041452; SH3.
Pfam; PFO0041; fn3; 5.
Pfam; PFO0041; fn3; 5.
Pfam; PFO0041; fn3; 5. ART; SM00408; IGC2; 15.
ART; SM00410; IG\_like; 34.
ART; SM00126; SH3; 1.
SSITE; PS00102; SH3; 1.
SSITE; PSS0002; SH3; 1.
nunoglobulin domain; SH3 domain.
JUENCE 16215 AA; 1841509 MW; 242C8765E00F7603 CRC64; Last sequence update) Last annotation update) \* PRT; 16215 AA. IFS3 PRELIMINARY; PRT; 16
IFS3;
OCT-2000 (TrEMBLrel. 15, Created)
OCT-2000 (TrEMBLrel. 15, Last sequence. 2002 (TrEMBLrel. 21, Last sequence.) 'n ઠે

۵	519	VGIDGGATCLEIPRVTANDAGWYQCTAQNIAGSTANRARLYVEVPREQPNYEQRRLNLPR	578
<u>&gt;</u>			4
۵	579	PTKVIEPEPIPGPEIIYLRHVERAKPHLRPGEEDRVYPPPQFIIPLONVQQTEGGRVHME	638
<u>&gt;</u>	ហ		4
۵	639	ARIEPVGDPTMVVEWYLNGRPLAASARATSVFKFGFIALDLLSIMGHDSGEYMCRVTNAS	698
≽	ហ		4
ā	669	GVAESRAILSVVQRPSIEQSSQNPNSLQYINQLEDYSRYQRTESIDEQLNQAPQFIRPLR	758
≿	ιΩ	-3TH71	0
ą	759	DLGEFEEGKNVHFEAQVTPVNDPSMRVEWYKDGLPITASSRITAIFNFGYVSLNILHLRA	818
≿	10		o.
ą	819	EDAGTYTVRAVNRIGEAISQSSIRVHSRSQVTADLGIPEQQRYIEKVEELEDYRKSQQRR	878
≿	10		0
ď	879	HVQEAAEAIAPPQFKTPIQNQLDLREHAHAHFEARLEPVGDSTWRVEWLKDGQPLEASSR	938
<b>≿</b>	10		6
ą	939	ITTYHNFGYVALTIKQLTIYDAGTYTCRAYNAMGQDTTVAQLTVISKNEIVSESQHPGGL	966
≿	10		6
ą	666	QKIQHLEDSSRYGRREEEETYITQAPRFLGPLKGTTKILEGQRAHFEARVEPQSDLGLVI	1058
à	10		13
ą	1059	EWYHNGRSITAANRIQTYYDFGYVALDISQVRAEDAGVYLVVARNKLGEAQQQATMIVET	1118
à	14		13
g	1119	RSSIDTSSMHRGLYEKTQNLENKPFVEPQYDIEEISKSKPVFVTPLSDPKPIHDGKNIHL	1178
ጵ	14		13
g	1179	ECRLEPMGDPTMRVEWFHNGRPVTVGSRFRTYYDFGFVALDIIKATAADSGEYTVRATNH	1238
à	14		13
g	1239	LGTAHTSACVRVIDHTDVVTETQNEQSLEQIQLLEDSRRRHHQEEDITIMQAPQFTRGLH	1298
à	14		13
ą	1299	NIETIEGTNVHLECRLQPVGDPSMRIEWFVNGKPVKTGHRFRPAYEFDYVALDLLGCYAI	1358
ò	14		13
g	1359	DSGVYTCQARNQLGEAVTSCSVRIIAKNDLILETQNESGLQKIQYLEDSTRHRRSEFVDE	1418
ઠે	14		13
QQ	1419	VVNIRPRFLTHPKSLTNTREGGHAHFECKIEPVTDPNLKVEWFKNGRPITVGHRFRPIHD	1478
ò	14		13
QQ	1479	) FGYVALDIVHLIAEDSGVYTCRAVNLIGSDETQVELQCRSGEQIVTVTQNEAGLEQIHYL	1538
ò	14		13
q	1539	) EDRSRYTRREEIDESTKQAPVFTTSLKNVEIKENQRAHFECRLIPVSDPSMRVEWYHNNL	1598
ò	14		13
Ę	1599	PLKSGSRFTETNNFGFVALDIMSTLPEDAGTYTCRAYNAVGEAITSAVAVVHTKKSIYLE	1658

ò	24
qq	1659 SQHETALPRLQHLEDGSKRQRISVQDEFVSQAPVFTMPVRDVRVAENQAVHFEARLIPVG 1718
ò	14
g	1719 DPKLTVEWLRNGQPIEASNRTTTMHDFGYVALNMKYVNPEDSGTYTCRAVNELGQAVTSA 1778
ò	16
QQ	1779 SLIVQSKTSIQLETQHEAAMHKIHQLEDHSRYQRREEEEYTVTTAPVFVTKLIGPSNLVE 1838
ò	17
qq	1839 GOSAHYECRIEPYPDPNLKVEWFHNGKPLSTGHRFRTTYDFGFAALDILTVYAEDSGEYT 1898
ò	17 16
q	1899 CRVTNNLGEAINSIVLNVTSRSSIIHETQHEEALTKIQHLEDTSRFQRKTDEEQFHAERP 1958
ò	
qq	1959 QFGRPLRNAKVNEGAPVHLEATLIPVNDPTMKVEWYCNGRPIQTGHRFKTTYDFGFVALD 2018
ò	31
qq	2019 ILYAHAEDTGTYMCKARNAIGEAVTTCAVNVTANKTLDLDTLDAGRLEKIRQLETYAPPP 2078
ò	31
qq	2079 KPVVEEKGQKPIFLTPLSNLEHLKEGEHAHLECRVEPINDPNLKIEWFCNGKOLPTGHRY 2138
ò	32 31
qq	2139 RTTHDFGYVALDILYVYGEDTGTYICKATNQLGEAVNTCNVRVLNRRSMILDTQHPDALE 2198
ò	32 31
QQ	2199 KIQKLESKVPNARTEVGDAPISPPHFTAELRGSTEIYEGQTAHFEAQVAPVHDPNLRIEF 2258
ò	32TNT/NI 36
đ	2259 YHNGKPLPSASRFHITFDFGYVSLDITHAVAEDAGEYSVRAVNALGQAVSSTNLRVIPRG 2318
ò	37GABLIR
qq	2319 TIISDTQHPEGLEKIRKLESTAPHQRQEPETPGTRQRPVFTQPLQNIDRINEHQTAHFEA 2378
ò	43
q	2379 RLIPVGDPNLKVEWYRNEKIIEDSSRITKQHDFGFVSLDISHIRKEDEGVYMCRAVNPLG 2438
ò	43 42
Q	2439 EAVITASMRVVSEASIQMDTQHPDSISRIHQLEKPLAPRPTEPERLFEKPIFTQLLTGPS 2498
ò	43 46
qq	2499 ELWEGTHAHFEARVVPVGDPSLKFEWFINGVELQMGSRLRTTHDFGFVTLDITAVVPEDA 2558
ò	47
Ор	2559 GVYMCRAYNAAGEAVSSTAMKVKTKSNIDGQPLIPESWEAIRLKEAAMNRVPEMFVDSTP 2618
ò	47
q	2619 QQAPVFTTHLQSYDKLHEGQHVLLEAQVEPRADPNLRIEWFKNGISLTTGSRIRSTFDFG 2678
ò	47
QQ	2679 LVTLSINGLRADDSAIYTCKATNQVGEAVSTSSLKIEDRHWLQAESLHPDSLPRIGELEA 2738

ò	47		<b>4</b>
Q	2739	PKEGRPEAPEPTYETPVF1THLNN1ECKESDNVRFECNVEPARDPTMS1EWFYNGQPLQA	2798
ò	47		46
a	2799	<b>AAKFKSIYDFGYCALDLTNSYAENSGVYTCKATNSKGSATTSGTLKCTGGKTMFLDTQHP</b>	2858
ò	47		46
g	2859	<b>QGEAGLEAVQETEEELANRYTSKTTKPETQYPPPVWTKPLQAEFHLSEAQPIHLEANVEP</b>	2918
ò	47		46
qq	2919	KEDPNLF1EWYFNGKMLNHGSRFKMTSEFGFVTMDM1EVYARDQGIYTCKAYNKAGEAFT	2978
ò	47		46
g	2979	STTI FCSSKENI I ESTQHPKGAEGLEQI QDLEDSLRKDGSKPEQPDLGI PPRFTTEFVNI	3038
ò	47		46
g	3039	ADIGEGELAHFEANLI PVGDQSMVIEWFYNGKVLEASHRVRTIYAFGTVALEVLGTKIED	3098
ò	47		46
a	3099	TGTYTCRATNKHGTAEISCNLECVDKPRGQKPRFTSHIQPLEGLKDGQSAHFECTLIPVN	3158
ઠે	47		46
g	3159	DPDLKVEWYHNGKLMRHSNR1KTVSDFGYVVLD1SYLQDHDSGEYVCRAWNKYGEDFTRT	3218
ò	47		46
d G	3219	TLNCGGRGGVFYDSLQPDSLQRIRELECPQGQQADTSAPLVAEPPKF1TQIVDVTKLVEG	3278
ò	47		46
8	3279	QSAHFEARLTPITDPDLVVEWYFNGKKLPHGHRFRTFHDFGIVILDILYCYEENSGVYEA	3338
ò	47		46
g	3339	RARNKYGEDVTRASLKCASKSSLILDSQLPRGMEGGLEKIANLEYSMVRTREETTEETKG	3398
ò	47	GAQFR	51
g	3399	1 : 1	3458
ò	52		51
q	3459	VILEISPVYPEDSGEYSCRAINEYGEAVTTATMKIQGKRSIIMESQLPKGMEGTIDRIAE	3518
ò	52		51
g	3519	LEGLGSRSTEFVPDDDTGKPPEFITSPFDMVIGENALAHFECRLQPINDPSMRVDWFHNG	3578
ò	52		51
a	3579	KALWAGSRIKTINDFGFVILEIAGCYQRDSGLYTCKATNKHGEATVSCKLQVKGRQGIVM	3638
ò	52		51
g	3639	<b>EPQLPSNFRTGTESLQKLEETWHKREELVTEDEQPNPPKFTEEIKDNLDVPEGGPIHFDC</b>	3698
ò	52		51
අ	3699	RVEPVGDPTMRIEWFYNGHVMATGSRVHQLNDFGFIALDVDYIYARDSGEYTCRATNKWG	3758
ઠે	52		51
a	3759	TATTSAKVTCKGKHNIVYESQLPEGMTSEKLKELERGRIPEAPKVVEEVFGPPKFTTQIT	3818
ò	52		51

24	5	S	ò
4898	) GQFLGVNGQGQHQGRSRQKKPKVRSKSLQPATKVIPWRKSSRPTRGRSLDKGVFLPGFKP	4839	qq
54		55	ò
4838	) SSTGQVESSAKLTVKKRRISAFQLRTIDSAEDESSSSGREDSAPESPHAFQPGQQPGOOF	4779	đ
54	5	52	ò
4778	) AQFKTTVTGKVKATSVQWFREGQLIPETPDFQMIFDGNSAVLLIGTTYEEDSGIFTVRVT	4719	qq
24		55	ò
4718	) YQLVISEAFPEDEGTYKCVAENKLGSIQTSAQLKVRPIENLDAPPTITALKDVSVTEGMP	4659	셤
54		55	ò
4658	) GSEKAPHIVEQLKSQTVEEGSKVIFRCRVDGKPTPTARWMRGENFVKPSRYFQMSRQGEY	4599	q
54		55	ò
4598	PSIKFKMLEEDSVHTLLIIEPFAEDSGRYECVAVNAAGEARCDGDCIVQSBAKPEKPTTP	4539	g
24		55	ò
4538	) ANLVVEERRRAGKGGIQPPSFVTTIQSTTVATGQLARFDAKVTGTRPLDVYWLKNGMKIQ	4479	Q O
54		55	ò
4478	GEPNPTVKWYRESFPIQNSPDLQIHTFSGKSILIIRQVFVEDSAVFSCVAENRGGTAKCS	4419	g
54		55	ò
4418	) LEITRKITATETTEVEHKGTIQERVVQGPVKPAKAPVFTKKIQPCRVFENEOAKFEVEFE	4359	qq
54		55	ò
4358	· SSQAKGMAQSYEENLQEKTSTTEVQAAPPKGIAQPSESSVHGREVHMNKQQQVQKEIQGD	4299	qq
54		55	ò
4298	HLKPKQYKPPTPDWQQNVKAKKSEDYYNKLQTLETEQLLKETNLRRDTHQYAIPGEKVVS	4239	Q
54		55	ò
4238	KVVARSDDYRNVLKNSPRPWYDYELAAYQKERQENELEKVFDERKQVLSEQSSHTLKGVE	4179	qq
54		55	ò
4178	PRPRVMWLINGHTVVHGSRYKLTNDGMFHLDVPKTRQYDTGKVEVIARNSVGESIATTEL	4119	q
54		55	ò
4118	PAHMQSIDRIREMEASWQVVPDEVDPDAKPRTKPVFVSKLEPQTVEEGDPARFCVRVTGH	4059	qq
54		55	ò
4058	HKNRFQPIYDFGYVAMNFGWVYPEDSGEYVCRATNLYGKDETRAIIKVSGKPGIVYDSQL	3999	q
54		55	ò
3998	   HLTEDDLFDPDRKQPPRFVTQIKEQLTLTEMAVTKFECQLAPVGDPNMKVEWFFNGKPLL	3939	qq
54	HI	53	ò
3938	DSGEYVCRAINNYGEDRTRATVSCKKLPTILLQNQVPRGMKRSDALTQMEATIKKYTSEV	3879	QQ
52			ò
3878	SVTVDEAEAVRFECQVEPKTDPSLRVEWYRNGKPLPSGHRYRNIFDMGFVSLDILYVYGE	3819	q

g	4899 EPVKSWTEETINLKATPIEKKKPAPKLEAAKVVLKSIKTERDQGIMSLGATLEQIIAGKT 4958	45
ò	55	מעחעה אייעם האוים עווא הפפה דפ בווא העומים הא הפפה מפה המפה את אייע העומים א אויע העוער אויע העוער הנהס.
g	4959 EKEAIPWITMREKLKAVESVQQQLNKFDLDEVYLQPLEGQIETEGQLPQQAQVEQVQRTK 5018	00.59 NNFNINVANBESIBEFABEIBEFBEBATIQFBEVQFVBEIFBEFQVNBVAUDENINFNFNF
ò	55 54	
gg	S019 EIQRLKSMESVEIMEMTDQIDKLITQQQNAKDLIPWKEMRQQLKSVQRVTKQIDKFKIEE 5078	6099 RKEEIIEKVEEVALKRVTRPKKELPQEATIEEVRLKPTQRTSIKPEEVKLEEVDLQHVEK
ò	55 54	
q	5079 VELRHLQAQQAITEEYQTGTAEETVVMIDESSKGSISKVLRRDEQLQYEDQSNIYKQKFI 5138	Db 6159 KEDEIVQEEKRKTRKVKKPKHEDLPEIPDAEPTQLEEAEHIELEKQPKPEEDQPQVPWKR 6218
ò		28
g	5139 TTEDVNIMHVSEREKLEAQRLIREQQAVNWRQQQQRPQLQPLTSVEDTVISQTSERQKLV 5198	6219 GEKKOPVEEVLEEKKWPSGKRRPLPEQOPEEVQLKPIPSKPIEEQOKPEKAIPGPQLVPE
ò	55	Ογ 55 · · · · · · · · · · · · · · · · · ·
쥠	5199 OQQSFIEEAQRQQFVQVEDSQMMSLEEYEHQKIINQRTQQEAFSWRQPREPQKFIQVEDS 5258	Db 6279 EKPESEEEELELEPLKLPEDKKPKEPKAKKEKKKRPKLKKATPSVDEVSEEVAEPFDEPI 6338
ò	55 54	55VKAVILTE
g	5259 TLLHLOERHDTGEQQLLQQQPVMMDRGRKKPDQPQYVQPQEQRVKEEFVEKPKTYEEMHD 5318	Db 6339 AEEDEVEEMPVDDVKVVAVSEDVLPEEEVVPTEETPEAKQKAHKKRTKRLKEASVEGQPQ 6398
ò	5554	Oy 63 62
g	5319 ELVEPTPIEQPOPVPVMWERGKKKPQPQEKTFEEAHDELVEPTPVQQPEPVPVMWERGKK 5378	6399 LLEAAIAEIEKVDEISQEISQKTITLLKKTEDTRPQFITTEQLIELDVEDVRRDLEMKVT
ò	55 54	63 62
q	5379 KVAQQETVLSQEVVQTSQVVEQQIVEETKKTAVRRVIPPREPEQKVEQVTLKPTPRPRPK 5438	Db 6459 SNIIKKEKRRVVLDDSQPLPELELITQKRIQEGIDKVADEELIEDQQLIQNQQETTTSEV 6518
ò	5554	Ογ 63 62
g	5439 EAVKAEEIQLKPLRSTRPVPQPVEAEQKAYEEATDELTEEPIPQPQPVMWERGKKKPQKP 5498	Db. 6519 IGQERKLVKKKKKEIKPPRITEKLRPRQCVPEEPTVLECKVEGVPFPEIKWYFNDILLFA 6578
ò	55	Ογ 63
셤	5499 QEEVTEIPKTLEIAVDTLEEEVPKPTEPQPQPVLWARGQKKPQKPDEQKQELPKSLEIAV 5558	Db 6579 SEKYEITVMEQVAKLKIAKVTPSDVGVYTCEAKNEAGVATSRTNIILEKEQGVPPQFTKP 6638
ò	55	63PEGAPN
q	5559 DTIEEDLIKPVQPEPQPVLWERKKKKRPQPQDVIEEKLDVAPTKTYEKAVDVLPDEPKVEE 5618	6639 LKIEFIEEKQPERLKVTVTCQVTGKPNPEVKMYRGIEEVIPSETVQMFYDEKTGDVALEV
ò	55 54	69
đ	5619 KPEPVLWQRGKKKIPKSEPTEEVHPDEVDAQIETVVKEDEMIVEEKRIKKTKRPKSTKE 5678	6699 INPTPNEAVVYSVQAQNQFGRAIGNANILSRVDEVPREILKAPTVTPLSAVVVPTGGTLF
ò	55 54	89
a	S679 VTEELFEEQPEEEISPEEEVPQKEVIEEIEEIVEEKRRLKKTKKPKLTQQVTEEFTPHEE 5738	6759 FEAKYDGLPRPEVKWMRNGREIIENEETIIETTTTTIKVVNMTRKRTGKYEVWAKNKV
ò	55 54	
đ	5739 IIKESEEVVQEQEEIVEEKKKVKKVKKPKTVAEKQLKEEEIPTEETVEEEETAEDQQLVV 5798	Db 6819 GEAKSSGSVVVSDQKPDEQIKPPRFIQPLEPKYFGEHEVAIIEAIVESEPLSSFQMFVHN 6878
ò	55 54	
g	5799 EESKKVKKVKKPTGTVEKTDVEELPGEEVPVEEVPVEEVPEDVAPEEELIEEQEEIVDQD 5858	6879 EPIKSSNEVRIVSQANKSTLLIENFQSKFVGPFTCRAENVGGSVTSTATVNLIPQEEAEE
ò	55 54	69
g	5859 EIQEQKRKVKKAKKPKKTIEKTEIEEEDQPEEEVLQEEIIGEQEEITERQRKVKSIKKP 5918	6939 FESPRFVEELVQPVEVMDGEALLLTCQVTGKPTPKVEWYHNAEKITENKETTISQDLQGV
ò	5554	Ογ 73· 72
q	5919 KKVVTEKTVDQTEQPEKPEESQAEEVKETVTEEPKKPKPAPEEAKVEQVEKISLKPAPRK 5978	Db 6999 CQLQITEVFPENEGQYECVATNKIGKSVSKTNVKIQAFEYIPDSEITGLTGSEEDLLDRT 7058
ò	55	Ογ 73 72
đ	5979 QRLLPEKEQVEEVLLKPVKKIVAVSEAEQPETPETEFEVKEFAITTTEDILDVTKKRVKK 6038	Db 7059 LSIDEQAPKIIKKLPEKIEPKEGEQAKLEVKVVGKPKPKVKWLRDDEQIFASEEYQIENF 7118

ò	73		80
Q	7119	EDGTSVLVINHVYPDDLGTISFEAXNPLGVAVTTALFAVEGIVGSKDYRKPEWVSQMEEM	7178
ò	81		80
gg	7179	OVALKAAKCSPSLLNEMRDCRAALGETAKFSIQFAGNPIPDIQWYFNNVOLRASEKYRMV	7238
ò	81	CGW	83
g	7239	VQEQEATLEIMKITSEDCGYYNCKLINEIGMTMTRAKFDISSTSTIVEETKAKTTVKKKS	7298
ò	84		83
g G	7299	GKKTMVKRSGASESQNVQKTEIRIIPTSAVETSMNVIKVKQPVSVLVEKSEISEVLVVKD	7358
ò	84		83
a	7359	REVADAEERSSQLIEEIEEEEEIEEKVQHDEEDEVEVQVEQKETYTSSKKIEITKTVELI	7418
ò	84		83
g	7419	RTKISEKIITIEDVQVLSHHEEVQWLLESIEAESFGQIGESALRDLATIGLLLRYGCEHY	7478
ò	84		83
g G	7479	EITYMYEQNIFISLKKPESQSALVQLVEREGHEELISQILSESSNEDETILAATVGFKPF	7538
ò	84		83
g	7539	IRMIQTYEITIEIVIRKFVREDFISQDWKICGKERIVETSQIIESHEAITHVKIETATTK	7598
ò	8		83
g	7599	VEKLFKKQEQEHVQNLEQQEQVKIQVQTKQIAQMNTKIKKHKKHKQQEQEVSETTIQCEQ	7658
ò	84		83
g	7659	KETLAHETSAELPQSETLEQIEESLSTYETLPIONLSKDTLQTVAVSVTTELSTPSPTAS	7718
ò	84		83
QQ	7719	RVQEEILPQKVLAINEEVLPLDEFGLRKESPRPKENKLTENIEVRLKHALNVSHAKTAES	1778
ò	84		83
g	1179	SKELPSKI PKSVKAQRKMKESRSLVVEAPNAEEAI EDLKPLKAVSQEVQSDILFSHEITE	7838
ò	94	ILOS	87
a	7839	EQHQALETIEKLKPTSAIEDTVQQKLLSQEELIIAEVLPSETVGRDVTDVRPPGETISPR	7898
ò	88	Cada	91
g	7899	LTPNMSLCITECQPEDSIGEMQQAAKERMETPSMSVTESKAVGGQELEVLENVDHMPLIT	7958
ò	92		91
QQ	7959	QPTKGLADYTIKAEEVPVQVQEIITFDSLERETVAKTQTAKSNALELFELSEGLVSSTAD	8018
ò	92		91
g	8019	SHSPIAEDLPIFEKDVKEATIDMQMQHHVTTSETVSNENAVKDLKAVDTPKMAEGTLGQS	8078
ò	95		91
QQ	8079	SALTIGETQQMNLVETTVELIEPNVESTKPAKGALTEAYGTAESNEETLLESLGLVPDDN	8138
ò	92		91
a	8139	RKI EQGKVNI SEGEYVAKVQTTTVTDTEGEFVSVAPKLVNPKFDFVEQSALQI KQDTTVE	8198
ò	92		91

66	0	100	ò
9278	9 GTVNLTSNSNLNSELVVSVVQEVTSVPSLGSLATVEPQELKAMPVTKSSTNLAYSEEVKG	921	a
66	0.	100	ò
9218	9 PQNSVNVCQQLAYEETPDIAFEPHALTRATTSSVPTFLKPAENATVNIYENIEGHGDFKP	9159	q
6	96	σ	ò
9158	9 ARIKSAEDHVHTNVSEDTAQAAADELQSLVTEEVVSVSSIQETYELKIPLQKTANLTQOT	6606	qq
95	9	σ	ò
9098	9 VVIEVVPIDNVGGIHLAPQPSTLLATLTSTDIVNQSHVIDTQVPLEMESEAQAPLDNIAQ	903	đ
95	96	σ	ò
9038	9 LLKDTHVAVQKAQQEYVAQVESNKVHVQMDNLVMHKEDIFENAEIENFCKPITEGTQLET	897	QQ
95	9	σ	ò
8978	9 SAVESIDSTFKVTSDSQQPPVFDKELSIPTVSPLEARAKPSLNLLQGTTTGDVIPLESSV	891	đ
95	96	σ	ò
8918	9 GLAMTTKTHPVEGIDVLLSSPPKPSLAQTNYEETQHEVRVRETQAIEESEELTDGRLLPV	8859	qq
95	96	0	ò
8828	9 EAMGQEQKVDKYNIQQAEITHDLPQVYATDLQQTFEAEKEITTREQSYVAATTDIIPSRL	879	g
95	9	o.	ò
8798	9 DQQIATNVQDSLSQSIIAEDQIAFETEQNLGLETTPTHKPKLLKDDQNLHAKLVDEATVY	873	q
95	9	o,	ò
8738	9 DHLYETKSSEMIVYDSSINSVDSEFPAGIVPQKSLVPFRHTMVTENVAFNASENFEILSA	867	qq
95	9	0	ò
8678	9 QEETLEHEEDLKAPLIPLEKAIPASSELHRLPLTEYVQEQQGTSDMTDFKVSNKCASPNI	8619	qq
9.5	96	o	ò
8618	9 LNPVLPALETIQSSIKSLHEINVRETDILEKEESLKDVDHISGRLAKIILDCTTGIAQVR	855	g
95	9	ō	ò
8558	99 VQLIESTTSLKTTTAVVSESTEELKDLNITQPVHIKPKPYESDQKISISEQTNVLEHVSS	849	g
95	96	6	ઠે
8498	9 NITRPQHMESLDRLDEQKVPYYQANVNIGBITLPNVEKIDSFDVLSDLNTPDYNKSSKGR	8439	g
95	9	6	ò
8438	9 LTRTEDLKPQTQTTESQFGLLQSLETSSCVTLEGESVLSVKERHPEQSAAIGTSSALQVA	8379	g
95	96	6	ò
8378		8319	g
95	12	6	ò
8318	9 IGVTSKPDMLESTSHIDAFQHPEFKTGDTILDENQQPLEVTNVQITESSTDIIDVLPNQK	825	QQ
16		σ	ò
8258	9 KEEILSSNIELAPQLATSNMFPAELKVTSIYEVQPGLTSSDIITEOTKSVSANQVFETMS	819	g

100 -----

ò

g	9279 1	NKQEVTKIETVEEDDKQPETTVTVEELPPQEEKPEEIQEIPEEVRVVETVTEDGKPKKKK 9138	
ò	100	. 66	
g	9339 1	IRTRVIKKVKGDKQEVTKIETVEEDDKQPETTVTVEEVPYEEEKPEEIQELPEEVRVVET 9398	
ò	100	66	
q	9399 1	VTEDGKPKKKKIRTRVIKKVKGDKQEVTKIETVEEDDKQPETTVTVEEVPYEEEKLEEIQ 9458	
ò	100	66	
g	9459 1	ELPEEVRVVETVTEDGKPKKKKIRTRVIKKVKGDKQEVTTIETVEEDDKKAETTVTVEET 9518	
ò	100	66	
g	9519	ELSAPSVGKVQLKKRVIVQKPEDAVTVFELPERKSVILSEKEDGTPTKTVIKTRIIKKIQ 9578	
ò	100	. 66	
q	9579 (	GPNMEVTKVQTVEEYEKAPQTIVSVEKFNTPFPELPEERLSEVVMLPDEVFESEAVDEEG 9638	
ò	100	7. 100	
g	9639	RLKMIKTKKRIIRKPALDNTEEVTEIGIIEQDNVEPIYSVKIQERPLTESKPEDSKLIEL 9698	
ò	101	VLYITRFDLELPDG 114	
q	6696	PEHVTELNVILPDGKKKRRTVKSRAFKKSLDDDLDEVTTIHIIEEEDKEPLTKVNIEVVP 9758	
ò	115	114	
තු	9759	SDEISITPIPIEELPEETVFTEELDENKKPKKKTTKTRTFKKRGPDDDEYFQIQTIDEEG 9818	
ò	115	114	
g	9819	KEPISLIRVVSDENIADIIDISKLDDEKVLKHKQKPHKHKDQYYKEYTITEPEEASADAL 9878	
ò	115	114	
g	9879	QKPTKDKTPKQKKTLETPIEEVDETVIIDEGTGEQTDQIAIKRKPRKVQGNVQVEAVDEK 9938	
ò	115	114	
g	9939	PIEKKEKAKKKKVVKTKRDEMDDYIHFLIHQEIPKTVLQPYQRTEMELPQRARRDSSFKQ 9998	
ò	115	114	
q	6666	PVKLTPMKIEKVEFKKPKONVEISSVVEFPQMLKLKAPKQRPQEEKKKKNEASFKNKKLKS 10058	
ò	115	NROV 118	
g	10059		
ò	119	120	
QQ	10119	LGAYESDHSDKSNKELLHPKYKRGKKEKIETPDESRKLKFGKGKVPQNEEASEEVNLKPV 10178	
ò	121	120	
q	10179	KLDIAEIEDAEMPVRTQEEEVVKKKKPKKSSKPEEGLQFEPIEFEEMERTSDIREESDTS 10238	
ò	121	120	
8	10239	VSVDTSTQEKPIYKKKKKVTPSPQKNQYKILPGQPREFEETPEDDLNLRKRQGERPDDDK 10298	
ò	121		
g	10299	ADTKLKPFYKFEVLDLEPEGVQAETVPLSETIAKEPKKKRKIKVKTEQEDNTIEIVPLSP 10358	
ò	121	120	
Q	10359	EDNDEQIFEITVTSSEIPQGDAKAKTIGKKKVKRMNKQELDDFVTELQEEPNQEVYETRM 10418	

ò	121		120
Op	10419	SDFYEVKLTELPSEMDSDKPTKRILRHEKGDEVQVLEIVESVVAPGEEPFYEINVISSAN	10478
ò	121	VTQL	124
QQ	10479	TEGDSEEITTDKIKKKSRKIKKDDLDAYIQQLINAEIPVTELEKYEKIDVDGKAKKPKKL	10538
ò	125		124
තු	10539	KAKTKKP11DEGETLQVGVTEHEPTKKLKTKKPEEKRNV1EKELAEHEAVPEYDEFL1NK	10598
ò	125		124
Q	10599	TESERPQEKRVEETEKDIVPIVDKVLADLNDCLPFVVVEEDLKDMPLATDVIALEDEKII	10658
ò	125		124
Q	10659	RKRKVRAKKDSKQYEIEIIETEKPGDIPDEARVIVITTEVSGDTIDGPAPSTTEAPKKSV	10718
ò	125		124
g	10719	RKVKKEKLKEFIVNIVEEAPLDHVSEIYEDVLRTPFRESSEKEDIPSFTTTVVEDEIVNP	10778
ò	125		124
qq	10779	VLPEKIKTVDDVRVPKDKKKKIDDNQKKIKISEFEPTPTSEDSTIEEYTPKLSEHDEDLQT	10838
ò	125		124
qq	10839	DEYSVDVKDSLPKSKKKSTKKQKKESLPGPISLYTIRIEETTPEPITEKIYEDGKEVVRV	10898
ò	125		124
đ	10899	INKRRIKKKAGPKEYLIEVIETYEDNNPEADVVIRTIETTPSIDSKPQEDHKIQVVQEKK	10958
ò	125		124
qq	10959	PKTESLDNY1QKLIDQEIPQVDHKEFKATVLETSPESKKAKKIKKHHKKTTEVIDGIPIT	11018
ò	125		124
qq	11019	VIEVTIQETETDDEDFKPDEVTLKEIDHENAEEAPKVLKSKVSEEKPKSKKEKSLEFKIA	11078
ò	125		124
QQ	11079	EEDKPKPVLEDISEDVQVVQIIEEDGTPKQVEIKKKKVSRKHGPKEQVFEITETKAIDEP	11138
ò	125		124
qq	11139	LSEVTVVEITDEQPQEEVLPAQEKKPIKKQKKLKPEDVNTYVVKVLEELTEPTQFETIPE	11198
ò	125		124
qq	11199	DADDKPQPVIEDISENVQVVQIIEEDGTPKQVEIKKKKVSPKHGPKEQVFEITETRPSDE	11258
ò	125		124
Q	11259	PLAEVTIVELTEEGLNKDIVIPQEKKTVKKPKKLKPEDIQSYVIRVLEEFNEPQWPASTE	11318
ò	125		124
Q	11319	KPIIEDIAESIEIVPVTEEDGITKEVEVKKKKKVSRKQGTKNQVFEIIETKTSDEPLAEVT	11378
ò	125		124
QΩ	11379	) ILELSGDKSQEVTILPKEKKPIKKTIKLKPEDVESYVVNVLEEFCEPQSFESPEPTEGEA	11438
ò	125		124
q	11439	) HETKTKKKPKKPIVKAPENVILIEEMAPETVIENIVNEIGEEVKQVKTTKKLKKEGPK	11498

ò	125	124	
셤	11499	EYLJEIKETYEENKPEGDIEITTTELVPEGSPDASDDQPVIVVQKIKKKRVKDVKDDLDKYI 11558	
ò	125	124	
යු	11559	QQLIEQEITKTPLEEYEPTEMDSKKKPKKVKSHNKKTIEVIDGLPVTIHEFNVEDIVSE 11618	
ò	125	124	
g	11619	PEDMETPKTLLDEIKEIPQLPDDSSKYLVNISDEFGEADKPIKQPTQDQPIKKEKPLKKK 11678	
ò	125	. 124	
8	11679	KDVEYPVSLEAFDHTVKVVSEPTLEGTVKEVTVKKRKVSRRKGSKDHIFEITETTSEDRP 11738	
ò	125	124	
g	11739	TAEVTVVELSSDEVLDSEEKPKHERKIVKKPKQLKKDDVEEYIINIIEEFIQPIPVGLVE 11798	
ò	125	124	
g	11799	DEVEKVQKEETKKPKKSPITYIATEQEDNDNNYDALVKEDLDQPIERALEKPSSPLEYTI 11858	
ò	125	124	
QQ	11859	SVEEDSVGEEQKQPKPKKISKPKSIKQPSVDKSPDYLVNVISEESIIDEPIPEDYVVTEA 11918	
ò	125	124	
g	11919	AEEKPSEEPTFKVEELETEAVEKEVTDDDKGETTKQSVTKRKIKKLVGPKEEIIEIVETK 11978	
ò	125	124	
a	11979	TGDTPEYEVIVTTEEVQEKSKEAPEEKKAKTVRKAKKIPKDDLQDYIQKLIEQDIPKTEL 12038	
ò	125	124	
g	12039	EKYEKIDLDEPVKMKRKPIKKVKQSEEQPKEETEEPIEDKPVEKISEYSEVDSDEPKLTV 12098	
ò	125	124	
g	12099	AVKEFIPEKPEEKPFEIVVLEETVESKREPDEEGKVREKVVKTKKIKQNRGSVEVVHDIV 12158	
ò	125	124	
පු	12159	EEIDTDTNESVITVTTTVPTETPDQDQPSVKQKRTKKIKKDEVEDFVKRVIEEEAPQPEG 12218	
ò	125	124	
QQ	12219	SVDLVVIEDFVPKPSSEKRKKKPIKDKHTSVEEETPHEDEVLLIESVPEDSPLSDDLITV 12278	
ò	125	124	
g	12279	VDSVPIEEEPENKVNQIEDTKKPEKKKRPKPSAKILEENVPEDTVEKPLEALHTDSDLEK 12338	
ò	125	. 124	
g	12339	PDVQEFSISIKEEEQKHTHPEKKKSSKISSEQPKQPSTEQYEISVTEHDLKPEEEKPFTV 12398	
ò	125	124	
QQ	12399	QVIQSETNVEETKDDTGKVHKQVTTKRMLRRPAGEGEIEIIEVVRDDQPEAEITIVEYEP 12458	
ò	125	124	
엄	12459	EPVNQDEKPKEPKKKTRKVKKDDIHDYIQKLIELETPKTELEKYEKIEFEPIVKDKPLDS 12518	
ò	125	124	
g	12519	PIDVLDESPKEVQKKDKKSRTICKGQCVEEEAPEQPEIPVQILEVKPVEVDVKEVITEDG 12578	
ò	125	124	

124	125		ò
13658	99 IVEETSVETAIKQKKTKKPKKDEEEAQLAIKVVESEAPVAEEVPSEAPESKIVEEEVIAE	135	g
124	125		ò
13598	39 EKKVAEKFDSYEFTLKETDEEKVITVDDQPEEEAPVEVVFKKKPKEPEAVEAFFVMTEPK	135	g
124	125	٦	ò
13538	79 BAEEEKQPVEETIVEVEKQEEKKKSEKPKSYEFKISETQSIEEKPIEVAEEAPEETPKVV	134	ద
124	25		ò
13478	419 VSAEISLPIEEPEQKPEQYEVELKITGTTPEEPNDVQIAVKEKVKTKPVKKVKEDKIVVV	13	셤
124	125		ò
13418	59 EDAPKEHQVKVIDFDERQETTEEVIEEKVVTRKKKPRPQOPEEFEVTLKEPKEEQIQPDV	133	g
124	125	н	ò
13358	99 BALVDKPIEIEKPKDVKVKEKKPKEAPVSEVVVIEEEPKPEEVPEBIPVEKKITTTVLEP	1329	q
124	25	Ä	ò
13298	39 PDEQALVTPKAEEPIPQEIEDKAIDDEKKPKKSKPKKVQPKEQEIAKEEPEEFEVSVKEE	1323	g
124	25	12	ò
13238	79 DKSKSEPETIVSEIVAGVPKEEEAIPEQDVKFRKPERDAPEETDSEIKLRPVPQASKDEN	1317	a
124	25	12	ò
13178	19 EVEIVEEQTKKPKDGEFVVEPFEPSEFDRPEYVPDELEQIEHPEIPEKVKKPSKTKYKPK	1311	g
124	25	12	ò
13118	59 YKKPEKAPKPEEKQEDVKLKLGKGKKKPKEEEAPENVTLKNI PQKPQEVEEEVELKOKPK	130	ద
124	125	ä	ò
13058	99 GAIKDNGELSRNIGEAEEILKFKPHKTKKIKKIKDDLEKVELEKYEKYISSEEEPEEKTP	12999	a
124	125	ä	ò
12998	39 TKVTILDATDVPKTVKLKPSKRKEKPAEELTVQLPKFRLKARMVLVEYPPAPLIPKTTDI	12939	qq
124	125	ä	ò
12938	79 KVVKKKTDDHDELIKKMLEQEIEKTELEKYEKIEFDVPKKLKPEFAALEPIKIERKEQKP	12879	පු
124	125	1;	ò
12878	19 IHEELVEEEQPEKILEVRVIDEVAEVEESQPIVEEVEDEEPQPATEETVEDVTKPKSKKK	12819	g
124	125	11	ò
12818	59 PEDTATAQITPSAQEEKSTQDDTKDTIQKTVKHKKTKPDTQKSVETSELPEVHKDYQISI	12759	g
124	52	12	ò
12758	99 PKPDKSQPISVLPDTTKPKKTKTPKTPKTEDTDQQVPDEPTETTVDTTDIPELTPTQTAQ	12699	g
124	25	12	ò
12698	39 EKLAPKPKKTVRKVKKDDLSDYVKKLIEEEIPKVDLEKYEKVEMPEKPVKLTVSDSIPEE	1263	Q
124	25	12	·ò
12638	79 KPVQEKTTKRVLKKIGPEEQTTFKITMIESEDNDSVTVIVDEEPEIASPQSIEEHPEQSK	1257	g

14798	9 IDEEEIKNVRIVTESDMHMYCSVVHISKVKKSQEGTYEVIATNREGEARLPITLKVRTTD	14739	ద
124	125		ે
14738	19 LSRRSMSRESSLADILEGIPPTFSKKPKAQYVDENTNVILECRLVAVPEPDIVWTFNGED	14679	a
124	Si	125	ેં
14678	.9 QDFQMFYDDDNVATLIIREVFPEDAGQFTVVAKNAAGFTSSTTELIVESPLSDHGSDATA	14619	g
124	S:	125	8
14618	9 KLPVFERPGPEDKPIAPRFIEKLOPIHTPDGYTVQFECKVEGNPRPQIAWFRETAIIKPS	14559	පු
124	ç.	125	ò
14558	9 NEAINLVEGEKVTVVVGRHSSEWWYVKKSTTEEEGWVPAQYLMEPEEYAQYVQNKLHEKID	14499	g
124	5	125	ે
14498	9 ODEEEEQFLIGIRHPKRDSVTYDEDSLTFKKKRKVVQQLFNEESENLNIMYSICNYIADN	14439	a
124 ·		125	ò
14438	9 IKIIQDFDDGEEPIIEEIRDDEDTIDEVEEPEEYFVEELPPDEVDFKLKPKKHPKPAYSV	14379	g
124		125	ò
14378	9 YADVENVTFRARSTKTKEDVDQEFNIALDSYAEEEISMSGKVKLKKPIKKTFSEAADEAK	14319	g
124	5	125	ò
14318	9 EAAAELSIKRQEEEYEEGEDIEEFVVSQQRKPKPLQITEEDEEAYTVKKLKRRKQVDIPE	14259	名
124	5	125	ò
14258	9 IIEEAVVIRKKPKKPFEPTVEDLEETEFSLSFKKPHTINEGVEEAATVLKKRPVKPTTLD	14199	a
124	9	125	ठे
14198	9 IVDAAIVKLKKPEPVDADEVVAEVTLKPKAKTEVTEEEFSVDVKLPKEKKERPVEIEEEE	14139	g
124	5	125	ठ
14138	9 EVQEEAKIVKKKPKKIDEVAVADELTVKVEEEVVPEPIVEEEVIEEFEIKKKPKEPEPED	14079	요
124	5	125	ò
14078	9 IEEIEEEIEEEKPAEYVIEVKESQPEAVEDKEVSLPKKKPKAPIVEEPEAEITLKPKVKSE	14019	8
124	5	125	8
14018	9 EVVEEPEABFLVKPKTPVQEVTEEAKITKSKKPVKEBEAAAELKVTITEEIPTEPEVQEI	13959	용
124		125	ਨੇ
13958	PQELVQEIBEIEIVEEPKAPEEQPTDFTFATKDSEKKPTVEELPEEQVTIQKKKKKAPVP	13899	8
124	9	125	જે
13898	IRRKKPKPEIKEEPEAEVTVSTPKPVEEVEATSSIAVIPEQPTEEEAADLKITIIEEETP	13839	9
124		125	à
13838	1 KETEPEKPABA1VEEEEPVVTEP1 EBAPKPEVFBEHKVRVI EETPRELVEBVI BEBVKV	13779	g
124		125	⋧
13778	I KTKKPKKKVTDVEAEELKIKITEEVPQEI PILEEVSEEEVITETKKTAPVVEEKTYKIG	13719	ရ
124	5	12	⋩
13718	9 EKPKEFTIRVSESEPKPEEPSVEQFTVKKRKPSVTFADEPATEIVIKESKPAEVVTEDAH	1365	ည

ò	125		
q	14799 1	KEAPQILEPLRNMVIREGESVVLSTQIVGNPPPKVTWYKDGKPVKNAKSDKDLHTLTLIT	14858
ò	125		130
g	14859		14918
ò	131		130
g	14919	KVSGNPVPEVQWLFNNTPLFPSERIQOVYDGENIELIIKDANPETDSGDYKCIASNPIGK	14978
ò	131		130
g	14979	TSHGARVIVEVDEVTFTKKLKKTITIBEVQSLTLECETSHVVTTKWFFNGKELSGMDHRV	15038
ò	131		130
g	15039	VVEDGKTHKLVIRNTNLRDSGTYTCKVKKQETQSTVEVLQRKPDFIKVLEDYEVTEKDTA	15098
ò	131		130
g	15099	ILDVELTTEATEVTWYKDGEKITPENKNVEFIKDGKARRLVIRDVTIHDEGQYTCKIEGQ	15158
ò	131		130
g	15159	ECSCELVVIELPPEIVEPLNDVAVTKGENAVFEVELSKGDALVKWFKNGKEIVFNERIQL	15218
ò	131		130
g	15219	AIDGKKQSLRIVKAKPEDVGEYSVQVGEQTSKAKLTVEEPLVDFVIRLPDITLATKTTDA	15278
ò	131		130
g	15279	ECTVQLSQPDVEVTWCKKGKP1KPNQKHEVFVEGTVRRLV1HDASDEDAGE1SCVAENVT	15338
ò	131		130
g	15339	SSTKLCVEELKLPPVITSDKDQTIKVKENDDVTFTVKYTGVPTPEACWTTRKVVIPKSKR	15398
ò	131		130
q	15399	TIPTIDEQSAKLTIKKVVDDDEGEYTVKLVNPVGEAEASLHLVIMRKPTAPGTPOPLEIM	15458
ò	131		130
g	15459	HDSITLYWKAPEDDGKSEIIEYILEYQDVKEEKWTEIRKIKDTTYTISKLKIDTEYVFRS	15518
ò	131		130
셤	15519	IAVNEVGPSPPSPLSPPIRLVPKVETKAPSVQEPLQDVVSELDKEVTLSCVFGGIPEPKV	15578
ò	131	TWSCLIT	137
g	15579	TWKKNGQVFESRSIRYENRVAKYTIEKTTIETEATYTCVATNEKGSAETSCRLKLOQKPV	15638
ò	138		137
qq	15639	LEVEDKYLTQKLRTGSILTIPATVRGYPQPTVTWHKETIEQKTTKSVTIETTETTSTYTV	15698
ò	138		137
g	15699	KKVTREQSGKYKVTATNESGTTYVECTVQVIDKPSRPQSLEIKDIKKDSIVLEWTPPVDD	15758
ò	138		137
g	15759	GGLDIEKYTLEKCDVQNNVMMKVSDFNKDIKSYAVQKLSMNAQYMFRVVAANPIGESEPT	15818
ò	138	EDTGFDL	144
q	15819	ESDPVTITKKFEKPSPPRGPTTVSGMNDTSFNLAWEPSETDGGSKIIEYIVEIREETETT	15878

36

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SDLAVLLGSAGQLWLAGQALDWRALYAGQQRRTLRLAPYPFQRERHWLDAPAAPQQDAQA 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988 AAVVRQALARARLRPEQIGYIEAHGTGTALGDPIELNALKSVFAHAPEAGRCAVGSVKTN 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGISHRRLATSHAFHSHMTEPILPAFADSVARLTLRAPAIPFVSNLTGAWIEPAQATDPG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1468 YWAAHLRGTVRFADGLOTLMOGGPHAWIEVGPGQTLSALARPCAGDALVLPSLGGGEGPK 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1228 VFMFPGQGAQQVGMARELYQEIAAFRAVVDRCAQVLRERAGFDLIQSLYGDGDPEASHLA 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHAGISSFGFGGTLAHMIVAQAPPAATAHGAQWPWHLLSLSAKTAPALEAMTEAVAGQLR 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLPDAALADAAYTHQAGRNAFAWRRMLVARDREDAAEALRARDPRRVFTAQVRPAVPAPV 1227
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                                                                                                                                                                                        588 GQGDRHPAEAAPDAPAQAADAPIAIIGLGCRFPGADDADAFWDALDGQVDAIGAVPQARR 747
                                                                                                                                 DAEAIDREQPFAFYGLDSMSAVQLAEALSVWMRVTVAPVVFWEHPNIARLAGFLAELSAA 687
                                                                                                                                                                                                                                               748 AAGTFDEPRAELPSQVRLGGFLDRVDAFDAAFFSISPLEAARMDPQQRLALEVAWQALED 807
                   508 QLVIVQELEFRQPVEPGMFECMASAVSMNVGVTPDVIVLVKAGAIPRTSSGKIRROQCRA 567
                                                                        568 DFLADRLPAMARWDRPVLAASPVPVAPGAPVLAAAREPVAVSAAVVEARLRAELAARLGL 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 RGRLMQSLPAGAMLSVALDEASLRAQLDGTLALAAVNGRQRCVVAGETTAVAALERRLDA
                                                                                                                                                                                                                                                                                                         808 AGIAASGLAGSTTGVFIGISTHDYENLQDRAGSELSVYSATGNAGSIVANRLSYCLDLRG
                                                                                                                                                                                                                                                                                                                                                                868 PSLAIDTACSSSLVAVHAACQSLRDGESTLALAGGVNLVLSTLSSEPFARAGMLSPDGRC
                                                                                                                                                                                                                                                                                                                                                                                                                          928 KAFDASANGYVRGEGCGVVVLKRLSDALRDGDPVRAVILGSAVMQDGRGNGLIAPNGSAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 GDLGFLHAGELYICGRLKDLIILNGLNİYPQDVELAAFESHARLRENGTIAFAVDRDDTE 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAYGMAEATLLIAFGWAIRFQGQPRCLPFSRLALQKGMAVAADDEADRIALASHGSALTG 387
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                                                                                                                                                                                                                                                                                                                        Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandder M., Choisne N., Claudel-Frenard.c., Cunnange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Rehsenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AHQEDTERY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 239; DB 16; Length 6889;
                                                                                                                                                                                                              Plasmid megaplasmid.
Bacteria: Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744917 MW; A7F31DCFFDED1D37 CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOMN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTITE; PS00606; B KETOACYL SYNTHASE; 1.
PROSITE; PS00237; G_PROTEIN RECEP F1 1; UNKNOW PROSITE; PS0012; PROSPHOPNITETHEINE; UNKNOWN_BROSHERMA; PS00P10 PROSPHOPNITETHEINE; UNKNOWN_BEQUENCE 6889 AA; 744917 MW; A7F31DCFFDEDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Pred. No. 8.4;
ive 27; Mismatches
                                                                                                  PRT; 6889 AA
                                                                                                                                                                  Probable peptide synthetase protein.
RSP0641 OR RS05860.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AL646079; CAD17792.1; -
Pro; IPR001227; Ac transferase.
Pro; IPR000954; Aminotran_3.
Pro; IPR000873; AMP-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bac luciferase.
Condensatn.
                                                                                                                             Created)
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Pfam; PF00668; Condensation; 4.
Pfam; PF00109; ketcacyl-synt; 1.
Pfam; PF00550; pp-binding; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000794; Ketoacyl-synt
                                                                                                                                                                                                                                                                                                                 MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50075; ACP_DOMAIN; 6. PS00455; AMP_BINDING; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGGILHLELLVAV--------
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aminotran 3;
                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00154; AMPBINDING
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                                                                                                  PRELIMINARY;
                          15879 YRSVGVTL 15886
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145 ---- GVTI 148
                                                                                                                                                                                                                                                       NCBI_TaxID=305;
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8	1588	:   ::  : SVEPSRAVTSMPVAAAMSSSVSNSASRAQAIQGALRGMVAKMLHADVARVDPDLPLLELG 1647
ò	78	77
qq	1648	ADSLMMVQAIGSIEQTYGVTVTVRQLFEELTTIAAIADYVDRQMPREARLEAAAEAPATV 1707
ઠે	78	77
q		PAAAVMPMPAPAPAAPVAAIAVDARPDAVPPLAAIPALPQSSLERLLSQQLDALSQLTAR 1767
ò	78	77
qq	1768	QLALFQGGTVAATAGGPASVAGETSPVVPTVMPAAVPVVAPAPASTAAPGGTHKPYVPYQ 1827
ò	78	77
<b>요</b>	1828	PVRVTAKADPFRDLSARQRAYLDGFVARYTERTRGSKALVQRYRPVLADNRVSAGFRFST 1887
ò	78	77
g	1888	KEMLYPVVSERSEGAYLWDPDGNVYIDLTWGFGVNLFGHRPAFVQEALDAQLKTGLELGP 1947
ò	78	LSVC
q	1948	OTRLAGEVAELVTRLTGLERVAFCNSGTEAIMLALRLARTVTRRDKIVVFAGSYHGWSDD 2007
ò	85	84
q	2008	TLMVADGAGTVAMAPGLQPGASAHTIVLDYGAPESLARIREHAHELAAVLVEPVQSRRPH 2067
ò	85	188
qq	2068	WQPREFLHALRELTREHGIALIFDEIIMGFRLHPGGAQAWYGIEADMATYGKVIGGGMPA 2127
ò	85	84
qq	2128	GMVAGSAAYLDAVDGGQWRYGDASYPQADTTFYAGTFCKHPLMLVAARAVLQRLAQEGPA 2187
ò	82	98
å	2188	: :  LQETLNARTAELVRRLNGVFADARVPVRAVHCGSSFRLLEASPSIDLLYYHLLAGGLYIW 2247
ò	89	888
Q	2248	EGRGMFLSTAHSDADVDRVVEIFADSVRAMLDGGFFEDGAPTPPSGGGGRSPFAAARVGG 2307
ò	89	88
qq	2308	PASTDAPVAPALAEAAVARLSAAPVPPATGGGIRFGISFFGHYASGYDAQKYRLLFEAAR 2367
ò	89	98
a	2368	YADAGGFSSLWLPERHFHAFGGLSPNPSVLSAALARETSHIQLRAGSVVLPLHHPVRVAE 2427
ò	89	88
Ω	2428	EWSMVDNLSQGRVGIACASGWHPNDFVFAPEAFGSHRELMFQRIEQIQALWRGEPLRVRD 2487
ò	89	88
q	2488	GSSREIEVKLFPMPRQPELPIWITIVGNPDTYRRAGEIGAGILTNLMGQTVEALECNLAL 2547
ò	89	88
qq	2548	YRQALVEHGHGVERSRVSVLLHTFVCEDAAEARAVARAPFIHYLRSSVGLFQNMVDSLGL 2607
ò	89	92
g	2608	QADVSTLSEDDRDYLLSVAYERYVEHSALIGSPATCRALVERLQAIGVDEIGCFIDFGVD 2667
ò	93	26

D.	2668	PDTVLGRLDQLALLKQSFETAAVDDDAAERYPLVPAQKGIWFECQISHEAALSYNTTTVL 2727
ò	93	65
g	2728	GLRGALDHAALARALQQVVDRHAALRSVVEADGEHQRVLPAVEVGLPLVDFSREADRDAA 2787
ò	93	101TDPGHADLV
g	2788	
ò	102	101
g	2848	RAACRGGAPGLPAASPFREQVERHQAYLRSDRYQQDRAYWRGQFGSLPPSLELSGRHARP 2907
ò	102	101
g	2908	SAPSHRARRHHLTIDGERYARLQQLSRKLGGTLFMTMLAGVAVLLQRLSGQAQMVIGVPM 2967
ò	102	101
g	2968	VVGRAEGSEASLVGCTLNLVPVRCDGSGDPSFAEFLGRIKRSVLEAHAHADYPFGHLLRD 3027
ે	102	101
Q	3028	LDLRASQRRPLAPVLFNLNRSLALPQFDALQAWLEQSPISFSPDDLTIDVMQLPDRLQVM 3087
ò	102	101
දු	3088	FQYQEVLFEHEAIERMAAQFVQLLDGIVADPACSIGRLALLSAEERRQIVDVWNAGEPVP 3147
ò	102	101
g	3148	EPSETLHAVFEAQVRRTPEAIAVEHEGWRVSYAELNARANRVAHALIGLGVGPDARVGLC 3207
ò	102	101
අ	3208	AERSVELVIGLLGILKAGGGYVPLDPSYPRDRLAYMLEDSAPVAVLAQSNTREPLGALSV 3267
ò	102	101
g	3268	PVLDLENPLEGEAEHDPQVTGLEPNHLAYVIYTSGSTGQPKGVLVEHRQVARLFTSTQPW 3327
ò	102	101
g	3328	FGFGAEDVWTLFHSFAFDFSVWELFGALLHGGRLVVVPKLTARSPQAFYALLCEAGVTVL 3387
ò	102	101
gg	3388	NOTPSAFROLMAAQQEAPAARHRLRQVILGGEALEVGALRPWYERAENAGTQLANMYGIT 3447
ò	102	104
g	3448	ETTVHVSYRALEAADAQGTGSPIGRRIPDLRVYVLDAHGEPVPVGVTGEMYİGGAGVARG 3507
ò	105	
g	3508	YLNRPELTAERFVVNPFHGEGRERMYRTGDLGRWLPDGSLEYQGRADAQVKLRGFRIELG 3567
ò	105	104
g	3568	EIEASLSQCAGVREAVVTVREDVPGEQRLVAYYVSGEAIEAQALREQLGGSLPAYMVPAA 3627
ò	105	104
8	3628	YVRLAHLPLTSNGKLDRKGLPAPEGHAYASTAYEAPOGEVEQTLAGIWOTLLGVERVGRH
ò	105	
QQ	3688	DDFFALGGHSLQAVRLVTGVRVQLGAELGLTALFAQPSLSAVAQAIVRGQGSALQAITAA
ò	105	104
පු	3748	I DRSEALPLSFAQQRLWLLAQMEGGSEAYHIPVGLRLKGELDEDALGRALDRIVARHEALR 3807

OGFLIRG 38  OYADYAV 39  CTILSADL 39  CTILSADL 39  CTILSADL 42  CTILSADL 42  CTILSADL 42  CTILSADL 42  CTILSADL 44  CTILSAD	1	011
THE EVREGGATOR VASADVGFALDRYDLGGGADRECTLAALSEREANTPFDLEGGELIGFUNTLARGE  CLVKLGEGEHVLLITWHHIVSDGASGONLARELGALYEAYBGGEDPLFALPIOYADYAY  GLYKLGEGEHVLLITWHHIVSDGASGONLARELGALYEAYBGGEDPLFALPIOYADYAY  WORRALEGGELGRGGAYMEGALARAGALSELESPERANTPFDLEAGE  VARGSATVSELLDRYKAKAKYLEAGAHGDLFEGOVVERVREVRSLSHSFIFGAVFBHINTEA  VALSTRALSELBSLARENATAKLDIQLELAEAGGRIVGTANYTRSEVEGLIGFVNTLALR  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGTAFERACOWRTPDAVAL  KHADQQUSYRELDARANRLAHHLRELGVAADVCVGLCVDRSIEMIVGGANTGTARRA  KHADQQUSYRELDARANRLAHHLRELGVAADVCVGLCVDRSIEMITGAGANATARRA  KHADQQUSYRELDARANRLAHHLRELGVAADVCVGCANABAADVGTATOLGGILKAGGANVC  CEFCQLAYVITTGGSTGQFKGVAYTHOGVASLVYSGCERFGVSSGSRVLQFASISFDAAV  SEIGMGLLCCACLVLAPAQALTHINAYGPTEATVCATWSRALTAQDAPSIGGPLGWRVYVU  1VAGEACPPSLYNLASGGRANINAYGPTEATVCATWSRALTAQDAPSIGGPLGWRVYVYSGE  0 SLENGCALAGIWGTLLIGVERVGRHDDFFALGGHSLDRYRTOLGABLTAGNATATOLGABLGTELGTERAO  0 SLENCORLAGIWGTLLIGVERVGRHDDFFALGGHSLGAVRLVAGWRTOLGABLGTERACON  0 TIEAQTLREGGAAVAGATREPTEGGAAVRANADAVRTOLGABLGTERACON  0 SELGEDALRRSLDRI VARHBALRTFRYTEEGGAAVRANADANASADVGFALDCOUDCOGADREDA  0 GECUCHACOUTCHAGANANATARFATEFFORMANADAVRANADANASADVGFALDCOUDCOGADREDA  0 GECUCHACUTCHAGANATARFATRETGGAAVGRANADAVRANADANATARFATOLGABLAGTERACON  0 TIEAQTLREGGAALAGIWGTLLIGVERVGTABARTFATOLGGARTACOUTCHAGATARFATOLGABLGTARACOUTCHAGATARFATOLGABLAGTARACOUTCHAGATARFATOLGGABLAGTARACOUTCHAGATARATATATACOUTCHAGATARACOUTCHAGATARACOUTCHAGATARATATACOUTCHAGATARACOUTCHAGATARACOUTCHAGATARACOUTCHAGATACOUTCHAGATATACOUTCHAGATACOUTCHAGATATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATACOUTCHAGATAC	ú	
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WORRWLEGGELGROCAYWEOALAGAPTLLSLPTDRARPAQODYAGGSVEVVPDETLSADL  KRLSORHGTTLFMTVLAGWSALLSRLSGOEEVVVGSPVANRTRSEVEGLIGFFVNTLALR  VDLSLRALSLESLARENATAKLDIGLELAEADGRIVGENVKPVRSLSHSPIFOAVFSWHNTBA  VDLSLRALSLESLARENATAKLDIGLELAEADGRIVGLVDRSIEMISERSTAGRYADYLOR  MIQAMVADDGQOVGRIALLGEAERAQVLQAMNATERAWPAATLPALFEAGVMRTPDAVAL  KHADQQVSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYVP  LDPDY POARLAYIFODAMLSVLVSKRALAGRLPTAMTGVVELUDAEPAWADYPPTPPOVO  GEPGQLAVVIYTSGSTGQPKCVAVTHQGVASLVYSGCERFGVSSGSRVLQFASISFDAAV  SEIGMGLLCGACLVLAPAQALAPGAALTHLDRERITHYTLPPAVLALMPFGALGILKAGGAYVP  1VAGEACPPSLVRLWSEGRTMINAYGPTEATVCATWSRALTAGDBABSIGGPIGNYRVYVUL  1VAGEACPPSLVRLWSEGRTMINAYGPTEATVCATWSRALTAGDBABSIGGPIGNYRYYVUL  GSLEYQGRADAQVKLRGFRIELGEIEARLSGCAGVSEAVYTVREDAPGEGAYASTAYBAPQ  AIEAQTLREQLGSRLPEYWVDAAYVRLEHLPLTPNGKLDRKGLPRPGGAYASTAYBAPQ  GEVEGTLLAGIWOTLLGVERVGRHDDFFALGGHSLQAVRLURGURGGSEAYHIPVGLRLK  SELSAVAQAIVRGCSALFAITVADRSGPLPLSFSGORLWFLAQWRGGSEAYHIPVGLARLK  SELSAVAQAIRSCORLDGGABRARRFVTEBGGANQRVASADVGFALDCVDLGGGADREDA	æ	
WORRMLEGGELGROGAYWEOALAGAPTLLSLPTDRARPAQDYAGGSVEWVPDETLSADL  KRLSORHGTTLFMTVLAGWSALLSRLSGGEEVVVGSPVANRTRSEVEGLIGFFWNTLALR  WNGSATVSELLDRVKAKVLEAQAHQDLFFEGWYERVKPVRSLSHSPIFGAVFSWHNTEA  WLGAMVADDGGQVGRIALLGEAERAGVLGAMDYLVGLCVDRSIEMIVGLGILKAGGAYDR  KHADQQVSYRELDARANRLAHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYDR  KHADQQVSYRELDARANRLAHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYDR  GEFGQLAYVIYTSGSTGQPKGVAVTHQGVASLVYSGCERFGVSSGSRVLQFASISFDAAV  SEIGMGLLCGACLVLAPAQALMFGAALTHLLDRERITHVTLPPRAVLALMFEGALPADCHL  IVAGEACPPSLVRLWSEGRTMINAYGPTEATVCATMSRALTAQDAPSTGPTPPQVO  GSLEYQGRADAQVKLRGFRIELGEIEARLSGCAGSSEAVTVREDAFGGAYATAYVSGE  ALEAQTLREQLGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKKGLPAPEGGAYASTAYBAPO  ALEAQTLREQLGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKKGLPAPEGGAYATAYVSGE  ALEAQTLREQLGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKKGLPAPEGGAYATAYVSGE  ALEAQTLREQLGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKKGLPAPEGGAYATAYVSGE  ALEAQTLRGUGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKKGLPAPEGGAYATAYVSGE  ALEAQTLRGUGSRLPEYMVPAAYVRLEHLPLTPNGKLDRKGLBAPEGGAYTTBLFPAQB  SLSAVAQAIVRGGGSALPAITVADRSGPLPLSFSGORLWFLAQMEGGSEAYHIPVGLRLFF  GEVEOTLAGIWOTLLGVERVGRHDDFFALGGHSLQAVRYASADVGFALDCVDLGGQADREGA	-	
KRLSORHGTTL.FMTVLAGMSALLÍSRLSGOEEVVVGSPVANRTRSEVEGLIGFFVNTLALR  VINYGSATVSELLDRVKAKVLEAQAHQDLEFECVVERVKFVRSLSHSPIFGAVFSWHNTEA  VDLSLRALSLESLARENATAKLDIQLELAEADGRI VGTLNYATALFERSTAGRYADYLOR  MIQAMVADDGQQVGRIAALLGEAERAQVLQAMNATERAMPAATLFPALFEAGVMBTPDAVAL  KHADQQVSYRELDARANRLAHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYVP  KHADQQVSYRELDARANRLAHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYVP  GEFGGLAYVIYTGGSTGQPKGVAVTHQGVASLLYSSGCERFGVSSGSRVLQFASISFDAAV  SEIGMGLLCGACLVLAPAQALMFGAALTHLLDRERITHVTLPPAVLALMFEQALPADCHL  IVAGEACPPSLVRLWSEGRTMINAYGPTEATVCATMSRALTAQDAPSIGGPIGNYRYVVL  OGN	8	WORRWLEGGELQRQGAYWEQALAGAPTLLSLPTDRARPAQQDYAGGSVEVVFDETLSADL
KRISORHGTTLFWTVLAGWSALLSRUEGGEEVVVGSPVANRTRSEVEGLIGFFVWTLALR  VNVGSATVSELLDRVKAKVLEAQAHQDLPEGGVVERVKPVRSLSHSPIFGAVFSWHNTEA  WLQAMVADDGQQVGRIALLGEAERAQVLQAMNATERAWPAATLPALFERSTAQRYADVLOR  KHADQQVSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYVP  KHADQQVSYRELDARANRLAHHLRELGVAADVLVGLCVDRSIEMIVGLGILKAGGAYVP  LDPDYPQARLAYIFQDAMLSVLVSKRALAQRLPIAWTQVVELDDAEPAWADYPPTPPQVQ  GEPGGLAYVIYTSGSTGQPKGVAVTHQGVASLVYSQCERFGVSSGSRVLQPAFFSPDAVA  1VAGEACPPSLVRLWSEGRTMINAYGPTEATVCATMSRALTAQDAESIGGPIGNVRYVVL  1VAGEACPPSLVRLWSEGRTMINAYGPTEATVCATMSRALTAQDAPSIGGPIGNVRYVVL  ON	-	110
VDLSLRALSLESLARENATAKLDIQLELAEADGRIVGTLAYATALFERSTAGRYADYLGR VDLSLRALSLESLARENATAKLDIQLELAEADGRIVGTLAYATALFERSTAGRYADYLGR MLQAMVADDGGOVGRIALLGEAERAQVLQAMNATERAWPAATLPALFERSTAGRYADYLGR KHADQQVSYRELDARANRLAHHLRELGVAADVLQAMNATERAWPAATLPALFERSTAGRYADYLGR LDPDYPQARLAYIFQDAMLSVLVSKRALAQREDIAWTQVVELDDAEPAMADYPPTPQVQ GEPGQLAYVIYTSGSTGQPKGVAVTHQGVASLVYSQCERFGVSSQSRVLQFASISFDAAV  SEIGMGLLCGACLVLAPAQALMPGAALTHLLDRERITHYTLPPAVLALMPEQALPADCHL IVAGEACPPSLVRLMSEGRTMINAYGPTEATVCATMSRALTAQDAPSIGGPIGNVRVYVL  ON	σ	KRLSQRHGTTLFMTVLAGWSALLSRLSGQEEVVVGSPVANRTRSEVEGLIGFFVNTLALR
VDLSLRALSLESLARENATAKLDIQLELAEADGRIVGTLAYATALFERSTAGRYADYLGR  VDLSLRALSLESLARENATAKLDIQLELAEADGRIVGTLAYATALFERSTAGRYADYLGR  MLQAMVADDGGQVGRIALLGEAERAQVLQAMNATERAMPAATLPALFERSTAGRYADYLGR  KHADQQVSYRELDARANRLAHHLRELGVAADVLQARNATERAMPAATLPALFERSTAGRYADYLGR  LDPDY PQARLAYI FODAMLSVLVSKRALAQRLPIAMTQVVELDDAEPAMADYPPTPQVQ  GEPGQLAYVI YTSGSTGQPKGVAVTHQGVASLVYSQCERFGVSSQSRVLQFASISFDAAV  SEIGMGLLCGACLVLAPAQALMPGAALTHLLDRERITHVTLPPAVLALMPEQALPADCHL  IVAGEACPPSLVRLMSEGRTMINAYGPTEATVCATMSRALTAQDAPSIGGPIGWRVYVL  IVAGEACPPSLVRLMSEGRTMINAYGPTEATVCATMSRALTAQDAPSIGGPIGWRVYVL  GSLGQCLAGINGTLLGFEIEARLSQCAGVSEAVYTVREDAPGGGRLVAYYVGE  GSLCQCACAGRADAQVKLRGFRIELGEIEARLSQCAGVSEAVYTVREDAPGGGRLVAYYVGE  GSLCQCALAGIWQTLLGVERYGRHDDFFALGGHSLQAVRTQLGARGCTLTELPAQP  GEVEQTLAGIWQTLLGVERYGRHDDFFALGGHSLQAVRTGLGARGCTLTELPAQP  GEVEQTLAGIWQTLLGVERYGRHDDFFALGGHSLQAVRTGLGARGCTTTLPVGLRLK  GELDEDALRRSLDRIVARHEALRTRFVTEEGQAVQRVASADVGFALDCVDLQGGADREGA	Н	110
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GELDEDALRRSLDRI VARHEALRTRFVTEEGQAVQRVASADVGFALDCVDLQGQADREQA	25	
	28	GELDEDALRRSLDRIVARHEALRTRFVTEEGQAVQRVASADVGFALDCVDLQGQADREQA

ò	125	124
음	4888	LATLSEREANTPFDLAHGPLIRGRLVKLGEQEHVLLITMHHIVSDGWSQGVLARELGSLY 4947
ò	125	124
g	4948	EAYRAGNADPLPALPIQYADYAVWQRRWLEGGELQRQGTYWEQALAGAPTLLSLPTDRAR 5007
ò	125	124
g	5008	PPQQDYAGGSVEVVFDAELSTGLRTLSQRHGTTLFMTVLAGWSALLSRLSGQGEVVVGSP 5067
ò	125	
g	5068	VANRTRSEVEGLIGFFVNTLALRVEVGGATVSELLERVKAKVLEAQAHQDLPFEQVVERV 5127
ò	128	127
g	5128	RPVRSLSHSPVFQAALSWLNTEAVGLSLELEGLTIEGVDAGQAAAKFDLTLELRETSEGL 5187
ò	128	127
g	5188	AGSLDYATALFDRATIERYLGYLHRLLKAMAADDSQEVNRIALLDEGERTQLLESWNETK 5247
ò	128	127
q	5248	APYPRASTIHGLFEAQVRRTPEAIAVVHEGQQVSYAELNARANRVAHALRRLGVGPDARV 5307
ò	128	127
g	5308	GLCAERSVELVVGLLGILKAGGGYVPLDPSYPQDRLTYMLEDSAPVAVLTOSNTREQLGA 5367
ò	128	127
g	5368	LSVPVLDLDGPLEEAEHDPQVTGLEPHHLAYVIYTSGSTGRPKGVMNEHRGVVNRLWWAO 5427
ò	128	127
g	5428	QTYRLDASDRVLQKTPFGFDVSVWELFWPLLAGARLVWARPEGHKDPAYLAATIEQAGIT 5487
ò	128	129
g	5488	TLHFVPSMLQLFLDQVEAGRCQGLRRMLCSGEALSHALQQRSLARFPHSELHNLYGPTEA 5547
ò	130	129
g	5548	AIDVTAWRCNAEIHPGVVPIGRPIANTQMYVLDGHQQPVPLGVTGEIYIGGIGVARGYLN 5607
ઠે	130	129
đ	5608	RPELTAERFVVNPFHGEGRERMYRTGDLGRWLPDGSLAYQGRADAQVKLRGFRIELGEIE 5667
ò	130	
엄	5668	ARLSQCAGVSEAVVAMREDVPGEQRLVAYHVSDEAIEAQTLREQLQASLPEYMVPAAYVR 5727
ò	130	129
g	5728	LEHLPLIFNGKLDRKGLPAPDGQAYASAAYEAPQGEVEQTLAGIWQTLLGVERVGRHDDF 5787
ò	130	129
qq	5788	FALGGHSLQAVRLVAQVRTQLGAELGLTELFAQPSLSAVAQAIVRGQGTALPAITVADRG 5847
ò	130	129
g	5848	EALPLSFAQQRLWFLAQMEGGSEAYHIPVGLRLKGELDEDALRRSLDRIVARHEALRTRF 5907
ઠે	130	129
g	5908	EVQEGQAVQRVASADVGLTLDWADLSAEAASEHQLGLLAEAWARAPFDLEQGPLIRGRLV 5967
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InterPro; IPR0012085, Adh zn_family.
InterPro; IPR004410; PabD.
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Pfam, PF02801; ketoacyl-synt_C, 6.
                                                                                       MEDLINE=96186896; PubMed=8635756;
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Pfam; PF00107; adh zinc; 1.
                                                                                                                                                                                                                                                                               Gene 169:9-16(1996).
EMBL; X86780; CAA60459.1; -.
HSSP; P25715; 1MLA.
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MEDLINE=9616695; PubMed=8635730;
Molnar I., Aparicio J.F., Haydock S.F., Khaw L.E., Schwecke T.,
Koenia A., Staunton J., Leadlay P.F.;
"Organia A., Staunton J., Leadlay P.F.;
Straptomyces hygroscopicus: analysis of genes flanking the polyketide synthase.";
                                                                                                                                                      6028 RWLEGGELQRQGTYWEQALAGAPTLLSVPTDRARPPQQDYAGGSVEVIFDETLSAGLRKL 6087
                                                                                                                                                                                                                                                                                  6088 SQRHGTTLFMTVLAGWSALLSRLSGQEEVVVGSPVANRTRSEVEGLIGFFVNTLALRVEV 6147
                                                                                                                                                                                                                                                                                                                                                                                                                 6148 GSATVSELLGRVKSRVLEAQAHQDLPFEQVVERVRPVRSLSHSPVFQAALSWLNTEAMVL 6207
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                              5968 KLGEQEHVLLITWHHIVSDGWSQGVLARELGALYEAYRAGNSDPLPALPIQYADYAVWQR 6027
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MEDLINE=95372374; PubMed=7644502;
Schwecke T., Aparicio J.F., Molnar I., Koenig A., Khaw L.E.,
Haydock S.F., Oliynyk M., Caffrey P., Cortes J., Lester J.B.,
Boehm G.A., Staunton J., Leadlay P.F.;
"The biosynthetic gene cluster for the polyketide immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSYPQDRLAYMLEDSAPVAVLAQSNTREQLGALSVPVLDLDRPLLEEAEHDPQVTGLEPH
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Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 MVMALQHVLVPRTLHVDEPSRHVDWTDGAVALVTENQPWPDMGRPRRAGVSSFGISGTNA 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 GSDTGVFMGAYPGGYGVGADLGGFGATAGAVSVLSGRVSYFFGLEGPAVTVDTACSSSLV
Aparicio J.F., Molnar II., Schwecke T., Koenig A., Haydock S.F., Khaw L.E., Staunton J., Leadlay P.F., Staunton J., Leadlay P.F., Staunton J., Leadlay P.F., Staunton J., Leadlay P.F., Stranton of the biosynthetic gene cluster for rapamycin in Streptomyces hygroscopicus: analysis of the enzymatic domains in modular polyketide synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Score 238; DB 2; Length 10223; Pred. No. 31; 17; Mismatches 25; Indels 9871;
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UNKNOWN 2.
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DR PROSITE; PSG0075; ACP DOWANN; 6.

R PROSITE; PS00066; B KETOACYL SYNTHASE; 6.

R PROSITE; PS00165; DEHYDRATASE SER THR; UNKNOWN 2.

R PROSITE; PS001015; PHOSPHOPANTETHEINE; 6.

R PROSITE; PS010162; QOR ZETA CRYSTAL; 1.

PHOSPHOPANTETHEINE; 6.

R PROSITE; PS010162; AA, I177169.
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Ω	999	FARIHQQVWGLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVVGHSVGELAA	625
_	23	0EDTERYVL	31
	626	GYVSGLWSLEDACTLVSARARLMQALPPGGVMVAVPVSEDEARAVLGEGVEIAAVNGPSS	685
•	32		31
0	989.	VVLSGDETAVLQAAAALGKSTRLATSHAFHSARMEPMLEEFRTVAERLTYQTPRLAMAAG	745
>-	32		31
0	746	DRVTTAEYWVRQVRDTVRFGEQVASYEDAVF1ELGADRSLARLVDGVAMLHTDHEAQAAI	. 508
>-	32	•	31
Ω	908	SALAHLYVNGVTVDWTALLGDAPATRVLDLPTYAFQHQRYWLEGADRAAAGGHPLLGPAV	865
>	32		31
۵	866	GLAEASGVLFTSQVSRSGDLWLQDQTVLPATAFAEMALAAADETGCGLVEELTVEALLLL	925
>	32		31
Ω	926	PDDGAVQVQTWVSEPDDAGRRQLSIHARYSDDELWTRLATATLATTGRVSGWQAGEAWP	985
>	32		31
۵	986	PAGAVPVEARVPSLRGVWRRGSEVFAEVALDDTHDATRFLLHPGLMTAAFAAVGEETPAA	1045
>-	32		31
Ω	1046	WQGLTLHARNAAELRVRLTSQDDETLSVEAVDSTGLPVLTARSLALDAVPVNEPATSATD	1105
>	32	TNFNIGA	38
Д	1106	:       LITLTWAGIATRQQQTGLTVGAFEDLAADGDAPVPDVVVFTALPGNDDPLAQTRILTAQV	1165
>-	39		38
Ω	1166	LRTVQEWIGGERFSDSTLVVRTGTGLAAAAVSGLMRSAQSEHPGRFILVESDDDALTPDQ	1225
>-	39		38
۵	1226	LAATVGLDEPRLRISDGRYEVPRLTRAHADEPEPERAWDPDGTVLITGGSGVLAGIVARH	1285
≥-	39		38
۵	1286	. LVAERGVRHLLLLSRGTPDRALLSELAELGAAVDTAACDVSDRAELARVLARVSPEHPLT	1345
≥	39		38
ڡۣ	1346	. AVIHTAGVVDDGVVESLSAQRLETVFRPKADGAWHLHELTRDADLAAFVMYSSAAGVMAG	1405
≥-	39		38
Q	1406	; AGQGNYAAANAFLDALAEERRAEGLPALAVAWGLWEDASGLTAQLTDTDRDRIRRGGLRA	1465
≿	39		38
Q	1466	; ISAEHGMRLFDNASRHSEPVLVAAPMEPVRDAEVPALLRSLHRPNVRRAALAGGAQWLAA	1525
≿	39		38
Q	1526	: LAPEERAKALLKVVRDTAATVLGHADARTIPVTGAFRDLGIDSLTAVELRNGLAKVTGLR	1585
≿	39		38
ð	1586	: LPATLVFDYPTPAVLAARLGELFTGENPVLVRTASVVGQDEPLAIVGMACRLPGGVSSPE	1645
≿	39		38
დ	1646	5 DLWRLVESGTDAISGFPADRGWDAESLFDPDPDAVGKSYCVEGGFLDSAASFDAGFFGIS	1705

ò	39	36
Q	1706	PREALAMDPQQRLIMEVSWEAFERAGIEPGSVRGSDTGVFMGAYAGGYGAGADLGGFAAT 1765
ò	39	38
g	1766	ASATSVLSGRVSYFFGLEGPAITVDTACSSSLVALYQAGYALRQGECSLALVGGVTVMAT 1825
ò	39	38
qq	1826	PQSFVEFSRKSGLDSDGRCKAFADSADGTGWAEGVGVLLVERLSDAQAKGHQVLAVVRSS 1885
ò	39	38
g	1886	AVNQDGASNGLSAPNGPSQQGVIRQALANAGLTTAEVDVVEAHGTGTTLGDPIEAQAVIA 1945
ò	39	38
g	1946	TYGQDRERPLLLGSLKSNIGHAQAASGVSGVIKMVMALQHNTVPRTLHVDEPSRHVDWAA 2005
ò	39	38
g	2006	GAVELVRENOPWPGTDRPRRAGVSSFGVSGTNAHVILESAPPAQFAEEAQPVETPVVASD 2065
δ	39	86
g	2066	VLPLVISAKTQPALTEHEDRLRAYLAASPGVDTRAVASTLAVTRSVFEHRAVLLGDDTVT 2125
ò	39	38
g	2126	GTAVSDPRVVFVFPGQGWQWLGMGSALRDSSIVFABRMAECAPALREFVDWDLFTVLDDP 2185
ò	39	38
q	2186	AVVDRVDVVQPASWRMMVSLAAVWQAAGVRPDAVIGHSQGBIAAACVAGAVSMRDAARIV 2245
ò	39	38
qq	2246	TLRSEAIARGLAGRGAMASVALPAQDVELVDGAWIAAHNGPASTVIAGTPEAVDHVLTAH 2305
ò	39	43
g	2306	EARGVRVRRITVDYASHTPHVELIRDELLDITSDSSSQAPVVPWLSTVDGSWVDSPLDVE 2365
ò	4	43
g	2366	YWYRNLREPVGFHPAVGQLQAEGDTVFVEVSASPVLLQAMDDDVVTVATLRRDDGDATRM 2425
ò	4	47 P816 47
q	2426	LTALAQAYVHGVTVDWPAILGTATTRVLDLPTYAFQHQRYWLRSVDRAAADGHPLLGTVV 2485
ò	48	47
පු	2486	DLPASDGVVLTGRVSLATHTWLADHAVRGSVLLPGTAFVDLVVRAADEVESDVVDELVIE 2545
ò	48	47
q	2546	TPLLLPQTGGVQLSVSVGGADESGHRAVMVFSQADNTDTWTRHVTATVSTSDSTVSLPEF 2605
ò	48	AQ 49
g	2606	aswppaqarpvsvadfydrlaaagteygpafqglqaawrdgdtvyaevvlaeeqaqeaar
ò	50	FRVH53
QQ	2666	 FAVHPALLDAAMHASVLHTPDTDQQSVRMPFSWNHVQIRATDTAMLRVAATPTTDGWSVR 2725
ò	54	53
QQ	2726	VADDTGRPVATIGSLVTRPVTADTLGSAADDLLTLVWTEIPTPQQSSLSVGRYEDLADGD 2785

ð	0y 54 53		
ក	Db 2786 VPVPDVAVYTARPEADGSPDPLVQTRTLJAQVLQTAQAWLGGERFTDSTLVVRTGTGLAA 2845	<u> </u>	Jabb Suchtan
ó	Ov 54	ò	
, ĉ	TATOR TOWNSHIP AND THE	qq	3926 HNGPASTVVA
ā (	Z846 AAVSGEMKSAQSEHFGKFVLVESDDDSEILENGEATIVGEDEFKEKVNDGKFEVFKLAKVN	ò	76 SL
ò i	TO THE TOTAL PROPERTY OF THE TOTAL PROPERTY	qq	3986 QAPVVPWLS1
Ö	2906 AAEPESETVWDPHGTVLITGGSGVLAGALARHLVTERGVRHLLLLSRTTADEGLLNELGE	ò	78
ő	0y 54 53	<b>Q</b> Q	4046 OAMDDDVVTV
ā	Db 2966 LGARVETADCDVSDRAGLARVLAGVSPEHPLTAVIQTAGALDDGVLETLTAQRLDTVLRP 3025	ò	
õ	Qy 54 53	QC	4106 ORFWAEGADF
ā	Db 3026 KADGAWHLHELTRNTGLAAFVMYSSAAGVMGNPCQGNLAAATAFLDALADQRRAEGLPAL 3085	-	
ò	Oy 54 53	. f	4166 FVELVVRAAD
Ω	Db 3086 ALAWGSSEETSDLIGLRTISAERGMRLFDSASHRGEPLLMAASLDPARAAEVPALLRSLR 3145	: à	
δ	Oy 54 53	· 8	4226 DAWTRHVSAT
Ω	Db 3146 RPVARRAASADGGVQWLAALAPAEREKALLKVVCDSAAVVLGHADARTIPVTGAFKDLGV 3205	ò	78
δ	Ογ 54 53	\$ E	ממטידים מיים אפני
Ö	Db 3206 DSLTAVELRNSLVKATGLRLPATMVFDYPTPTALAARLDELFTGENPAPVREPVPAVAQD 3265	3 8	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ố	Oy 5453	ž á	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ជ	Db 3266 EPLAIVGMACRLPGGVSSPEDLWRLVESGTDAVSGFPTDRGWDVEGLFDPDPDAAGKSYR 3325	2 2	1240 VKAIGSAIL
6	Qy 54 53	ò 1	
ជ	Db 3326 AEGGFLDTAAGFDAGFFGISPREALAMDPQQRLLLEVSWEAFERAGIEPGSVRGSDTGVF 3385	α 	4406 IELFIPUQIO
6	Qy 5453	ò	78
ជ	Db 3386 IGAFPVGYGAGAAREGYGATAAPNVLSGRLSYFFGLEGPAITMDTACSSSLVALHLAAQA 3445	ପ୍ର	4466 QVLQAVQAWI
	Oy 54 53	ò	78
i	3446 LRNGECSMALAGGYTVMATPEVFTEFARGRASDGRCKAFADSADGAGFSEGAGLLLVE	qq	4526 QLAATVGLDE
ić	, r	ò	82
<b>o</b> 7	ביידוליים אחש זל אונא ז אל מדיומל ל מחליות אחשינים אל מלימ ארים מודולים אחש זל אונא ז אל מדיומל א מחלים אחשינים אל מלימי אומל מחלים מל מל מל מימי אומל מחלים מחלים אחשינים אל מלימי אומל מחלים מל מל מל מל מל מל מל מל מל מל מל מל מל	q	4586 PAETAERPLO
<b>5</b>	3506 KESDAKKNGHQVLAVVKGSAVNQDGASNGFTAFNGFAQQKVIKQALANAGLITAEVDVVE	ò	82
o i	0y 54 59	qa	4646 PGDRVFGLVG
5 6	3366 AMGIGII DGDFIEAQAVIAIIGQDKEQFELLGIEKSNVORIQAAAGVSGVIKNVALLQAS	ò	87
ò i	09	qa	4706 SVLIHAAAGC
<u></u>	3626 TVPRTLHVNEPSRHVDMSAGAVELVTENOSMPVTGRPRRAGVSAFGVSGTNAHVVLESAP	۸٥	87
o	60	ପ୍ଧ	4766 LDTTDSRGVE
Õ	3686 PAQSVNNAQPVATPVVASELVPLVISAKTLPALTEHEDRLRAYLAASPGADMRAVGSTLA	ò	87
oʻ	65	අ	4826 DLMDAGPDRI
Ω	Db 3746 LTRSVFEHRAVLLGHDTVTVTGTGTAVSNPRVVFVFPGQGWQWLGMGSALRGSSVVFAER 3805	ò	87
ŏ	Qy 65 64	; f	4886 OOLDANGTVI
ם	Db 3806 MAECAAALSEFVDWDLFAVLDDPAVVDRVDVVQPASWAVMVSLAAVWQADGVRPDAVIGH 3865	2	87
6	Фу 65 64	<del>,</del>	ò

a	3866 SQGEIAAACVAGAVSLKDAAKSVILKSQAIAKCLAGKGAMASVALFAAEEELVUGANIAA	0 3 4 0
ò	65GAP	75
đ	3926 HNGPASTVVAĠAPEAVDRVLAVHEARGVRVRRIAVDYASHTPHVELIRDELLDITAGIGŚ	3985
ò	16 SL	77
q	3986 QAPVVPWLSTVDGTWVEGPLDVEYWYRNLREPVGFDSAVGQLRAEGDTVFVEVSASPVLL	4045
ò	78	77
Q	4046 QAMDDDVVTVATLRRDDGDATRMLTALAQAFVEGVTVDWPAILGTATTRVPDLPTYAFQH	4105
ò		77
qq	4106 QRFWAEGADRSVAGGHPLLGVAVELPESDGVLLTGRVSLATHAWLADHAVRGSVLLPGTG	4165
ઠે	78	77
đ	4166 FVELVVRAADEVGCDVVDELVIETPLLLPSSASVHLSVSVGEADESGRRGVTVFSRADGA	4225
ò	78	77
Q Q	4226 DAWTRHVSATIGVSGAALSLPELAAWPPAQAQPVGLGDFYDRLTGAGYEYGPAFQGLQAA	4285
ò	78	77
đ	4286 WRDGDTVFAEVALAEEQAEEAARFAVHPALLDAALDAGILNTLDNAEQGVRLPFSWNGVQ	4345
ò	78	77
Q	4346 VRATGSATLRVADNPTSDGWSVRVADDSGRPVATVDSLVTRPVTADTLGSAADDLLTVVW	4405
ò	78	77
පු	4406 TEIPTPQQTGLSVGRFEDLADGDVPVPEVVVCTALPDSSENPLAPLDPPDPLVQTRTLTT	4465
ò	78	77
đ	4466 QVLQAVQAWLAGERFTDSTLVVRTGTGLATAGVSGLMRSAQSEHPGRFVLVECDDNLTLQ	4525
ò	7815S/C	81
Q	4526 QLAATVGLDEPRLRVCDGRFEVPRLARANTPESSPLTIPGDRAWLLEQSHSGTLRDLALV	4585
ò	82	81
g	4586 PAETAERPLQSGEVRVDVRAAGLNFRDVLIALGTYPGEAVIGAEAAGVVLENGPEVQDLA	4645
ò	82GWSOT	98
QQ	4646 PGDRVFGLVGGGFGAVAIADRRMLGVIPDGWSFTTAASVPVVFATAYYGLVDLAGLSAGE	4705
ò	87	. 98
g	4706 SVLIHAAAGGVGMAATQIARHLGARIYATASTGKQHVLREAGLEDARIGDSRTTGFREMV	4765
ò	87	96
g	4766 LDTTDSRGVDVVLNSLSGDFVDASLDLLPRGGRFVEMGKTDIRDPHQVTADRPGTSYQAF	4825
ò	87	98
g	4826 DLMDAGPDRLREIIADLLALFAQGVLLPLPVRAWDIRQAREAFSWMSRARHIGKIVLTVP	4885
ò	87	98
q	4886 QQLDANGTVLVTGGSGVLAGIAARHLVAEQGVRHLLLLSRSTPDDALINELGELGARVDT	4945
ò	87	06

8	4946	AICDVSDRAGLARILAGVSPEHPLTAVIHTAGALDDGVVESLTAQQLETVLRPKADGAWH	5005
÷	16		06
g	2006	LHELTRDADLAAFVMYSSAAGVLGSGGQGNYAAANAFLDALAEQRRGEGLPALAVAWGLW	5065
ò	91		06
QD	9905	EDASGLTAEMTDTDRDRIRRGGLRAISAGHGMGLLDAASRHGEPVLLAAAMEPVREAEVP	5125
ò	91		06
a	5126	ALLRLLHRPVARRAASTGGSSVQWLARLAPVEREKALLKLVCDGAATVLGHADASTIPAT	5185
ò	91		06
g	5186	AAFKDLGIDSLTAVELRNSLTKATGLRLPATLVFDYPTPTALAARLGEWFVGETPVPVRT	5245
ò	91		06
g	5246	SVSVVAQDEPLAIVGMACRLPGGVSSPEDLWRLLESGTDAVSGFPTDRGWDVENLFGPAA	5305
ò	91		06
Op	5306	GDSYRLQGGFLDAAAGFDASFFGISPREALAMDPQQRLVLEVSWEAFERAGIEPGSVRGT	5365
ò	91		06
g	5366	DTGVFMGAYPGGYGIGADLGGFGATASAVSVLSGRVSYFFGLEGPAITVDTACSSSLVAL	5425
ò	91		06
qq	5426	HQAGYALRQGECSLALVGGVTVMATPQTFVEFARQGGLAGDGRSKAFADSADGAGFSEGV	5485
ò	91		06
g	5486	GVLLVERLSDAQAKGHQVLAMLRSSAVNQDGASNGLTAPNGPSQQRV1QAALSNAGLAAH	5545
ò	16		06
g	5546	EVDVVEAHGTGTTLGDP1EAQALLATYGODREQPLLLGSVKSNLGHTQAAAGVSGV1KMV	5605
ò	91		06
qq	5606	MALQRGFVPRTLHVDEPSRHVDWSAGAVALVTENQPWPDMGRARRAGVSSFGISGTNAHV	2665
ò	91		06
QQ	9995	ILESAPPTQPADNAVIERAPEWLPMVISARTQSALTEHEGRLRAYLAASPGVDMRAVAST	5725
ò	91		06
g	5726	LAITRSVFEHRAVLLGDDTVTGTAATDPRVVFVFPGQGSQRAGMGEELAAAFPVFARIHQ	5785
ò	91		06
g	5786	QVWDLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVVGHSVGELAAGYVSGL	5845
ò	91		06
a	5846	WSLEDACTLVSARARLMQALPAGGVMVAVPVSEDEARAVLGEGVE1AAVNGPSSVVLSGD	5905
ò	91		06
g	5906	EAAVLQAAEGLGKWTRLATSHAFHSARMEPMLEEFRAVAEGLTYRTPQVSMAAGDQLTTT	5965
ò	91		06
g	5966	. EYWVRQVRDTVRFGEQVASYEDAVFVELGADRSLARLVDGVAMLHGDHEAQAAVSALAHL	6025
ò	91		06
g	6026	: YVNGVTVDWPALLGDAPATRVLDLPTYAFQHQRYWLEGTDRMAAGGHPLLGEAVAVPGSD	6085

ò	91	06	5
QQ	6086	GVLLTGRVSLATHPWLADHAVRGSVLLPGTGFVELVVRAADEVGCDVIDELVIETPLLLP 614	145
ò	91	06	0
gg	6146	QTGGVQLSVAVAESDDSGRRAVTVFSRADNVDTWTRHATVTVSNSDTTLSLPDLSAWPPA 620	205
ò	16	06	0
S	6206	QAQPVNVADFYDQLTVVAYEYGPAFQGLQAAMRDGDTVHAEVALAEEQAQDAARNAVHPA 62	265
ò	91	06	0
g	6266	LEDAALHAGILNTPDTEQGVRLPFSWNQVQVHAVGSAMLRVAVTQAADGWSVRVADDTGR 63.	6325
ò	91	06	0
g	6326	PVATIGSLVTRPVTADTLGSTTDDLLALTWTEIPAPQETSLTIGRFEDLADADVPVPEVV 63	6385
ò	91	06	0
g	6386	VFTARPDSSENPLAQTRTLTAQVLQKIQAWLAEERFTDSTLIVRIGTGLAAAAVSGLMRS 64.	445
ò	91	93	m
g	6446		505
ò	94	66 63	en.
g	9059	WDPDGTVLITGGSGVLAGIAARHLVAERGVRHLLLLSRSAPDGALISELGELGAQVATAV 65	6565
ò	94	66 63	e G
g	9959	CDVSDRPGLVRVLADVSPEHPLTAVIHTAGVVDDGVVESLTAQRLDTVLRPKADGAWHLH 66	6625
ò	94	66 63	<u>س</u>
g	6626	ELTRDADLAAFVMYSSAAGVFGSAGOGNYAVANAFLDALAEQRRAEGLPALALAWGLWEG 66	6685
ò	94	96DP	ທ
g	6686	TSGLTANLTDTDHDRIRRSGMRAISAEHGMRLFDGASRRRDPVLVAAAMEPVREAEVPAM 67	6745
ò	96	100 GHADL 100	100
q	6746	LRSLHRPVARRAASGGAVRCLAALAPEERAKALVKVVCDSAATVLGHADVDSIPVTAAFR 68	6805
ઠે	101	10	100
g	6806	DLGVDSLTAVELRNSLTKATGLRLPATLVFDYPTPGALAARLEELFTGENPVQVRTPVSA 68	6865
ò	101	10	100
엄	6866	VGQDEPLAIVGMACRLPGGVSSPEDLWRLVESGTDAISGFPTDRGWDVENLFDSDPDAAG 69	6925
ò	101	10	100
g	6926	KSYCVEGGFLATAANFDASFFGISPREALAMDPQQRLVLEVSWEAFERAGIEPGSVRGSD 69	6985
ò	101	01	100
g	9869	TGVFMGAFPGGYG1GADLEGYGATAGLNVLSGRLSYFFGLEGPAVTVDTACSSSLVALHO	7045
ò	101	01 V 10	101
g	7046	AGYALROGECSLALIGGUTVMATPHTFVEFSRORGLASDGRCKAFADSADGTGWSEGVGV	7105
ò	102	LYITRF	101
d	7106	:   LLVERLSDAQAKGHQVLAVVRSSAVNQDGASNGLSAPNGPSQQRVIRQALANAGLTTAEV	7165

⋧	108	
ð	7166	DVVEAHGTGTTLGDP1EAQAVIATYGQDRDQPVLLGSVKSNVGHTQAAAGVSGVIKMVMA 7225
≿	108	107
ą	7226	LOHGLVPRTLHVDEPSRHVDWTDGAVELVTENQSWPEAGRPRRAGVSSFGVSGTNAHVIL 7285
à	108	
ą	7286	ESAPPTQAVDDVRPADAPVVASVMASELVPLVISAKTQSALAEYEGRLRAYLAASPGVDM 7345
à	108	107
g	7346	RAVASTLAMTRSVEEHRAVIVGDDTVSGTAATDPRVVFVFPGGGSQRAGMGAELAAAFPV 7405
à	108	110
8	7406	 FARIHQQVWDLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVIGHSVGELAA 7465
ò	111	115
9	7466	AYVSGLWSLEDACTLVSARARLMQALPAGGVMVAVPVSEDEARAVLGEGVEIAAVNGPSS 7525
à	116	. 115
qq	7526	VVLSGDEAAVLQAAEGLGKWTRLATSHAFHSARMEPMLEEFRAVAQGLTYHAPGVVMAAG 7585
ò	116	119
В	7586	   DRYMTAEYWVRQVRDTVRFGEQVASYEDAVFVELGADRSLARLVDGVAMLHGDHETQAAI 7645
ò	120	gvT 122
g	7646	   GALAHLYVNGVTVDWTALLGDVPVTRVLDLPTYAFQQQRYWAEVGRSADVSGAGLDAVGH 7705
ò	123	122
g	7706	PLLGAVVALPGSDGVLLTGRVSLATHAWLADHAVRGSVLLPGTGFVELVVRAADEVGCDV 7765
ò	123	122
g	7766	VDELIVEAPLLLPQTGGVQVSVSVGEADESGHRVVTIFSRADNADTWVRHVSAVISTSDS 7825
ò	123	122
g	7826	TVSLSEFASWPPAQAQPVDVTGFYDPLMAEGYEYGPAFQGLQAAWRYGDTVFAEVALAEE 7885
ò	123	122
g	7886	QVREAARYPSVHPALLDAALHACTLECADAEVGVGLPFSWDGVRVHAGGSAMLRVAVTQA 7945
à	123	122
g	7946	ADGWSVRVADEIGRPVANVGSLVTRPVTADALGSAADDLLALTWAEIPAPEGTGLTVGRF 8005
ે જે	123	122
g	9008	EELVSDGDVPVPEVAVFTALPDNDDDPLEQTRKLTGQVLQAVQEWLGGERFSDSTLVVRT 8065
ò	123	122
g	8066	GTGLAAAGVSGLMRSAQSEHPGRFVLVESDDDALALDQLAAAVGLDEPRLRISDGRFEAP 8125
ò	123	122
q	8126	RLTRTHAAEPESEKVWDPDGTVLITGGSGVLAGIAVRHLVTERGVRHLLLLSRSAPDEAL 9185
ò	123	QuG
qq	8186	 INQLGELGARVETAACDVSDRAALAQVLAGVSPEHPLTAVIHTAGVLDDGVVESLTAQRL 8245
è	126	125

	0	14(	ે
139	6 TVFVEVSASPVLMQAMDDDVVTVATLRRDDGDATRMLTALAQAYVHGVTVDMRAVLGDVP	9266	g
	0	140	ò
		9206	g
139		136	ò
9205	S AQDVELVDGAWIAAHNGPASTVIAGTPEAVDHVLTALRQRGAGAADHVDYASHTPHVELI	9146	쉱
135	:	136	ò
9145	 ; wqaagvrpdavighsqeeiaaacvagavsmrdaarivtlrsqaiarglagrgamasvalp	9086	, d
135		134	ò
9085	; GSALRDSSVVFAERMAECAAALSEFVDWDLFAVLDDPAVVDRVDVVQPASWAVMVSLAAV	9056	q
133		134	ò
9025	YLAASPGVDIRAVASTLAVTRSVFEHRAVLLGDETVTGTAVSDPRIVFVRGGGGWQWLGM	9968	g
133		134	ò
8968	GVSSFGISGTNAHVILESAPAQSVGDTAGSTPVLVSELVPLVISAKTQPALTEHEDRLRA	8906	g
133		134	ò
8905	toraagusguikmumalohsmuprtlhudepsrhudwäagaveluaenopwpetgrprra	8846	g
133	SH	132	ò
8845	VIRAALSNAGLAPHEVDVVEAHGTGTTLGDPIEAQAVIATYGQGRGEPLLLGSLKSNVGH	8786	원
131		132	ò
8785	FADAADGTGWAEGVGVLLVERLSDAQANGHQILAVVRSSAVNQDGASNGLSAPNGPSQQR	8726	g
131		132	ò
8725	FTVDTACSSSLVALHQAGYALRQGECSLALVGGVTVMPTPQTFVEFSRQRGLSADGRCKA	8666	QQ
131		126	8
8665	FERAGIEPGSVRGSDTGVFIGAYPGGYGIGADLGGFGTTAGAASVLSGRVSYFFGLEGPA	8606	QQ
125		126	ò
8605	WDVENLYDPDPDAPGKSYSVQGGFLDAAAGFDASFFGISPREALAMDPQQRLMLEVSWEA	8546	q
125		126	ò
8545	FTGENPAPVRGPVSAVAQDEPLAIVGMACRLPGGVSSPEDLWRLVESGTDAISGFPTDRG	8486	ą
125		126	તે
8485	GHADTST1PATTAFKDLGIDSLTAVELRNSLAKATELRLPATLVFDYPTPTALAARLDEL	8426	q
125		126	à
8425	AAPMEPVRDAEVPALLRSLHRPVARRAAAAGGARWLAALAPAEREKALLKLVSDGAATVL	8366	දු
125		126	à
8365	EGLPALAVAWGLWEDASGLTAQLTDTDRDRIRRGGLRAISAEHGMGLFDSASRHSEPVLV	8306	ą
125		126	≿
8305	DAVLRPKADGAWNLHELTRDADLAAFVMYSSAAGVLGSGGOGNYAAANAFLDALAEQRHA	8246	ą

MLTGRVSL 9385	142	GGVQLSVS 9445	142	KPVDVAGF 9505	142	DAALHAGI 9565	142	VATIGSLV 9625	142	FTALPDSG 9685		SEHPGRFV 9745	142	PDGTVLIT 9805		DVSDRAGL 9865	142	LTRDIDLA 9925	142	SGLTAKLT 9985		RLLHRPVA 10045	-DLGV 146	KDLGV 10102	nadaceae;
326 ATRVLDLPTYAFQHQRYWABAGRSADVSAAGLDAVGHPLLGAVLAMPGSDGVMLTGRV	140TGFTGF	 386 ATHAWLADHAVRGSVLLPGTGFVELVVRAADEVACDVVDELIVEAFLLLPQTGGVQLS	143	446 VGEADESGHRAVTVFSRADSADAWVRHVSATVSVSDTTVPTSDLTAWPPAQAKPVD	143	506 YDQLTRAGYEYGPAFQGLQAAWRDGDTVFAEVALAEEQTQDAARFAVHPAVLDAALHAG	143	566 LNTPDADRDTVRLPFSWNHVQVHVTGSATLRVAMTRVADGWGVRVADDIGRPVATIG	143	626 TRPVAADALGSAVDDLFALTWTEIPVSQQVGVTVGKFEDLADGEVPMPDVVVFTAL	143	686 DPLAQTRRLTAEVLQAVQVWLAGERFTDSTLVVRTGTGLAAAAVSGLMRSAQSEHPG	143	746 LVESDDDTLTPDQLAATVGLDEPRLRVIDGRYEAPRLTRTGVAEPEFEGVWDPDGTVL	143	806 GGSGVLAGIAARHLVAERGVRHLLLLSRSAPDEALISELAELGAAVVDTAVCDVSDRA	143	866 ARVLAGVSPDHPLTAVIHTAGVLDDGVVESLTARRLDTVLRPKADGAMNLHELTRDI	143	926 AFVMYSSAAGVLGSAGQGNYAVANAFVDALAEQRRAEGLPALALAWGLWEDASGLTAKL	143	986 GTDHDRIRRSGLRTITAERGMRLFDIASROGEPVLVATPMEPVREVEVPALLRLLHR	143	0046 RRAASTGDSSAQWLVGLAPEERAKALLKVVRDSAATVLGHADARSIPATGAFKDLGV	12 15168 PRELIMINARY; PRT; 9376 AA. 15168, 15168, 15168, 15168, 15168, 15168, 15168, 15168, 15168, 15168, 15168, 15168, 151698 (TrEMBLrel. 08, Last sequence update) 151699 (TrEMBLrel. 20, Last annotation update) 1516990/210 synthetase. 15169 1516990/210 syntingae). 1516990/210 syntingae). 1516990/210 syntingae). 1516990/210 syntingae). 151690/210 syntingae). 151690/210 syntingae). 151690/210 syntingae). 151690/210 syntingae). 151690/210 synthetase gene 151690/210 synthetase gene 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase 151690/210 synthetase
00 90	ò	.6 qa	ò	op 8	ò	op 96	ò	36 QQ	ò	op 96	ó	op 96	ò	.6 qa	ò	DP 96	ò	96 40	ò	42 63	ò	Db 99	ò	DP 10(	RESULT 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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29;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1040 QAGILYHHISAEQGDPYTLKALFALSDRAQLDDFSGALQGVINRHDILRTAVLWEDLDEP 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100 VQVVLRQAELHVTELLLDPVDGPVDEQLHQRFDRRHYRLDVRTAPLMRIVFSHDPVNDRW 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: | |
| 1220 RDMLGDIDEPTLPFGLQDVQDRGRNLEEASVTLAAELNLRLRAQARQAGVSVASLMHLAW | 1279
                                                                                                                                                                                                                                                                                                                                                                          980 AAGGGSEVVVPANLIPEHCDRITPQMLPLINLSQAQIDHVVKDMPGGVANVQDIYPLAPL 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1160 LAMLLCHHLVSDATSLSVILQEIQAHLLGQGNALGEAVPYRNYVAQARLGVSEAQHEAFF 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1400 YQLPVDLNVDDLGDAFTLTIQAVQQISATRIGEYMQVALRNLVDALEHTPQAALNSLSIL 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1460 PDDERELLITGFNDTAHPYPRDVLIHQLIEQQAAQRPDACAVRGDSGTLLTYAELNQQAN 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1280 ARVLGNVSACEQVVFGTVLLGRMQAGDGADRALGMFINTLPLRVDIGATTVAEGLKATHE 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1340 RLTALLGHEHAPLVLAQRCSGVAAPTPLFSALLNYRHSVVSDVRQKLPGLGGSSLRHRRP 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1520 QLAHRLIELGVEPDTRVAVSLRRGAĖMVÄLLGILKAGGAYVPIDPDLPDARQAYMLSDS 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1580 APRAVLTSHELLADLPDLGVPALVLDGRDDSALLKKQPTGNPDAKALDLQPNHLAYVLYT 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1640 SGSTGTPKGVMNEHLGVVNRLLWARDAYQVNSQDRVLQKTPFGFDVSVWEFFLPLLTGAE 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1700 LVMARPSGHQDPDYLAQVISDAGITLLHFVPSMLDVFLEHRSTRDFPQLRRVLCSGEALP 1759
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                 Ouery Match 30.7%; Score 237; DB 2; Length 9376; Best Local Similarity 1.2%; Pred. No. 27; Matches 94; Conservative 24; Mismatches 28; Indels 7809;
R InterPro; IPR000873; AMP-bind.
R InterPro; IPR001842; Condensatn.
R InterPro; IPR001801; Ppantne_attach.
R InterPro; IPR001031; Thiosererase.
R Ffam; PF00501; AMP-binding; 9.
R Ffam; PF00505; pp-binding; 9.
R Pfam; PR00157; Thiosererase; 1.
R RRINTS; PR00154; AMP-BINDING; 9.
R PROSITE; PS00455; AMP BINDING; 8.
R PROSITE; PS00455; AMP BINDING; 8.
R PROSITE; PS00012; PH0SPHOPANTETHEINE; UNKNOWN_S.
R PROSITE; PS00012; PH0SPHOPANTETHEINE; UNKNOWN_S.
R PROSITE; PS00012; PH0SPHOPANTETHEINE; UNKNOWN_S.
R PROSITE; PS00012; PH0SPHOPANTETHEINE; UNKNOWN_S.
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g	1760	O RALORRFEQHLKGVELHNLYGPTEAAIDVTAWECRPTDPGDSVPIGRPIANIQMHVLDAL 181	6.1
ò	14	.4	
අ	1820	:0 GQLQPMGVAGELHIGGIGVARGYLNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANG 187	6/
à	14	4	
g	1880	O ALEYLGRNDFQVKIRGLRIEIGEIEAALAKHPAVHEAVVTAREDIPGDKRLVAYYTQTAE 193	68
à	14	.4	
g	1940	O HTAVDLETLRGHLQQVLPEYMVPAIYVLLEAMPLTSNGKLDRKALPAPDGDALISRGYEA 1999	6
à	14	.4	
g	2000	O PQGEIEEQIAVIWQDLLGVEQVGRHDHFFELGGHSLLAVSLIDRLRKQDLNLNVNTVFTA 205	6
à	14	4 13	
a	2060	0 PSVREMALAISQEKQALFRAPANRIPAHCTQLTPDMLPLVELSVAQIELIASAVPGGAAN 211.	6
⋩	14	4	
ဥ	2120	O IQHIYPLAPLQEGILFHYLLNLERDAYLVRSTIEFDSRARLDAFLEGLQTVIDRHDVLRS 2179	6
⋧	14	4	
ą	2180	SVHWVGLPQAVQVVHRQAQSPIHTLTLRPDEDALSQLDRLSDPGRLRLDLRQAPLLLAYI 223	6
⋩	14	4	
ð	2240	ARDPDSERWLLALIDHHMISDHVTLELILEEIRLLMRGOSAELLPPQPYREFVAQTLASP 229	o
≿	14	4	
ð	2300	SSAHEAYFTGRLADVDSPTAPFELLEVQGDGNDVEESELALSSDLCARIRTQARERGMSP 235	6
≿	14	4	
ą	2360	AVLFHVAMAQVLARCTGRDDVVFGTAVTGRLQGTLGAERAMGMFMNTLPVRVQLATQSVQ 241	σ,
≿	14	13	
Ω	2420	ELVMATHRDLSELLSHEQASLALAQRCSSVATGVPLFSSLLNYRHQNEDSQLQWPGLRLL 247	6
≽	14	13	
Ω	2480	DSAERTNYPLCLSVNDYGSDLGLLIHSVQPADPQRLCAMMQCALEQLTDALAHTPQKEVT 253	6
≥.	14	4 13	
۵	2540	O QLDVLPAAERNLLLETFNQTRQDYPTDLCIQHLFEAQVRTQPDAIAVAFQAQRLSYAELN 2599	Ø
<u>≻</u>	14	417	
مِ	2600	ROANRLAHHLIGLGIGPDDRVAICVERGVEMMVGLLGVLKAGAAYVPLDPAYPAERLAYM 265	6
≽	18	3	
۵	2660	IEDSQPAALMTQRHLQEYLPTLTLPLVLLDDDQRKTFTERDDNPVVEALGVRNLAYVIYT 271	6
<u>≻</u> -	18	3 17	
Q	2720	SGSTGNPKGVMIEHRGLVNYSVDAARLFDLSPTDTVLQONTLNFDLSVEEIFPALLAGAT 277	6
>	18	17	
Д	2780	LTPSREIFGSEGTENHGINPTVLHLTAAHWHTLVAEWHKQPQVAEGRLQHVRLINVTGDA 283	6
>	18	17	
Q	2840	) LSAOKLKLWDEVRPAHTRLINTYGPTEATVSCTAAYVSHDAAAGSEGSGNATIGKPMANT 2899	·

ò	18	VFQAHQED	25
gg	2900	:       : RIYLLDAHQQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERPLADPFSESPDARMYKTGD	2959
ò	26	TERYV	30
g	2960	:   LARYMADGRIEYLGRNDFQVKVRGFRIELGEIEARLGNCTGVKEAVVIAREDNPGDKRLV	3019
ઠે	31	L1	32
g	3020	AYVVAQPQSQLTAADLRAELAPQLAEYMLPSAFVLLDELPLTPNRKLDRKALPAPDADAL	3079
ઠે	33	NUN	35
qq	3080	ISRGYEAPQGETETQIVAIWQDLLGIEQVGRHDHFFELGGHSLLAVSLIERLRKQGLNLN	3139
ò	36		36
q	3140	: VKTVFTAPTVREMALAISQDKHVLFQVPANRIPAHCTQLTPDMLPLVELSVAQIELITSA	3199
ò	37		36
q	3200	VAGGAANIQDIYPLAPLQDGILFHYLLNRERDAYLMRSMIEFDSRARLDAFLEGLQTVID	3259
ò	37		36
셤	3260	RHDILRSSVHWIGLPQAVQVVHRQAQLPVHTLTLTPEEDALSQLDRLSDPGRLRLDLRQA	3319
ò	37		36
g	3320	PLLLAYIARDPNSERWLLALIDHHMISDHVTVELILEEIRLLMRGQSADLLPPQPYRDFV	3379
ò	. 37		36
g	3380	AQTLASPSSAHEAYFTRRLADVDSPTAPFELLEVQGDGNDVEEAKLALNSDLCIRIRTQA	3439
ઠે	37	20°E	39
g	3440		3499
ò	40		39
С	3500	LTTQGAQELVMATHRDLSELLSHEQASLALAQRCSSVATGVPLFSSLLNYRHQGEDNRLO	3559
ઠે	40		39
g	3560	WPGMRLLDGTERTNYPLCLSVNDYGSELDLIIHSMQPANPQRLCAMMQCALEQLTDALAH	3619
ò	4		39
g	3620	TPQMAVTQLDVLPAAERNLLLETFNQTRQDYPTDLC1QHLFEAQVRTQPDA1AVAVOGGR	3679
ò	40		39
g	3680	LSYADLNRQANRLAHHLISLGIVPDDRVAICVERGVEMMIGLLGVLKAGAAYVPLDPAYP	3739
ò	40		6.9
qq	3740	AERLAYMITDSQPAALLTLPGLQDRLPALSMPLVLLDDEQYQGLAECDDNPVVPTLGVRN	3799
ò	20		6
g	3800	Layviytsgstgnpkgvmiehrglvnysvdaarlfdlsqsdtvlqqntlnfdlsveeifp	3859
ò	20		0
q	3860	allagatlapsrei fgsegtethgi optvlhlttahwhtlvaewhnopqaaeorlohvrl	3919
δ	. 20		<b>4</b> 0
g	3920	INVTGDALSAQKLKLWDEVRPAHTLLINTYGPTEATVSCTAAYVSYDAAAGSEGSGNATI .	3979

		,,,
96E qa	980 GKPMANTRIYLLDAHQQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERFLADPFSESPDA 4	4004
0,		
Db 4040	RMYKTGDLARYMADGRIEYLGRNDFQVKVRGFRIELGEIEARLGNCKGVKEAVVIAREDN	4099
oy . 6	61 60	,
Db 4100	PGEKRFVAYVVAQPQTQITAAELRAELAPQLAEYMLPSAFVLLDELPLTPNRKFDRKALP	4159
o,	61TEPEGAPNIT-ANLTSSLLSV	0
Db 4160	APADDAFASREHVEPQGATEIALAQIWQŚLLDLERVGRHDQFFELGGHSLLAWRLISQAR	4219
٥٪	81 8	80
Db 4220	HQLGVELGLAALFAHPEVSALAVAIAQAGRSKFPDIVPVARDQAWPLSFGQQRLWFLAQM	4279
	81 8	80
Db 4280	EGASAAYHI PAGLSLHGNLNLKALQRALERI VARHEGLRTTFMQGDDGQPVQRI SPADTG	4339
ò	81 8	80
Db 4340	FNLQMHDLQGLADAEEKLQALASEESLQSFDLQQGPLIRGRLIRMAEDHHVLLLTLHHIV	4399
ò	81 -CGWS	84
Db 4400	 SDGWSVDVLTRELSALYAAFSQDQDDPLAPLELQYLDYAVWQRRWLSGDVLQQQSNFWQQ	4459
ò	88	84
Db 4460	TLADAPALLMLPTDRARPALQDYAGAALPVVFDKDLTRGLKALSQRRGSTLFMTVMAAWA	4519
ò	85	84
Db 45;	4520 GLLGRLAGQDDVVIGTPVANRTRSEVEGLVGLFVNTLAIRVDLSDKPTAETLLARVKQQT 4	4579
ò	85	6
Db 45	4580 LDAQAHQDLPFEQVVEVINPLRSLSHSPIFQAMLSWENNEASDLTLGDMTLKSIELAADT 4	4639
δ	8 06	6
Db 46	4640 AQFDLTLDMAEVDEQLVGTLEYATALFDESTMRRYLGYFQRVLEAMVADDQQVLEHVALL 4	4699
ò	3 06	68
Db 47	4700 GADEREHLLAGLNATEAPFPQDRTIHQLFEERVQAQPDAIAVAFGAQRLSYAELNRQANR 4	4759
à	90	93
Db 47	4760 VAHHLISLGIKPDDRVAICVERGVEMLIGVLGVLKAGAAYVPLDPAYPAERLAYMIĖDST	4819
ò	, 56	93
Db 48	4820 PSALLAQRDVQAHLPTLDLPLVLLDEDQRTTLSERDDNPVVETLGAHNLAYVIYTSGSTG	4879
ò	þ6	93
Db 48	4880 VPKGVMVEHRGLFAVSAAWEQLYALHAPLNHLQMAGFFDVFSADLIRSLAFGGTLVLCPR	4939
ò	94DPGHADLVL	102
Db 49	4940 ETLMDPPALYRLLSEESIGFADFVLAVLNALLGWVEETGHDLSFMRTVVCGSDIWTAHSA	4999
O,	103	102
05 qa	000 RQLRKLCGDHVQVVQAYGVTEASIDSTCFEFEATSQVDGVLPIGRALANTRIYLLDELGQ	5059
ó	103	102

3 8	103	YITR 106
5 8	9 6	 
Q Q	5120	ELEAKLAEVAGVAESUVALVEDSSOSIFIKALITATION SAVAGAVESUS SE
ò	101	106
qq	5180	GPALTPRALRQQLQLNLPEYMIPAAFVRMAALPLSANGKLDRRALPEPDADAFDQHDFEA 5239
ò	107	106
q	5240	ADGPLETAIAAIWADVLGVAQVGRHDDFFALGGHSLLVMRVLAQVRQQLNLEVSPSVFFA 5299
ò	107	106
đ	5300	APVLRQFAERLGNTQDNARVAIKPVQRSGALPLSYAQQRLWFLAQLEGGSAAYHIPAGLR 5359
ò	107	106
qq	5360	LRGNLDQASLQRALDRIVARHEALRTTFVQEQGQPAEQRISAAETGFRLQLQVLAGQTDA 5419
ò	107	106
qq	5420	EDKLLAIAAQEASEHFDLVNGPLVRGRLVRMANDNHVLLVTMHHILSDGWSTGVLNRELG 5479
ò	107	106
qq	5480	ALYAPFRQGAGDPLPALPVQYVDYALWQRDWLSGDVLQQQRQYWQQALAGAPALLTLPTD 5539
ò	107	106
q	5540	RPRPAQQDYSGQTLELVLDTQLTRGLKALSQRHGSSLFMTVMGAWAALLGRLSGQDDVVI 5599
ò	107	106
qq	5600	GTPVANRMSAEVENLIGFFVNTLAIRVDLSGTPSVEALVRQVKQRTLAAQANQDLPFEQV 5659
ò	107	110
g	5660	VEVVQPQRSLSHSPIFQAMLSWQNNEDTALVLGDLTLQGVAVAGDTAKFDLALDIGEVDG 5719
ò	111	110
සු	5720	QLIGTLEYATALFDESTMRRYRGYFLRLLEAMAADDQQVLEQVPLLDTAEREYLLKDINA 5779
ò	111	110
<sub>업</sub>	5780	TERTYPVGQLMHRLFEAHAEAAPQAIAVRQGEQTLTYAELDSRANALAOHLRKHGVGPGT 5839
ò	111	110
g	5840	RVAILLDRSVELLASMLATLKCGAAYLALDRLAPEERLRFMLEDSEAIMLLSRSDLTAPD 5899
ò	111	110
q	5900	MIPRLDLDTLELSALNQEPVVPATEVAGETPACIIYTSGSTGVPKGVIVTHNGIVRLVQD 5959
ò	111	110
qq	5960	NGYYDFSAEDRVAFSSNPAFDASTPEIWGALLNGCQSVIIEPQVLLEPVAFAALLKRHGV 6019
ò	111	110
qq	6020	TAMISSTALFNLYAGLIPEALAGLRMIMCGGERADPASFRRVREHSAQVRLFNGYGPTEG 6079
ò	111	110
qq	6080	TTCATSYEIFDVLPDTLSLPIGKPNANVRVYVLDARREPVPMGVVGDIYIGGTGVALGYL 6139
ò	111	

۾	6140	NRPELTAERFSEDPFSOOAGARLYRTGDLARWLPDGNLEYLARNDGOVKVRGFRVELGEI 6199	
	121		
۾ .	6200	ESVLHLYDGVRNSVVVAHEASPGDTRLVAYYTVHAGVAAPDPEDLRAQLSADLAEYMVPS 6259	
≿	121	120	
ą	6260	VFVRLDALPLTLNGKVDQKALPVPDLNAMFERTYVAPEGATEQALAEIFQELLGLERVGR 6319	
≿	121	120	
ą	6320	HDGFFELGGHSLLAAQLVSRVRQQLNGDMALRQLFNHPTVAELAKVVDGLQTVDSDSIEP 6379	
≿	121	120	
ą	6380	IERNAPLALSFSQQRLWFLDRLDPGASSAYHMPMSLLLRGELDHRALKAALDRLVARHĘS 6439	
≿	121	120	
ð	6440	LRTTFELHGEQPVQVIAAADSGFALAEDDLRSQPYEQASLNASRIADSEAAAPFDLRQGP 6499	
<u>~</u>	121	VTO 123	
ą	6500	LIRGRLLRLADDEHMLLITQHHIISDGWSVGVLINEFTALYQAFTEQRPDPLPALSIQYA 6559	
⋩	124	LGGACSPT	
ą	6560	DYAAWQRRTFTGERLAEQADLWREHLGGAPTLLSLPTDRPRPVVQSYRGGAVPVTIDA 6617	
⋩	132	137	
ð	6618	ALHQRIERFCQAHNVTLFMGLLSAWSVLMTRLGNBRDVVIGVPSANRGRTETENLIGFFV 6677	
≿	138	137	
ą	6678	NALALRVDLTQNPSVAQLLEQVRQTTLAAHEHQDIPFEQVIEALQPPRSMSHSPLCQVAL 6737	
≿	138	137	
ą	6738	SLDNTSIGGELKLPGLSLHPVLQAHETAQFDLMLTLASENGALNGVIEYASDLFDRSTVE 6797	
⋩	138	137	
ą	6798	RFAQHFHTLLEAMVEDVAQPVLGLPLLSPAQRLASPALLQPKAVFASGLMVHQRFEQFAA 6857	
.≿	138	137	
ą	6858	AHPONIALVFGRHEVSYOALNRRANRLAHELLAQGVRPDDRVAILAERGTOMICAVLAVL 6917	
⋩	138	137	
ą	6918	KSGAAYVPLDPTYPTERLGYLLTDSAPVALLAQSACLDVLPAHSVPVLTLGADNDSADLA 6977	
⋩	138	. 137	
ą	6978	DESVDRNPEPAALGLSREHLAYVIYTSGSTGLPKGVLVEHGNVARLFDATAGQFNFGHED 7037	
⋩	138	137	
ą	7038	VMTPFHSFAFDFSVWEIWGALCYGGKLVIVPSEVARSPDDFYALVCEQQVTVLNQTFSAF 7097	
à	138	137	
ą	7098	RQFIQARERSPQEHALREVVFGGEALDFRSLQPWTARTPLSRTRLVNMYGITEITVHATY 7157	
ጵ	138		
g	7158	YPISQSEIDTAMPSLIGPALDDLCLRILDDYQQPVPVGVNGEIYIGGAGVARHYLNRTEL 7217	
ጵ	138	137	
g	7218	NAERFIADPYALQSGARLYRTGDVAHYRSDGGVVNVGRNDSQIKIRGFRIELGEIEAQLL 7277	

કે ક	·	APHMI.PSARVTIR 7337	7
g C	9/7/	37.4.100	;
ò	ογ 138	137	~
qq	Db 7338 TWPLTTNGKLDRAALPAPDQFATVSRDYEAPLGAIETTLAAAWQELLGVERVGRQDHFPE	GVERVGRODHFFE 7397	97
ò	Оу 138	137	7
QQ	Db 7398 LGGHSFLVISLIERLRQIGLLLDVSTVFSAPTLQAMAAVLAGGTAAERVAPANLIPVDCT	RVAPANLIPVDCT 7457	57
ò	0у 138	137	7
QQ	DD 7458 ALTPDMLPLVKLTRQELEHIVADVPGGVANVQDIYPLSSLQEGILFHHLLQSEGDAYLMR	HLLQSEGDAYLMR 7517	17
ò	Ογ 138	137	7
qq	Db 7518 TLATFDSRALLDKFLGALQVVINRHDIMRSSLRWQGLPQPVQVVHRQAQLPVIQLDTAPG	AQLPVIQLDTAPG 7577	77
ò	Ογ 138	137	7
QQ	Db 7578 EDALQMLRERTNTYHMRLDLQQAPLIAAYITYDTRQEKWLMALLDHHLISDNVTLRLIMG	LISDNVTLRLIMG 7637	37
ò	Оу 138	137	7
QQ	Db 7638 EIQAVMDGRADALPPSQPYRNFIARAACVSQAEHEAYFRQLLGDVDTTTAPYGVLDVRGG	TTAPYGVLDVRGG 7697	97
ò	Ογ 138	137	7
qq	Db 7698 DATILRSVQDLSDDLSARIHSTARAQGVPTSVLFHAAWGLVVAATSGRDDGIFGTVLSGR	RDDGIFGTVLSGR 7757	57
ò	0у 138		7
qq	Db 7758 SQGTSGANHALGMPINTLPMRIRLQQNSVRDIVQDAYQQLSGLLTHERAPLALAQRCSAV	RAPLALAGRCSAV 7817	11
ò	Ογ 138ΕDTG	141	-
q	Db 7818 DASLPMFTVILNCRHGDLVNTAGENIEDMGEEQEGVHFLGSETRTNYPIEIAVANEANGF	PIEIAVANEANGF 7877	77
ò	Оу 142	141	н
q	Db 7878 SLTAQSIDGIDPHRIAAYLGQAVAELVNALEQDPARLASSLEVIPQAERQLLLNDFNDTA	ERQLLLNDFNDTA 7937	37
ò	0у 142	141	-
đ	Db 7938 SDFAPAVPIHALFEDQVRRNPDAVALVYEDRQLSYRQLNRRAMHVARQLLQLGVQPDERV	QLLQLGVQPDERV 799'	97
ò	Qy 142	br	-
d Q	Db 7998 AICAERSLDMIAGLLGVLKSGAAYVPIDPAHPADRMAFMLQDSQPRALLTQGALSLPVGD	LLTQGALSLPVGD 805'	57
ò	Oy 142	141	-
qq	DD 8058 TPLMLLDSAESLLAADDQAFDANPVVDGLTAENLAYVIYTSGSTGQSKGVMVEHRSVFNF	KGVMVEHRSVFNF 811	17
ò	Ογ 142	141	-
QQ	Db 8118 WNVLTRTTHQHCPTPATVALNAGFFFDMSIKGISQLFSGHKLVIIPQLLRANGSELLDFL	LLRANGSELLDFL 817'	77
ò	Oy 142	141	-
đ	Db 8178 EAHQVHAFDSTPSQLDTLLSAGLLERSSYQPVSVLLGGEAINASTWEKLRNCPTIRLYNM	KLRNCPTIRLYNM 823	37
ò	0y 142	141	-
q	Db 8238 YGPTECTVDATIDLIRDLGEKPSIGRPIANVQVHVLDARGEPAPLGVAGEIHIGGSGVAR	AGEIHIGGSGVAR 829	197
ò	Оу 142		-
g	Db 8298 GYLNRDELSAERFIVDPFSDAANARLYKTGDLGRWLADGTLEYMGRNDFQVKVRGFRIEL	IDFQVKVRGFRIEL 8357	5.7

DR Pfam; PF00109; ketoacyl-synt; 6.  DR Pfam; PF02801; ketoacyl-synt_C; 6.  DR Pfam; PF02801; ketoacyl-synt_C; 6.  DR TIGRFAMS; TIGRO0128; fabD; 6.  DR PROSITE; PS000129; ACP DOWAIN; 6.  DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 6.  DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.  KW Phosphopantetheine; Transferame.  SQ SEQUENCE 11096 AA; 1150415 MW; 776CAEAFCAESSIDD CRC64;	Query Match 30.5%; Score 236; DB 2; Length 11096; Best Local Similarity 1.1%; Pred. No. 51; Matches 99; Conservative 18; Mismatches 31; Indels 8882; Gaps 30;	Qy 1 AAG3 	Qy 4	Oy 4			<b>QALPRGGAMLAIRATEDEVTP</b>		Db 684 HLTDDVSIAAVNGPTSVVVAGTEEAVAAIGARFTAQDRKTTRLRVSHAFHSPLMDPMLAE 743 Qy 10	Db 744 FRAVAAGLTYHEPRIPVLSNLTGTVAAVADLCSADYWVRHVREAVRFADGVTALTDRGVT 803		Db 864 GTGARRADLPTYPFQHQRFWPTAARAAQDVTAAGLGAADHPLLGATVELADGAGYLFTSR 923	LSVRTHPWLADHGVQGRALLPGTAFVELAVRAGDEAGCDRVEELTLAAPLVLPERGGVQL	Ογ 18	Db 984 QVRVGAPDAAGRRTLGIFSRVEDGFDLPWSQHATGVLTAGAGAPDPTFDATVWPPSGAEP 1043		10	VL 1		SVDSLVSREVPADAPGAAGTVHRDSLFHVEWTPLQGRPGPAPATVAVLGPDPDALADTLR		Db 1224 ATGIRTTAPRDLAALADAEGPVPDLVVTTLTTTPGAPVPDAAHATTAAVLALAQOWLADD 1283
Qy         142           Db         8358           GEIENVLLAVPGIREVVVIARNDSQGDSDSQRLVAYVCGESVAAEHLRSELLRHLPEYMV         8417           Qy         142           Db         8418           PSAFVQLDALPLTANGKLDRRALPAPGQDALASKVYEAPQGETEEAIAEIWKALHLDQV         8477           Qy         142	Db 8478 GRNDGFLELGGHSLLAVQLLSRLRRKLGTRITLRELFDAPTVRGLASLVNAAAPGEAQSI 8537 Oy 142 141	Db 8538 PRANRSGRLPLSFSQQRLWFLDHLDHAAGAAYHLPMALRLTGALDTAALEATLDRLVARH 8597 Oy 142 141	DD 8598 ETLRTRFELVDGEPVQKIAPADSRLPLLKQDLRDLSGDERTSTLARLGQENATQLFDLTK 8657 Qy 142 141	Db 8658 GPMLRGHLLRVADAEHVLLITLHHIVSDGWSNSVLAQEVSALYAAFSQGQKDPLPALPLO 8717 Ov 142	8718 YVDYAAWQRQSLDGPALQAQIDFWRKHLEGAPSVLNLPLDRPRPAIQSYTGGMVEHVFSP	Qy       142       141         Db       8778       ALSADLRAFSQAQGSTPFMVLLAGWSMLMSHLSEQTDVVVGTPVANRQHPELEBMIGFFA       8837	Oy 142 141	Db 8838 NTLALRVATDRETRLNDMLDRIKSLTLAAYNHQDLPFEQVVSALQPTRNVSHSPLFQVML 8897	Qy 142		RESULT 13 Q9L4W3 ID Q9L4W3 AC Q9L4W3; DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE NysC. GN NYSC.	OS Streptomyces noursei. OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.	OX NCBI_TaxID=1971: RN (1)	RP SEQUENCE FROM N.A. RC STRAIN=ATCC 11455;	DLINE=20334850; PubMed=10873841; auta8et T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.	RA Valla S., ZOCCREV S.B.; RT "Biosynthesis of the polyene antifungal antibiotic nystatin in RT Streetcomyces noursei ATCC 11455: analysis of the gene cluster and	duction of the biosynthetic pathway."; em. Biol. 7:395-403(2000).	DR EMBL; AF263912; AAF71776.1; DR HSSP; P25715; 1MLA	DR InterPro; IPR001227; Ac transterase. DR InterPro; IPR002085; Add zn_family. ND InterPro: IPR0104410; PahD	DR InterPro; IPR00194; Ketoacyl-synt. DR InterPro; IPR003880; Ppantne_attach.	am; PF00698; Acyl_transf; am; PF00107; adh_zinc; l.

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ò	35	34	
a a	1284	RFADARLVLVTRGATDGTDPAAAAGGLIRTARTENPGRFALLDLAPDTGRPDPETLATA 1343	
ò	35	NIGAELLR 42	
g	1344	LAASHDEPDLAVRGTDVHAARLARVPLATEPTTWNPDGTVLITGGTGGLGAVLARHLVAT 1403	
ò	43	DPS	
a	1404	HGVRHLLLASRRGPAADGADDLTAELTGLGATVHIAACDVADPAALADLLGTVPAGHPLT 1463	
à	46	45	
g	1464	VVVHTAGVVDDGVLGSLTPQRLDTVLRPKADAAWHLHEATRHLDLDAFVLFSSVAATLGS 1523	
ò	46	45	
පු	1524	PGQANYAAGNAFLDALAARRAATGLPATSLAWGPWTQSVGMTSSLSDLDVERIARSGMPP 1583	
ò	46	45	
ą	1584	ÎTLEQGTALFDAALAAGPAALAPVRLDLPVLRTQGDIAPLLRGLIRTPVRRTAAQVSQTA 1643	
ò	46	LGAQF50	
g	1644	DGLAQRLAGLDAAARREALLELVRTQIAQVLGHADATEVETGRQFQDLGFDSLTAVELRN 1703	
ò	51	09	
20	1704	ALNTATGLRLPATMVFDYPTPHALADHLRDELLGTEAESTTAVPVPTRTAGTDDPIVIVG 1763	
ò	51	S3	
Q	1764	MACRYPGGIASPEDLWRLVSQGADATGPFPTNRGWDLDNLYDPDPDRPGRTHVRAGGFLH 1823	
ò	54	53	
g	1824	DAGSFDADFFGMSPREAWATDSQQRLLLELSWEAVERAGIDPASLRDSGTGVFAGVMYND 1883	
ò	54	53	
g	1884	YGTTLTGDEYEAFRGNGSAPSVASGRVSYTLGLEGPAVTVDTACSSSLVALHWAAQALRA 1943	
ò	54	53	
a	1944	GECSLALAGGVTVMSTPSTFVEFSRQRGLAPDGRSKAFAEAADGVAWSEGVGMLVLERQS 2003	
ò	54	53	
g	2004	DAVRNGHEILAVVRGSAVNQDGASNGLTAPNGPSQQRVIRQALASGGLSTADVDAVEAHG 2063	
ò	54	58	
a	2064	TGTTLGDPIEAQALLATYGRDRPENPLLLGSIKSNIGHTQAAAGVAGVIKMVMAMRHGV 2123	
ò	53	1ITE	
g	2124	 LPQTLHVDAPSSHVDWSVGAVELLTEQTAMPETGRARRAGVSSFGISGTNAHVVIEQSPT 2183	
6	63		
g	2184	AVPATPASADRSVEEPPAVPWALSGKTPDALRDQAARLLAHVEAHPALRPVDISYSLIAT 2243	
ò	63	29 93	
a a	2244	RTAFDHRAVVLGTDRAEALRALTALAAGETDPAALTGTVRTGRTAFLFSGQGSQRLGMGR 2303	
ò	63		
QQ	2304	VLYERFPAFAEALDTVLTALDAELGHPLRDIIWGEDAQLVDRTGYTQPALFAIEVALFRL 2363	

ò	у 63	62
Q	b 2364 LEAWGITPDFVAGHSIGEIAAAHVAGVLSLGDACRLVVARAVLMOSLPEGGAMI	AVOATE 2423
ò	у 63	62
q	b 2424 DEVLPLLTDDVSIAAVNSPTSVVVSGYENATLAVARHFADQGRRTTRLRVSHA	FHSPLMA 2483
ò	у 63	62
q	D 2484 PMLDDFRAVVESLTFTAPTTPVVSNLTGELAPAEALCSADYWVRHVREAVRFADGI	GIRTLA 2543
ò	у 63	69
a	D 2544 DRGVTTFVELGPDSVLSAMAQESAPEGAGTIPLLRRDRPEEQAVLAALCHLQVLGVEADW	GVEADW 2603
ò	γ 70 γ	69
Q	D 2604 SATFRGLDPVRVDLPTYAFQHRWFWPAARPARPDDVRAAGLGAAEHPLLGAAVQLPDDDG	1LPDDDG 2663
ò	у 70 у	69
QQ	D 2664 ALFTGRLSLRTHPWLADHTVLGTVLLPGTALVELAVRAGDETGSGHLEELTLAAPLTLPE	APLTLPE 2723
ò	y 70y	69
q	b 2724 DGATLLQVRVGSADDTGRRTVTVHARPDDTADRTWTLHATGVLATTPPAAAAFDTTVWPP	OTTVWPP 2783
ò	γ 70γ	69
qq	b 2784 ADAEPLTTDDCYAHFTTHRFAYGPAFQGLRAAWRAGDVLYAEVALPESATDEAAAFGLHP	AFGLHP 2843
ò	λ 70	69
q	b 2844 ALLDAGLHAALLADDRDTGLPFSWEGVTLHASGATALRVRLAPNGPNGLSVTAADPAGNP	ADPAGNP 2903
ò	y 70TAN	. 27
QQ	b 2904 VATVTRLLARPLDAEQLTIHSALTRDALFHLDWTPVPLPDTANSAPPALLGPDTAVLADA	TAVLADA 2963
ò	73	80
q	D 2964 LGDPAVARHATLDDLLAGDTTPPATVLVPLGAPLDGDTAQHAHALTRSALTLVQOWLATD	20WLATD 3023
ò	у 81	08
엄	b 3024 RLADSRLVFVTHGAVATDDAPPTDLAAAAVWGLIRSAQTENPGTFTLLDLDTBPDSTTAL	PDSTTAL 3083
ò	y 81	08
qq	D 3084 SRALTLDEPQLLLRAGRARAARLTRTPAPTTTTHTPWSADGTVLVTGGTGGLGGLVARHL	GLVARHL 3143
ò	у 81С	82
Q	D 3144 VRSCGVRHLLLTSRSGVGAAGAAGLVAELESLGARVVVAACDVGDGSAVAELVAGVSESX	AGVSESY 3203
ò	у 83	82
q	D 3204 PLSAVVHAAGVLDDGVVGSLTPERLAAVLRPKVDGAWNLHEATRGLDLDAFVVFSSVAGV	FSSVAGV 3263
ò	y 83yyouTiy	87
d d	D 3264 FGGAGQANYAAGNAFLDALMVHRVAGGLPGVSLAWGAWDQGVGMTAGLTERDVRRAAESG	RRAAESG 3323
ò	88 A	87
qq	3324 MPLLTVDQGVALFDAALATGSAALVPVRLDLAALRTRGDIAPLLRGLVRAPLRRTAATGL	
ò	ki	87
qq	3384 ATGADTGLVQRLGRLDHAQRHEALLDMVRSSAALVLGHADGNAIDAERAFRDLGFDSLTA	GFDSLTA 3443
ò		18

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a	3504 VVVGMACRFPGGVTSPEDLWRLVDDGTDAITTFPTNRGWDLDNLYDPDPEHFGTSYTRSG 3563	g G	4584 LHРАББВАБНА
ò	.66 86	ò	104
Q	3564 GFLHEAGEFDPAFFGMSPREALATDSQORLLLESSWEAIERAGIDPLTLRGSATGVFAGV 3623	d d	4644 VADTAGRPVAAI
ò	76 86	à	104
q	3624 MYSDYGSILGGKEFEGFQGGSAGSVASGRVSYALGFEGPAVTVDTACSSSIVALHWAAQ 3683	Q	4704 GHAQDQDGRPAA
ò		ò	104
8	3684 ALRAGECSLALAGGVTVMSTPSTFVEFSRQRGLAPDGRSKAFAEAADGVGWSEGVGILVL 3743	QQ	4764 TGTGTGTGTGTE
ò	96	ò	104
Q	3744 ERQSDAVRNGHEILAVIRGSAVNQDGASNGLTAPNGPSOORVIROALASGGLSTADVDAV 3803	q	4824 AFVTTGATAAGG
ò		ò	104
g	3804 EAHGTGTTLGDPIEAQALLATYGRDRDPENPLWLGSLKSNIGHTOAAAGVAGVIKWWAW 3863	셤	4884 QLLLRALHTDEPC
ò	26	ò	109
qq	3864 RHGVLPQTLHVDAPSSHVDWSVGAVELLTEQTAWPETGRVRRAGYSSFGISGTNAHVIVE 3923	qq	4944 YPAALAPLTGHEV
ò		ò	109
đ	3924 QPALVESPAAEPSGREPGVVPLPLSGKSPEALRDQAARLLAGLAERPALRPLDLGYSLAT 3983	a	5004 APGDQVMGMITGS
ò		ò	109
පු	- - 3984 TRSAFDHRAVVLATDRADAVRALTALAAADADLSAVVGDTRTGRHAVLFSGOGSORLGMG 4043	OP	5064 EKVLVHAGAGGVG
ò		ò	109
qq	4044 RELYERFPVFAEALDVAIDHLDAALPAQASLREVMMGDDVELLDETGWTQPALFAVEVAL 4103	đ	5124 FAEVAGDRGLDVV
ò		ò	112
යු	4104 FRLVESWGVRPDFVAGHSIGEIAAAHVVGVFSLEDACRLVAARATLMQALPTGGAMIAIQ 4163	qq	5184 AWVVPETIGTMLA
ò		ò	112
셤	4164 AAEDEVTQHLTDDVSIAAVNGPTSVVVSGAESAARTVADRLAENGRKTTRLRVSHAFHSP 4223	q	5244 WKPEGTVLVTGGT
ò		ò	112
යු	4224 IMDPMLAEFRAVAEGLSYATPTLPVVSNLTGRLATADDLCSAEYWARHVREAVRFADGVS 4283	qq	5304 VVAACDVGDGSAV
ò	101	ò	112
q	4284 TLENEGVTTFLELGPDGVLSAMAQQSLTGDAATVPALRKDRDEETSALTALAHLHTAGLR 4343	g	5364 WNLHEATRGLDLD
ò	101	ò	112
ద	4344 VDWAAFFAGSGATRVDLPTYAFQHATYMPTGTLPTAHAAAVGLTAAEHPLLNGSVELAEG 4403	Q	5424 AWDQGVGMTAGLT
ò	101	ò	112
q	4404 EGVLFTGRLSLQSHPWLADHAVMGQVLLPGTALLELAFRAGDEAGCDRVEELTLAAPLVL 4463	<del>ය</del>	5484 RGDIAPLLRGLVK
ò	101	ò	
q	4464 PERGAVÇTQVRVGVADDTGRRTVTVHSRPEHATDVSWTQHATGTLTMGSAPADTGFDATA 4523	අ	5544 SGDGVDPSRAFRD
ò	101 103	ò	112
		Д	5604 PDAESDPDEPGDP7

g	4524	WPPADAEPLATDDCYARFTTLGFAYGPVFQGLRAAWRAGDVLYAEVALAESTGDEATAFG	4583
ò	104		103
đ	4584	LHPALLDAALHASLVAHEGEESNGGLPPSWEGATLYATGATALRVRLTPTGTDGRSVAIA	4643
ò	104		103
QQ	4644	VADTAGRPVAAIDNLVSRRVSGDQLTGAAGLARDALFTLDWNPVPENLVPENPVPENTGG	4703
ò	104		103
Op	4704	GHAQDQDGRPAAATVALVGADGTAIAADLTAAGIHTTLHPDLTTLATTDADVPXTVLIPL	4763
ò	104		103
Op	4764	TGTGTGTGTGTESTDG1GTGAAESDASAPSPAEVAHTLSTAALALVOEWTAQERFAGSRL	4823
ò	104		103
qq	4824	AFVTTGATAAGGTDVMDVAAAAVWGLVRSAQSEAPDTFVLIDRDPGPAGTHDRTAAAERG	4883
ò	104	ITRED	108
업	4884	OLLLRALHTDEPQLALRDGGVLAARLARFDTAAALTPPADRAWRLDSTAKGSLNGLALTP	4943
ò	109		108
QQ	4944	Y PAALAPLTGHEVRVEVRAAGLNFRDVLNALGMY PGDDVGSFGSEAAGVVVEVGPEVTGL	5003
ò	109		108
q	5004	APGDQVMGMITGSFGSLAVDDARRLARLPEDWSWETGASVPLVFLTAYYALKELGGLRAG	5063
ò	109		108
qq	5064	EKVLVHAGAGGVGMAAIQIARHVGAEVFATASEGKMDVLRSLGVADDHIASSRTLDFEAA	5123
δ	109	737	111
q	5124	: FAEVAGDRGLDVVLNSLAGDFVDASMRLLGDGGRFLEMGKTDIRAADSVPDGLSYQSFDL	5183
ò	112		111
Db	5184	AWVVPETIGTMLAELMDLFRTGALRPLPVRTWDVRHAKDAFRFMSMAKHIGKIVLTLPRS !	5243
ò	112		111
QQ	5244	WKPEGTVLVTGGTGGLGGLVARHLVRSCGVRHLLLTSRSGVGAAGAAGLVAELESLGARV !	5303
ò	112	Z.	111
Q	5304	VVAACDVGDGSAVAELVAGVSESYPLSAVVHAAGVLDDGVVGSLTPERLAAVLRPKVDGA !	5363
ò	112		111
qq	5364	WNLHEATRGLDLDAFVVFSSVAGVFGGAGQANYAAGNAFLDALMVHRVAGGLPGVSLAWG !	5423
ò	112		111
Op	5424	AWDQGVGMTAGLTERDVRRAAESGMPLLTVDQGVALFDAALATGSAALVPVRLDLAALRT 9	5483
ò	112		111
qq	5484	RGDIAPLLRGLVKAPIRRAAATTPGDTGLAEQLTRLQRAERRDTLLALVRDQAAMVLGHT 9	5543
ò	112	[	111
QQ	5544	SGDGVDPSRAFRDLGFDSLTAVELRNRIGAATGLRLPATAVFDYPTADALAAHLLTELLG 5	5603
ò	112		111
QQ	5604	PDAESDPDEPGDPTAGPTDDPIVIIGMSCRFPGDIGSPEDLWRLLGDGADVVTDFPTNRG \$	5663

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	5664 WDLDNLYDPDPAHAGTSYARTGGFLHDAADFPGMSFREAMATUSQQRLLLESSWEA 5723	ò	125 124
	112	q	6804 RTVSVTALSATAGLARDALFRLDWASAPEPACQPDDTVTVIPAVAVVGTETSELTSELTA 6863
	5724 IERAGIDPLTLRDSRTGVFAGVMYSGYGTRLDGAEFEGFQGQGSALSVASGRVSYTFGFE 5783	ò	125 124
	112	; a	6864 ALRAAGADVDVRTTLSTDEPAPALIALPLVASDQTGTAEAAPVPAAVHDLTRRALALVQT 6923
	5784 GPAMTVDTACSSSLVALHLAAQALRGGECTLALAGGVTVMSIPDTFIEFSRQRGLAPDGR 5843	ò	
	116 115	; a	6924 RLOEQHFADTKFVFVTRGATVGRDVAAAAVWGLVRSAQSENPGCFALVDLDPDGAVGAAA 6983
q	5844 SKPFSESADGVGWSEGVGMLLLERQSDAVRNGHQILAVVRGSAVNQDGASNGLTAPNGPS 5903	ò	
	116 115	; A	6984 LVAALVSGEPQLAVRGDVLRVARLVRRPLTEVGAGADGTGDGVGGGSGVSFSGEGAVLVT 7043
QQ	5904 QORVIRQALASGGLSTADVDAVEAHGTGTTLGDPIEAQALLATYGRDRDPENPLLLGSIK 5963	ò	
	116 115	g Q	7044 GGTGGLGAVLARHLVAEYGVRDLLLVSRSGERAVGAGELVAELAGVGARVRVVACDVTDR 7103
a B	5964 SNLGHTQAAAGVAGVIKMVMAMRHGVLPRSLNITEPSSHVDWSAGAVELLTEQTAWPETG 6023	ò	
ò	116 115	qC	7163 AAVVELVGGHAVSAVVHAAGVLDDGMVGALTGERLSAVLRPKVDAVWHLHEATRGLDLDA 7163
8	6024 RARRAGISSFGISGTNAHVILEQPEAARHSAPEEADTAEAAAKAPATAHLPVMPWALSGK 6083	ò	
ò	116 115	: සි	7164 FVVFSSLAGVFGSPGQANYAAANAFLDALMTRRRAEGLPGLSLAWGPWSLTDGTSGMLAD 7223
g G	6084 TPEALRAGAARLLAHLQGRPELAPADIALSLATGRSGFTHRAVVLSTDRDEATRALSALA 6143	ò	125 124
ò	116 115	; A	7224 AEADRLTRSGVPPLTAEQGLALFDAALATGDATCVPVRLDLSALRAQGEVPPLLRSLIRG 7283
q	6144 TTAASDPSALTGTVTMGRCAVLFSGQGSQRLGMGRELYERFPVFAEALDVVIDHLDAALP 6203	à.	125 124
ò	116 115	ą	7284 RSRRAAAAESATATGLRERLVGLNPVERQEVLLDLVRGQVALVLGHADADDVHPARAFRE 7343
g	6204 AQAGLREVMWGDDVELLNETGWTQPALFAIEVALFRLVESWGVRPDFVAGHSIGEIAAAH 6263	ò	125 124
ò	116 115	q	7344 LGFDSLTSVELRNRLNTVTGLRLPATMVFDYPTVEVLVSYVLDELLGTDAEVATVQPAAV 7403
Q	6264 VVGVFSLEDACRLVAARATLMQALPAGGAMIAVQATEDEVIPHLTDEVAIAAVNGPTSVV 6323	ò	125130ACSP130
ò	116 115	: A	7404 AVADDPIVIVGMACRYPGGVASPDDLWRLVTDGVDAVSPPPTNRGWDVESLYHPDPDHLG 7463
20	6324 ISGAEEATQTVAQHFADQGRRTTALRVSHAFHSPLMMLAEFRAVAEGLSYATPTLPVVSN 6383	ò	
ò	116 124	g qg	7464 TSYTRSGGFLHEAGEFDPGFFGMSPREALATDSQQRLLLESSWEAIERAGIDPVSLRGSR 7523
QQ	6384 LTGQVATADELCSAEYWVRHVREAVRFADGVTALEAEGVRTFLELGPDGVLAAMARETVA 6443	δ	131 130
ò	125 124	d d	7524 TGVFAGVMYSDYSAMLASPEFEGFQGSGSSPSLASGRVAYTLGLEGPAVTVDTACSSSLV 7583
g	6444 DDTVTVPVLRRNMPEERTLLTALGRLHTTGTPIDWAALLAPTGARPVDLPTYAFQHRPFW 6503	ò	131 130
ò	125 124	q	7584 AMHWAMQALRSGECGLALAGGVTVMSTPAVFVDFARQRGLSPDGRCKAFADAADGVGWSE 7643
Dp	6504 PSGPRDTADAAAVGIAGASHPLLNGIVELADEEGLLFTGRLSLQSHPWLADHAVMGQVLL 6563	ò	131 130
ò	125 124	දු දු	7644 GVGVLVLERQSDAVRNGHEILAVVRGSAVNQDGASNGLTAPNGPSQORVIRQALASGGLT 7703
g	6564 PGTALLELALRAGDEVGCDHVEELTLAAPLVLPERGAVQTQVRVGVADTTGRRTVTIHSR 6623	ò	131 130
ò	125 124	qq	7704 AGDVDVVEAHGTGTTLGDP1EAQALLATYGRDREPERPLLLGSVKSNLGHTQAAAGVAGV 7763
a a	6624 PARATTTDSDTHTGTDTPWTQHATGVLVAGLPATATVPFDATVWPPAHAEPVDLADFYAS 6683	ò	131 130
ò	125 124	q	7764 IKMVLAMRHGVVPRTLHVDAPSSHVDWSEGAVELLSEQAAWPETGRVRRAGVSSFGISGT 7823
셤	6684 RAGEGFGYGPAFOGLRAAWRRDGEVFADVALPEAGRTEAEAYGLHFALLDAGLHAAWLVA 6743	ò	131

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žä	PF00698; Acyl_transf; 2.	ò	11 10
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3 2	PROSITE; PS00606; B KETOACYL SYNTHASE; 4.	ò	11 10
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S	SEQUENCE 7829 AA; 874065 MW; E19BDDA392F325C1 CRC64;	6	
o a	Query Match 30.1%; Score 233; DB 5; Length 7829;		1171 ENIRLPFVAEEKQIDRSAIVSFGITGTKTVVTTERVSQLNVDNIQNCYLLPVSAKTKDGL 1230
íΞ	ss 90; Conservative 25; Mismatc	ò	11
ò	1 AAGGI 5	qq	1231 KKACLSLIEMIDNSCESLYDISTTLQKQKTNFKWRTAVVGSSHADVVLKLKQFLTSEHNT 1290
q	151 ÄÄVGIETACSSSLVAFHLARQAIQSGETKLALVCGANHVGSRSFHSLYNSHMVSPNGRLA 210	ò	11LVAV
ò	5	g	1291 SLTNWHISTSHHSIGCSTFFHNIPEFEDHYSMFCHRLRFEPHSNTNSIYHLLAVVYALIR 1350
g	211 AFDRSANGFVRAESFAVAVLCSKQFAEENNLLIHCECVGSAFNSDGKTPSLTAPNPISQY 270	ò	15 14
ò		ପୁ	1351 VILKHKLTNSFAVGGFNSLIVLAAVDAAPSHYLNDLLHAFANDDVRMMKRIARDVTISIE 1410
සු	271 EVQLEALKNIDKDSVQLVTCHGTGTKLGDQVELTAINRSFKSDIRVMSPKSSMGHGEGAA 330	ò	15 14
ò	6 10	q	1411 NVKLLNLNGEPITTARQAVEATIDQKVKNVRLPETTLILSPSRAYEFASQLETIQDYYKL 1470
QQ	331 GLIGVLQSLYSMQHGIIPNQLHLELPSEDLGEDKSMGFVNEEMELNRVAISSYGFGGTNA 390	ò	15
ò	11 10	; d	1471 IGEKFTOGGOVDFAGIFGTPIKLIDLPEYPFNRKSFWLPIPDSVPSNEKGEKPLIPKSYE 1530
g	391 CAIIEKPEKPSLVQKESYAESNVLFLSAKSHESLKLQIEEYTQFMAQSDSAMEDILYTVN 450	6	15
ò	11 10	; A	1531 FLLKSQKWQHVQNHVVDSKIVLPGATSIRLVHQLNGKPTVELSNIDFLNKITPSEAPSVV 1590
đ	451 ERKTKYDFRAAVFGKDNEEIARKLQDGDYSLTNLQESTFEVEFGEGNEKLWLLRMLYEKN 510	ò	15 14
ò	11 10	g G	1591 KIEEQDGLEKLVFGETDAISFKLTELQNFNPIPNERLNAEVHHTDNIYERFANSHLTYRN 1650
g	511 ETFHSTVDKYCKLAETCGFPEARTALFFPFKLTLTPLTYNVSRLISSMATFELLVQYNTL 570	ò	15 14
ò	11 10	qa	1651 EFQMVDSLKYTMGKGEVRFVSMKDLDILIDGTLQAIVGCYFFENTNDNSPFVPFTIDQLS 1710
යි	571 PNKLRGKGLGQIFCLAVAKVITFESAVQLIKGVVAEANLTDILGDIELKSSKIPIEIQHL 630	ò	15 14
ò		QQ	1711 ILNGDISQKQLHAVLKYDSSGNFINGDATVYDALGNIILHISNVTFKRLNGOSAPSLTSK 1770
g	631 KSTKKKILPIHISGELKETAKPNLMTFIVNGEEILELDPVRKVQKLICQLFACGFDPAVK 690	ò	15 14
ò		qo	1771 TVDSSKITKKVENEDQKRASKAMLHVWFEENFGWTDIDNTTGFFDLGLTSIQAVKLRNAI 1830
g	691 FRGRIVKTPTYSFLKRQFWPEVQTAMTTNIVDEQTNSSLSDAEIESTVRTIVKQFLDIEE 750	ò	15 14
ò	:	qo	1831 KSNYPNASSTCVFDYPSIDLLSGYLSTLNDPQVTETSTGEDDIQKDLTEDHKPTRLAENP 1890
g	751 DDINLLETGAVDSLTSIEMVEAFGTAVNQTMPFDLLEAYPTILNIVDFLKTLVTTVPVTK 810	ò	15 14
ò		qq	1891 IGYMAAACRLPGGVSSPSELWELLKIGKNASSRIPATRVPTRNTLISGSKYGNPVEGGNF 1950
g	811 ATTSIHKKTSELSTSDINVIACDYQFAGVEGEKELMDTLLTSRLTTGKISDIRKKQCEGD 870	ò	15
ò		셤	1951 ITQDVTQFDPSFFKISKSEAELIDPQQRLLLECVQECLENSGVIETSNVGVFVGLMEKEY 2010
අධ	871 AGLEVGLLKQDISMFDNSFFAIAKDEAEFLDPQHRLLLNAAYNALEKSGLTSIFDADLFL 930	ò	15 16

		=	QQ	3091 DGN
<u>ප</u>		QDMMESSSILAMLGSMAAVIAGRVNYIFGCYGPSVTIDTACSSSLVALEMAINALLDNRC 2070	ò	92
ò	17 -		qq	3151 CR
අ <u>ය</u>	2071 S	LMLELAKPNF	ò	26
ò	17 -		qq	3211 LS
QQ	2131 н	HYMSTIQSVNVNHGGRSVSLTAPNGVAHKMLLTSVINQSPSLAIDYWEAHGTGTPLGDPI 2190	ò	26
ò	23 -		q	3271 AK
q	2191 E	EFNTLSSILQNIIIGSVKASLGHGEASAGTCGLLKLFLMLTYQYVPTLIHFHVLNKDINA 2250	ò	31
ò	23 -		qq	3331 HT
g	2251 G	GSIRLPIIGEDSELVSAGISSFGVSGTNAAAIAFNDNNKLEPYIFIHKYYILPISAKNQI 2310	ò	44
ò	23 -		q	3391 LE
đ	2311 S	SLDNLEKQILSVIPLTDVPICNIASALANNRSHFTIRNALIVSNSGIVNSKMEGKPHRVA 2370	ò	44
ò	23 -	22	qq	3451 NW
g G	2371 K	KKDRYHVKLCDSLLDASLLQYDVINETYTVASLKNPQSFAMKFAIIKFLTSLSEYIEIVA 2430	ò	44
ò	23 -	22	g	3511 DL
qq	2431 8	SDGEELLAVLLANGSLKWENFNKTWIELPIGSLLTEFADHDLNSTTSSSIKSYQTQPESH 2490	ò	44
ò	23 -		q	3571 MC
a	2491 N	NLDSPMELMKLIMKLYITGYDVDWATVYSPVEQFIALPNYQFNKQTLWFEERLEIVDHYL 2550	8	44
ò	23 -	22	. A	3631 TI
q	2551 I	IGTIDEESEDTLILKNQISELRHPQFFKGKPLDVGTMSEIAIEALKIRNEIPFSIQNLKT 2610	ò	
ò	23 -		; E	3691 AV
QQ	2611 E	ELITLTKPAMLETNVTRNEDDEGFNVSAYIDGQRLFSLNASSVEIQNIEVPAVEVQIPDK 2670	ìò	50
ò	- 92		3 8	3751 TL
Q	2671	VVYLKECPNAVIRRHRNMVYVDSRAEQSPFRTANIVLNEIIGFAPTPSDMFIEILGVLPS 2730	8	50
ò	- 52		: E	7811 DY
đ	2731	VHYMVQVDDGALWQFQMISQDKRVLSNIYVLKDAKGLEIFTIRMHKKSTLLSSQEASIVA 2790	}	51 80
ò	. 92		; d	
g	2791	AKTLOMAVRHKVCLAVGDVIESGLDIDESQLSTGFSELGIDSLATVDLLNRLNQKYFPEI 2850	8	
ò	56		; <u>4</u>	3931 CL
qq	2851	ELTTSDLFDNPSIIDLSIMIEQLLNEKGITEPSEPNTPKTSLRGRKLSIPAVRAQVLAQI 2910	ò	58
ò	. 92	25	q	3991 SA
q	2911	EFVENYNSKQKEVQAEAPSSSSECSNHLEESDATVDRTEIRRKVSLAVFDLATETLSAED 2970	ò	58
ò	. 92		QΩ	4051 RN
Ωρ	2971	LQSKGFTELGMDSLSIVDFVNRLNDKYFPDDEITASDIFDYPTVDELSDHIVRKKSSSVP 3030	ò	58
ò			đ	4111 EK
q <sub>0</sub>		PAASEIMKETMNGISTSVDAEHTKLENLSQSFMLLENQNSINPTLKMIWSNQTIKLVKPS 3090	ò	58
ò	56		qq	4171 FE

q	Db 3091 DGNFLFELNANGGQEKEIQKHFTGPNNIIIDLKGFHEGSTETLYMSLLNLVKS	LNLVKSISKLEIQ 3150
ò	Qy 26Qy	25
q	3151 CRFGVSQEFGLGNSISRAFMKTVAAEKNPLISFAWYQNVQOVSFVD	SDSPITGNWLITGG 3210
ò	Qy 26Qy	25
q	3211 LSGIGLEIGKFIANNGAENVILISRROPTAKALRDILSTELTHI	GLARKTIVLKLIKNIS 3270
ò	76T	30
đ	3271 AKLIVFQSFKLSFSTKKYISDLFSKKVTFFYNLLQSKCFSKHFHWL	FEWLEVYLIKOWTV 3330
ò	Oy 31LINLNIGAELLRD	43
qq	3331 HTIAADINDKEKLIRELTKLNVGITGIIHSAGVLKDSKIERQNKES	FNQVFTPKANGFHV 3390
ò	Oy 44	43
qq	3391 LEEIEKHFNYKIENFIMMSSFTAACGNEGQLNYGVSNAYLEY	QVQRRRRQGKSGCAIQWG 3450
ò	Qy 44	43
q	Db 3451 NWIDTGMATDENVRKFLANLGFLGQHNKDALKYLRACILTKPELIMVANIDWNVI	ANIDWNVILKNRK 3510
ò	Qy 44	43
qq	Db 3511 DLPKDLINTGILPFEDFTGKMNESEFPLSNGDFEKVSMNFSVEDEEEVLELIKEKVSSIL	
ò	Ογ 44	43
q	Db 3571 MCSPTKLKNNKNIMDMGLDSKLIVEFLNFINSTFKISVNLSDAYNHPT	TLEKLAAHIFEQM 3630
ò	Qy 44	43
셤	Db 3631 TIVDHPVNSVKSEEIFKSTDFCPIFGINIFFDNKNDFDKAKSTAVKLLENGEQLPTAGKY	LENGEQLPTAGKY 3690
ò	G	SLGAQ 49
gg	1691 AVSVVGKSIRDVVSKIKEAAPQQIKLCQESSKCVLMLTGQGSQYPM	IGRÓLVENYEIFRT 3750
ò	Ολ 20	64 46
q	Db 3751 TLQSCLKKCDEYLQGDVSLWEILFNTDHYKLLQLTKHMQPIMFCFGYATAQLWLSLGIVP	ATAQLWLSLGIVP 3810
ò	20	F 50
đ	Db 3811 DYYLGHSVGELVAGVLAGIMSIEDGLRLIVERGKAMENIAGLGALLAVQREIADEVLRKF	NVOREIADEVLRKF 3870
ò	51	HLVKM 57
qq	Db 3871 KVSVATINSPKQVVFAGTKSVLDAALAFVKGQGKQATYVNQQYPFHSNLIQETHLVSLRQ	
ò	Ογ 58	57
g	Db 3931 CLADIKFSAGRTPLVSNVTGQIINTFSEAYIVKHTVSAVKFVDCVETLQAKGVTVWIDAG	rloakgvtvwidag 3990
ò	Ογ 58	75 57
පු	Db 3991 SAAVLATFVKRIIQPTELSKHRIVQTCKEKESDVDNLVQACLELEQSGLPI	SGLPISWTTLYGCG 4050
ò	Oy 58	57
g	Db 4051 RNADERLVEFPMTHNDIIKNDEFELLEGHQLNGKIVVAGAYQLFKIDQLVKLKAAGMELM	OQLVKLKAAGMELM 4110
ò	Qy 58Qy	57
q	Db 4111 LKNVKFLKPWYIEDNREYQIQWNSDMTIELIVNSVIVCSLEVEPQNSVLKLETI	SENEKP
ò	28	57
qq	Db 4171 FEVHDFYETLFRNGLQYDSGFRRIESARRSDKRCFSQIKSSPFAWPLIDSAMHSITASVV	LIDSAMHSITASVV 4230

3		
;		
a	4231 PRRPDCYFLPVAMGSVTMKDTNSFTLPNLHAQTVITSETDKFIQVNVALLAGDTPICEVR	KFIQVNVALLAGDTPICEVR 4290
ò	58VILTEP	63
g	4291 NMTIVVLKTEPVHTRIPNSIETVETPPKSEIEIVGFDISLPYNQISENSENWQHLKTNTV	PYNQISENSENWQHLKTNTV 4350
ò		63
đ	4351 KQKLHNRSLKQDHARVALLDSDARYWDPEYFGIRPSEAKFIDPQQRLLLCSVAKLLDSLL	IDPQQRLLLCSVAKLLDSLL 4410
ò		63
엄	4411 ITSLTSNTGVFIGCSANEFSHIVYAYGYKDPRAEWSGGTSNSALAGRIAHWLKLKGPVVT	NSALAGRIAHWLKLKGPVVT 4470
ò		63
qq	4471 LDTACSSSFYALSAACDALRTGQCEYAIVGTVNLVMHEMTTDVLQNAKMTVDDFCKAFDV	TDVLQNAKMTVDDFCKAFDV 4530
ò	64	71
g	:       : 4531 DANGYKRSEAVCSMLLTKSPNIDSVATITNYATGHNGTSSSLFTPNGLSQLEVMQRATNP	SLFTPNGLSQLEVMQRATNP 4590
ò	72	NLTSSLLS 79
ф	4591 LEKILEIQTHCTGTKLGDPIEINAISKLVSSACKIGSVKSNIGHTEGSSGLVSLCSSLMS	NIGHTEGSSGLVSLCSSLMS 4650
ò	08	62 18
qq	4651 FRSKYRVAQLHLKCPTNSIKTNKMICRFIGEDADENNSILINNFGFTGSNCSVVLKPKNA	INNFGFTGSNCSVVLKPKNA 4710
ò	08	64 19
q	4711 ISEHFVSSEVFYPILLSSHSAKSLQKYVQVLCEFISNSAKSLHDIMMSLFQKKIHVHRQF	SLHDIMMSLFQKKIHVHRQF 4770
ò	08	62 18
g	4771 IIFNFKRKIAVTSLDGFVEVRDERLEKLKHPCSVFLKEGVVHFDKDKSFQRVDLPSIVFN	VHFDKDKSFQRVDLPSIVFN 4830
ò	08	VC 81
οg	4831 NTLHWALDSYRDEIDRHESQQMSFKNIFYEKVLLETPMPQQNPISKVVCIGRLDLIPKIE	QNPISKVVCIGRLDLIPKIE 4890
ò	82	81
Q	4891 IDEVSSFANGIIVFHPISNSIFEYLKLAKVWSLISRNQNVFIIICCFENGTSHTEWTGTL	FILICCFENGTSHTEWTGTL 4950
ò	82	18
qq	4951 RSLASEKMIPYKFVSIDKVDALKLEFNHEYMFEAIFYSKRGRYVERLRKVNPTFKFAPQY	GRYVERLRKVNPTFKFAPQY 5010
ò	82	81
g	5011 EKCLISGGTGGIGSAIINELKPKSSVIITRKNIASEDGKTFLSSDITRLDISHKFNYVFH	PLSSDITRLDISHKFNYVFH 5070
ò	82	18 81
q	S011 LAGIVNNSLHENVKRDSLDEMVSIKLQGAKNLMKCCDETSHFVFSSSIANVLGSYGQSNY	SHFVFSSSIANVLGSYGQSNY 5130
ò		GW 83
g	5131 AFSNGLVTSFLETSSTKSTIIHWGPWKDVGMLAQPERREIVKQIESNGWKLLPNQDAISV	IVKQIESNGWKLLPNQDAISV 5190
ઠે		83
g	5191 FYTQFMETHEQIIVFDGDFDTIVARQPHLQKLLSEVVEKTKVKEEIKKKSLNFEEIFFEI	rkvkeelkkkslnfeelffel 5250
ò		83
g	5251 VGITDISSKLNIPFMDLGIDSLCMENLRYSLNKNFDLELTVSEMFENATYQKLQTYVETL	IVSEMFENATYQKLQTYVETL 5310

ò	84	
QQ	5311	RKAKHSESLSHDRVSSQVSNKEDDTRVAVIGWSAEFSGSSNIHEYWENLMDGICSTGNNK 5370
ò	94	95
Q	5371	YLLKNPFGFDNKFFNLTDEDARVLDPQVRKFIQHAYLALENSGYVKQKHELRCGVFAGAE 5430
ò	96	56
q	5431	PSDYGRADDHDDAMRKLFVMNMNSYLASYASYCLDLKGEAVSVYSACSTALVAVANAVKS 5490
ò	96	96
qq	5491	IQSGSMDYALVGAA8IAEVSGALSGFDDQKKTMFSKSGVCRPFDKDSEGIVRGSGVGCFV 5550
ò	96	36
q	5551	LKRYSGALLDNDNVHFVIKDFAINNDGHSRASFMAPNPAGQLKCMTDVLARFTNKEKERI 5610
ò	96	98 9н
QC	5611	SFVECHATGTTLGDTIEMNSLRTAYSFKNKLAIGSCKANIGHAYAASGLAALVKCAKMLQ 5670
ò	66	. 86
qq	5671	TGIIPPQVNFSEFRDGMGQFFTVNGKKSTISQNSLISIDSFGIGGTNVHMVIEFPARSOE 5730
ò	66	DLVLY
q	5731	:   :
ò	104	103
qq	5791	TYLSVANNNBELLKIRTNKKTWFNGKSPKIALFFAPQGIQFTNILPNEYLKNSAYRREVEY \$850
ò	104	103
đ	5851	LCELASSFGIPSLEGILYPTKNFDHLIHATQFAQIAIFVQCMAIFKAIKNVFNPTCLIGH 5910
ò	104	103
g	5911	SVGEYADAVISGALKTEEALKLLIKRSELIGKTEKARMLMVWNYEKOLPSHVHVSAIIDA 5970
ò	104	103
QQ	5971	NTKCVVGPVETIDNLEKYFINNHIKYRNIETKHGFHSKMFHCISKEFEFFCESFATKVPL 6030
ò	104	103
Q	6031	IPMISSITGSEIKIFDSKYCTMHLTNPVNLELVVDHIMKLDIDIIVEVGPTGVLSNLLAK 6090
ò	104	103
අ	1609	RNSKIVVVPTCGTKKHPKISLGECIGQL#SNGVDIRKLTPKLAVDGQVPGYCFDERQFGE 6150
ò	104	103
đ	6151	KNOKISOKLNRFSYYKESWKPVSSELEETKPVRFTVCDGSLNGISEPVLVYLLRKSEDIH 6210
ò	104	
q	6211	KNYFDVELFLKSSPRCSTVVFVGMDNSPSVHLSLGLIRCYQLVSRIDLKYVENFENIAMS 6270
ò	110	
q	6271	IVIQKVLTANGLYFRIDSTGLCKHGFRTTEIPSRLHPVSRGHALVFGANGFIGSIVFRLL 6330
ò	113	113
QQ	6331	QEMGMNVIPISRASIPSCDITNIKDVQNVFKSLGFKKFSVVINCVGVETSAKMNKTSLEQ 63
\$	113	112

සි	6391 EIVLSPKTFGSVNILKCLEEFSIEVDKLVNFSSLSSVVPLLGNFDYASANCFVEALTKQG 6450	DR DR	
ò	113 DGNRQVRGVT 122		Pfam; PF00698; Acyl_transf;
ద			Pram; Pruolos; adn_snort; 3. Pfam; PF00109; ketoacyl-synt
ઠે	123 122		Pfam; PF02801; Actodoy1-87110 Pfam; PF00550; pp-binding; 6
g	6511 SSVNPADIATKSIAFHRTDENGSEVKAVESLKLPKSTSCEFVIABIWKETLGISILNDAN 6570		PROSITE; PSS0075; ACP DOMAIN
ò	123OLGG 126		PROSITE; PS00343; GRAM POS A
g	 6571 PNFFSLGGDSLSALQVVWKVQKKTDRIVDVNDLFDNPTLQEFTKFVKNLTTEKFAGNTND 6630	¥ 5 5	PROSITE; PS0003; HIE 1, ON PROSITE; PS00012; PHOSPHOPAN Phosphopantetheine: Transfer
ò	127	SOS	SEQUENCE 9477 AA; 988132
q	6631 KISYDAIPLTNSQTQMFMLRQIDTTSKYNLIFKITISYETKFVWEFLKYSLHSLIAYQPS 6690	O	Query Match 29.9%;
ò	127	ΣW	92; Conservati
g		ò	1 AAGGILH
ò	132 WSCLITEDT 140	QC QC	86 ASGGFLHDAPDFDADFFGISPR
<b>Q</b>	:    6751 NSRIHIVFNQHHILTDGWSMTVLSDTVSSLYAAYRGETSFPSKTKQTISQVAMGTKSSGD 6810	ò	8
ò	141	qq	146 IGAMAQDYRVGPADGAEGFOLT
g G	6811 IKEALEYYQNTYHTIIPYDSETGNTSPSYVRISKLIPSKIWQKLVGLSKLYNTMYNLAL 6870	ò	8
ò	141	q	206 TQALRAGECTLALAGGVTIMSG
g	6871 SVFCDAVRSFTGQADILLAYAISGRNADNSELIGYFMNNALFKTSLPFEILRLEEILNIV 6930	ò	8
ઠે	141	qq	266 VLERLSDAVRNGHEILAVVRGT/
g	6931 LNSLEKSRSFATIPFYQMVEQNRKLNEISLFFNFRQKLDYPTVSMFGAKCEIEHLSLNNA 6990	ò	8
ò	142 FDLGVTI 148	qq	326 VVEAHGTGTTLGDPVEAQALLA1
පු		ò	8
		QQ	386 AMRHGTLPRTLHAEEPTHHVDWS
RESULT 09L4X3	.T. 15	ò	8
A G	Q9L4X3 PRELIMINARY; PRT; 9477 AA. Q9L4X3;	q	446 IEQAPEPOPEDAATAQDDAAGS?
ដ្ឋ	01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)	ò	8
DE DE	01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Nysi.	qa	506 RRPDLLDLAHSLATTRAGFEHRU
S S	NYSI. Streptomyces noursei.	ò	
ខ	Bacteria, Firmicutes, Actinobacteria, Actinobacteridae; Actinomycetales, Streptomycineae, Streptomycetaceae; Streptomyces.	đ	566 TRLAVLFTGQGAQRLGAGRELA
X S	NCBI_TaxID=1971; [1]	ò	8
8 2 2	SEQUENCE FROM N.A. STRAIN=ATCC 11455;	g	626 RTAYAQPALFAVEVALYRLIES
R &	MEDLINE=20334850; PubMed=108/3841; Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,	٥ <b>٠</b>	60
8	siosynthesi	qq	686 RLMQALPDGGAMIAVQASEADV
RT	reptomyces noursel ATC 11455; analysis of the gene cluster.	ò	8
2 2	Jem. B101.	qq	746 AADGRKTRRLRVSHAFHSPLME
S S	SSP; P81989; 10E5.	ò	8
222	nterPro; IPR002198; nterPro; IPR004410;	qa	806 ADYWVDHVRHAVRFADGIDWLA
ž	nterPro; 1PR		

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29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAPLLAGHEDQVAIAAVNGPSAVVLSGAEATVTALAEQL 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REAVAMDPQQRVVLESAWEAFERAGIDPTSVKGSRTGVF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGNTGSVLSGRISYTFGTVGPAVTVDTACSSSLVAVHLA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATYGQNRPADRPLLLGSVKSNLSHTQAAAGVAGVIKMVM 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSQGAVRLLTDTTDWPATGAPRRAAVSSFGISGTNAHTI 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STPATAPVVPGVVPVLLSGRTPDALRGQAAALRAALDTG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAVLLATDHPALTDGLTALADADDPAAAPAWITGTTRAE 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AARFPAFATALDAALDAFTPHLDRPLREVLWGTDAALLD 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFGVRPDHLAGHSVGEIVAAHLAGVLSLADAATLVAARG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPMLDAFRAVVEDLTLQPPLLPVVSNLTGKPATVAQLTS 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARHDTTAFLELGPDGVLSAMAQDCLDAADADAVTLPALR 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPGTFIEMGROGGLSADGRCRSFGDTADGTGWAEGVGIL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAVNQDGASNGLTAPNGPSQQQVIQQALVNARLAAGDID 325
                                                                                                                                                                                                                                                                                                                                          ; Score 231; DB 2; Length 9477;
Pred. No. 57;
27; Mismatches 29; Indels 7868; Gaps
                                                                                                                                                                            AAIN; 6.
ACYL SYNTHASE; 6.
DS ANCHORING; UNKNOWN_1.
DRANOWN 1.
DPANTETHEINE; 6.
Sferase.
ncyl-synt.
NA_binding.
ne_attach.
                                                                                     3.
nt, 6.
nt_C; 6.
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Ор	1946 S	  PEFEGFQGSGSSPSLASGRVAYTLGLEGPAVTVDTACSSSLVAMHWAMQALRSGECGLA 2005
ò	21 -	20
đ	2006 L	LAGGUTVMSTPAVFVDFARQRGLSPDGRCKAFADAADGVGWSEGVGVLVLERQSDAVRNG 2065
ò	21 -	20
đ	2066 н	HEILAVVRGSAVNQDGASNGLTAPNGPSQORVIRQALASGGLTAGDVDVVEAHGTGTTLG 2125
ઠે	21 -	20
q	2126 D	DPIEAQALLATYGRDREPERPLLLGSVKSNLGHTQAAAGVAGVIKWVLAMRHGVVPRTLH 2185
ò	21 -	20
q	2186 V	VDAPSSHVDWSEGAVELLSEQAAWPETGRVRRAGVSSFGISGTNVHVIVEQAPGAKAIAA 2245
ઠે	21 -	20
QQ	2246 A	AGAARRTPGAVPVLLSGRGRSALRGQAARLLGHLQARPDAELVDVALSLATTRSRFBQRA 2305
ò	21 -	20
g	2306 A	AVVAQDRDQLIASLGALAADRPDPAVVEGEAAGRGRTAVLFTGQGSQRAAMGRELHEVQP 2365
ò	21 -	20
QQ	2366 E	EFAAAFDAVCAVFDPLLDRPLREVVFAEDGSDEAALLDETGWTQFALFAVEVALFRLVES 2425
ò	21 -	20
qq	2426 W	WGVRPDFVAGHSIGEIAAAHVAGVLTLEDACRLVAARATLMQALPTGGAMIAIQATEDEI 2485
ò	21 -	AHOEDT 26
qq	2486 P	:   aahlddtvalaavngposvvisgdeeaaetiaatfaergrktkrlrvshafhsprmdgml 2545
ò	27	
q	2546	DAFRIVAĘGLTYRAPRIPLVSDLTGRRADDAEVCTAEYWVRHVREAVRFADCVRTLRDAG 2605
ò	27 -	
g	2606 7	ATTFLELGSDGLLTAMAEDTLGDDHDAELVPMLRAGRAEELAAATALARLQVRGVDVDWA 2665
ò	27	
Q Q	2666	aylagtgarrtdlptyyafqhayywpqlptpaalaaadpadqolwaave <b>rg</b> dareladil 272s
ò	27	34
Q	2726 (	GLGEQDLTPLDSLLPALTSWRRGNQEXHLLDTLRYRVEWTRLSKPTAPVLDGTWLLVASD 2785
ò	35	34
g	2786 1	ATAADQPALLDGLADALGSHGARVRRLLLDDSCADRAVLAERLARTADVDAATQVLSVLP 2845
ò	35	34
g	2846 1	LDERDADDCPPLTRGLALTVALVQALADTGAQGRLWTATRGAVSTNPADPVTHPVQAAAW 2905
ò	35	34
g	2906	GLGRGVALEHPRLWGGLVDLPQVFDERAGQRLAGILAVKDAPDGEDQVALRATGVSGRRL 2965
ò	35	. I I ! .
q	2966	VRHTVEALPTAAEFTATGTVLITGGTGGLGAEVARWLARAGAQHLVLTSRRGPDAPGAAE 3025
ò	43	42

Q	3026	LRAELEGYGPSVSVVACDVADRDALAAVLTALPEELPLTGVVHTAGVGHYGPLDTLSTAE 3	085
>-	43	<b>b</b>	23
Ω	3086	FAGLTAAKLAGAAHLDALLADRELDFFVLFGSIAGVWGSGNQSAYGAANAYLDALALHRR	3145
>	43	SdO	45
Д	3146	ARGLAATSVAWGPWAEAGMAADDAVSETLRRQGLGLLDPAPAMTELRRAVVRQDVTVTVA	3205
>-	46		45
Ω	3206	DVDWQRYAPLFTSARPSALIAGLPEVRALAADERTEQDATGASEVVTRVRALAEPEQLRL	3265
>	46		45
Д	3266	LTDLVRTESATVLGHSSADAVPEGRAFRDVGFDSLTAVELRKRLGAATGLSLPSTMVFDY	3325
>	46	LGAQFRV	52
Ω	3326	PTPLELAQYLRAEILGAVLEVAGPVATGGADDEPIAIIGMACRFPGGVSSPEQLWDLVAS	3385
>	53		52
Ω	3386	GTDAISEFPVNRGWQTGHLFDPDPDRPGTTYSTQGGFLHEADEFDPTFFGISPREALVMD	3445
>	53		52
Ω	3446	POORLLLETTWESFERAGIRPETLRSTLTGTFVGSSYQEYGLGAGDGTEGHMVTGSSPSV	3505
>	53	JH	54
Ω	3506	LSGRLSYVPGLEGPAVTVDTACSSSLVALHLACQSLRNGESNLAVAGGATIMTTPNPFIA	3565
>	5.5		54 .
Д	3566	FSRQRALAKDGRCKAFSDDADGMTLAEGVGVVLVERLSDAQRNGHPVLAVLRGSAINQDG	3625
>-	5.5		54
۵	3626	<b>ASNGLTAPNGPSQQRVIRQALANARLAPGDIDALEAHGTGTPLGDPIEAQALFATYGRDR</b>	3685
>	55	VXMV	28
Д	3686	DPESALLLGSVKSNIGHTQSAAGIASVIKMVMALRHSELPPTLHADAPSSHVDWSAGTVR	3745
>	59	TIL	61
Ω	3746	:   LLTQARAWPETGRPRRAAVSSFGISGTNAHVLLEQAPVADTPAEERPAVAPVPIAAGVVP	3805
>	62		61
Q	3806	WVVTARSAAALRGQAERLLAHAETVGTALPAAGPLDIGLSLVSARARFEHRAVVVPPAGT	3865
>	62		61
Д	3866	DPLAALRAVATDGPSPVVARGVADVEGRTVFVFPGQGSQWVGMGSQLLDESAVFAERIAE	3925
>	62		61
Ω	3926	CAAALAEFTDWSLVDVLRGVVGAPSLERVDVVQPASFAVMVSLAALWRSRGVLPDAVVGH	3985
>	62		61.
۵	3986	SQGEIAAAVVSGALSLRDGARVVALRSQAIGRALAGRGGMMSVALSVDVLEPRLVEFEGR	4045
>	62	393	64
Q	4046	VSVAAVNGPRSVVVAGEPEALDALHARLTADDIRARRIAVDYASHSHQVEDLHEELLEVL	4105
>	65		64
Q	4106	AELAPRTSEVPFFSTVTGDWLDTARMDAGYWFRNLRGRVRFADAVADLLAAEYRAFVEVS	4165

ò	65	79
đ	4166	SHPVLSMAVQEAIDEAGVPAVAAGTLRRDQGGTDRFLLSAAEVFVRGVDVDWAGLFEGTG 4225
ò	65	94
q	4226	ASRIDLPTYAFQHEHLMAVPPAPEAVAAADPDDAAFWTAVEDGDVSALTAALGTDEDSVA 4285
ò	65	99 94
Q	4286	AVLPALISHRRARRDRSTVDAMRYRVAWKPLGGTLPHPSLIGIWLLVTADGIDDTDVAGA 4345
ò	65	99 94
g	4346	LETYGAEVRRLVLDEECVDRAVLRERLAGAEDVTGIVSVLAAAERTDAVPGTSLVLGTAL 4405
ò	65	99
요	4406	TVALIQALGDAEIDAPVWALTRGAVSTGRADELTAPVQAQVTGIGWTAALEHPQRWGGTL 4465
ò	65	99 94
g	4466	DLPAALDARAAQRLAAVLSGALGSDDQLAIRPSGVFTRRIVRAEATAGRPAGTWTPRGTT 4525
ઠે	65	99 94
g	4526	LVTGGSGTLAPHLARWLAQRGAEHLVLISRRGTAAPGAAELVAELAESGTEATVAACDIT 4585
ò	65	99 94
g	4586	DRDAVAALLADLKADGRTVRTVVHTAATIELHTLDATTLADFDRVLHAKVTGAQVLAELL 4645
ò	65	99
සු	4646	DDEELDDFVLYSSTAGMWGSGAHAAYVAGNAYLAALAEHRRANGLPALSLSWGIWADDLK 4705
ò	65	99
g	4706	LGRVDPQMIRRSGLEFMDPQLALSGLQRALDDNENVLAVADVDWETYHPVYTSGRPTPLF 4765
Š	9	99
g	4766	DEVPEVRRLTAAAEQSAGTVAEGEFAAALRALSDAEQORTLLETVRTEAASVLGLSSAED 4925
ò	65	99 94
g	4826	LTDQRAFRDVGFDSLTAVGLRNRLASVTGLTLPSTMVFDYPNPAALAAYLHGELAGARSA 4885
ò	65	99
පු	4886	AAGAAAVPTGAPDADDPIAIVGMSCRYPGGVGSAEDLWRIALDEVDAISGFPADRGWDAE 4945
ò	65	99 94
q	4946	GLYDPDPPDRPGRTYSVQGGFLRDVAEFDPGFFGISPREALSMDPQQRLLLETAWEAFEHA 5005
ò	65	75 TANLTS 75
음	2006	GIDPVGQRGSRTGTFVGASYQDYASGVPNSEGSEGHMITGTLSSVLSGRVSYLFGFEGPA 5065
ò	76	75
g	9905	VTLDTACSSSLVAMHLACQSLRNGESSLALAGGVSIMSTPMSFVGFSRQRALAEDGRCKA 5125
ò	16	75
Вр	5126	YADGADGMTLAEGVGLVLLERLSDARANGHQVLAVIRGSAVNQDGASNGLTAPNGPSQQR 5185
ò	16	SLLSVCG
q	5186	I   I

Search completed: March 20, 2003, 12:41:58 Job time : 273 secs

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773
1 AAGGILHLELLVAVGPDVFO.....SPTWSCLITEDTGFDLGVTI 148
                           GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human Von Willebra	Human addrecanase	Human ADAM-TS-like	Human Von Willebra	Human ADAMTS-M	Human Von Willebra	Amino acid seguenc	Amino acid sequenc	Human ORFX ORF2432	Human titin (conne
SUMMARIES	AAE24448	AAU97641	AAU79217	AAE24449	ABB04153	AAE24450	AAG63826	AAG63829	AAB42668	AAU05396
DB	23	23	23	23	23	23	22	22	21	22
% Query Match Length DB	148	242	933	1353	1416	1427	203	1120	118	26926
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	99.6	99.6	68.4	35.2
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T. niveum Cyclospo Human ORFX ORF1143 Human ADAMTS-7 ami Human ADAMTS-7 ami Human ADAM Lype me Human 27875 ADAM-T Ruman 27875 ADAM-T Streptomyces nours S. venezuelae pik Human metalloproce Streptomyces nours Amino acid sequenc Human secreted pro Streptomyces averm Novel human diagno Drosophila melanog Novel human diagno Drosophila melanog	Ø	protease fragment #1.  9 protease; vWP-cp; therapy; ensyme; omboembolic disease; preeclampsia; henoch-Schonlein purpura; la; haemolytic-uraemic syndrome;	Nurecek P, Schwarz H; Ner R, Tagliavacca L;
AAR44929 AAB41379 AAB41379 AAB72283 AAB72283 AAB700913 AAE00913 AAE00913 AAR30129 AAY51898 AAY51898 AAY51898 AAS3752 AAG65267 AAG65267 AAG6521044 ABB69110	AAY39301 AAB70969 AAB70969 ABC2216 AAM23830 AAM23830 AAM2360027 AAU360027 AAU85008 AAR25450 AAR25450 AAR25450 AAR25450 AAR25450 AAR25450 AAR25450 AAR25450	8 AA. eaving leavin 1, Thr copaen	Furlan M, Turec Kerechbaumer R
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111111111111111111111111111111111111111		RESULT 1 AAESALH48 ID AAE XX AC AC AC AC AC AC AC AC AC AC AC AC AC	30 22 122 122 123 123 221 21

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This invention relates to the cDNA and protein sequences of a novel than aggrecanase polypeptide. The protein of the invention may be used to inhibit the proteolytic activity of aggrecanase, or to inhibit the aggrecanase wediated cleavage of aggrecan in cartilege. The expression of the invention is useful for developing inhibitors of aggrecanase protein. The cDNA sequence encoding the aggrecanase protein of the invention is useful for designing probes for obtaining DNA sequences encoding other aggrecanase molecules. The cDNA sequence is also useful for detecting mRNA encoding aggrecanase in a given cell coppulation, and thus for detecting or disgnosting genetic disorders convolving the aggrecanase is irregularly transcribed or tissue disorders in which aggrecanase is irregularly transcribed or expressed. The DNA sequences may also be useful for preparing vectors for gene therapy applications. An inhibitor of the protein is useful continuacy by blocking the enzyme's proteolytic activity. An aggrecanase protein inhibitor and a method for inhibition of its activity aggrecanase protein vectors cartilage, by blocking the enzyme's proteolytic activity. An are useful for treating various aggrecanase—sescoideted conditions including osteoarthritis and other inflammatory diseases. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ADAM-TS-like protein; cardiovascular disorder; angina; vascular system; congestive heart failure; myocardial infarction; ischaemic heart disease; arrhythmia; hypertensive vascular disease; embolism; secondary arterial hypertension; peripheral vascular disease; embolism; chronic peripheral arterial occlusive disease; acute arterial thrombosis; inflammatory vascular disease; chronic obstructive pulmonary disease;
                                   Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide, which are useful for treating aggrecanase-associated condition such as osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKWVIL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 773; DB 23; Length 242; 100.0%; Pred. No. 1e-32; 1ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VTQLGGACSPTWSCLITEDIGFDLGVTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 33-34; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU79217 standard; Protein; 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ADAM-TS-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 242 AA;
N-PSDB; ABK52579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory ve
liver disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 102
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AAU79217
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                                                                                                                                                                                                              The invention relates to an isolated or substantially pure von Willebrand factor-cleaving protease (wWF-cp) polypeptide. wWF-cp is useful for controlling which involves providing wWF-cp as a ligand, contacting a solution comprising wWF with the polypeptide ligand under conditions where wWF is bound to the ligand and recovering from the ligand purified where wWF wWF-cp is useful for producing anti-vWF cp polypeptide antibodies wWF cp polypeptide antibodies wWF cp polypeptide antibodies from the animal. wWF-cp and isolating the anti-cwWF cp polypeptide antibodies from the animal. wWF-cp is useful for tromboembolic disease such as thrombotch thrombocytopaenia or thromboembolic disease such as thrombotch thrombocytopaenia or heamolytic-uraemic syndrome. wWF-cp and also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                         Novel isolated or substantially purified Von Willebrand factor-cleaving procease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDFSLGAQFRVHLVKMVIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aggrecanase; osteopathic; antiarthritic; antiinflammatory; human;
cartilage; osteoarthritis; inflammatory disease; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 773; DB 23; Length 148; 100.0%; Pred. No. 3e-33; arive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morris EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolfman NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU97641 standard; Protein; 242 AA
                                                                                                                                                                               Claim 1; Fig 3; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001; 2001WO-US32458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000US-241469P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human aggrecanase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Racie LA, Twine NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-452389/48
          WPI; 2002-479950/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 AA;
                                 N-PSDB; AAD39331
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WPI; 2002-479950/51.
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                                                                                               (BAXT ) BAXTER AG.
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          30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB04153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a human ADAM-TS-like protein and the polynucleotide encoding it. The protein of the invention is useful for treating cardiovascular disorders including diseases of the heart and vascular system, such as congestive heart failure, myocardial infarction, ischaemic heart diseases (e.g., stable angina, unstable angina), artial cand ventricular arrhythmia, hypertensive vascular diseases (e.g., all cardiovascular diseases (e.g., all carterial thrombosis and embolism, inflammatory vascular disease, acute are useful in diagnostic assays for detecting diseases and abnormalities or musceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences which encode the protein. The sequences are also useful for modulating ADAM-TS-like protein activity in a disease condition. This sequence represents the human ADAM-TS-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, Von Willebrand factor-cleaving protease, VWF-cp, therapy, enzyme, transgenic animal; immunisation; thromboembolic disease; preeclampsia; thromboct thrombocytic purpura; TTP; Henoch-Schonlein purpura; thrombosis; neonatal thrombocytopaenia; haemolytic-uraemic syndrome; transgenic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKVVVL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                               New purified human ADAM-TS-like protein, useful for identifying modulators of protein activity for treating cardiovascular or liver disorder or chronic obstructive pulmonary disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 773; DB 23; Length 933; 100.0%; Pred. No. 2.7e-31; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Von Willebrand factor-cleaving protease fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTQLGGACSPTWSCLITEDTGFDLGVTI 148
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                                                                                                                                                                                                 Claim 25; Fig 2; 106pp; English
                       28-SEP-2000; 2000US-235881P.
25-JUL-2001; 2001US-307393P.
26-SEP-2001; 2001WO-EP11124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 148; Conservative
                                                                                                              WPI; 2002-383274/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        933 AA;
                                                                                                                         N-PSDB; ABK49356
                                                          (FARB ) BAYER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                     Xiao Y;
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The invention relates to an isolated or substantially pure von Willebrand factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for comprising vWF with the polypeptide ligand under conditions solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified where vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunishing an animal with vWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for twe producing a preparation of prophylaxis and threapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura (TTP), thench-Schonlain purpura, precelampais, neonatal thrombocytopaenia or haemolytic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELDDGNRQVRG 120
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                                                                                                                                                                                                                                                                                 urlan M, Turecek P, Schwarz
Kerschbaumer R, Tagliavacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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100.0%; Score 773; DB 23;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Furlan M,
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                                                                                                                                                                                                                                                                                 Laemmle B, Gerritgen HE, Fu
Scheiflinger F, Antoine G,
Zimmermann K, Voelkel D;
20-NOV-2001; 2001WO-EP13391
                                                                            22-NOV-2000; 2000US-0721254
12-APR-2001; 2001US-0833328
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The present sequence represents a ADAMTS protein, designated ADAMTS-M, that exhibits the characteristics of the ADAM (A Disintegrin And that exhibits the characteristics of the ADAM (A Disintegrin And Metalloproteases) and contains a thrombospondin domain (TS). The protein is encoded by the CDNA given in the specification describes a newly isolated polynucleotide, comprising a nucleotide sequence encoding an ADAMTS-M polypeptide as a given in the specification, one metalloproteinase, disintegrin domain, prodomain or its thrombospondin submotif. The polynucleotide, polypeptide and agent are useful for manufacturing a medicament for treating a subject in need of altering activity or expression of ADAMTS-M. The polynucleotide, ADAMTS-M polypeptide and agent are useful for manufacturing a medicament for treating architis (setcoarthritis and rheumatoid arthritis), inflammatory bowel disease, Crohn's disease, ashima, Alzheimer's disease, organ transplant toxicity and rejection, cachexia, allergy, cancer (e.g. solid tumour cancer including colon, breast, lung, prostate, brain or haematopoietic malignancies including lenkaemia and lymphoma), osteoprosis, atherosclerosis, aortic aneurysm, congestive heart fallure, myocardial infarction, stroke, head trauma, spinal cord injury, neurodegenerative disease, Parkinson's disease, sutchimmune disorders, spinal cord injury, neurodegenerative disease, pain, depression, suntriple sclerosis, abnormal wound healing, burns, infertility or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, useful in gene therapy, particularly for treating or preventing e.g. arthritis, Crohn's disease, Alzheimer's disease and organ transplant toxicity and rejection, comprises ADAMTS polynucleotide and encoded polypeptide -
                                                                                                                                                                                                                                                                 /label= Mature ADAMTS.M protein
/note= "The mature form of the ADAMTS-M protein is
processed by furin cleavage of the prodomain"
Parkinson's; migraine; pain; depression; multiple sclerosis; burn; infertility; diabetic shock; gene therapy; ADAMTS-M; A Disintegrin And Metalloprotease; thrombospondin domain.
                                                                                                                                                                  /note= "The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wachtmann TS, Walsh RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        410..473
/label= Thrombospondin_submotif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1099. 1156
/label= Thrombospondin_submotif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.424
label= Heparin-binding_domain
                                                                                                                                                                                                                                                                                                                                             /label= Metalloprotease_domain
                                                                                                                                                                                                            14..97
|abel= Furin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                  147..272
| label = Zinc-binding_motif
                                                                                                                                                                                                                                                                                                                                                                                                                        Disintegrin_domain
                                                                                                                 Location/Qualifiers
                                                                                                                                      l..97
/label= Prodomain
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                                                                                                                                                                                                                                                                                                                                                                                                      324..394
/label= D:
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                                                                                                                                                                                                                Cleavage-site
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                                                                               Homo sapiens
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                                                                                                                                    Peptide
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diabetic shock. The polymucleotide and polypeptide are also useful for diagnosing the diseases above. The polymucleotide is particularly useful in gene therapy for treating the diseases cited above.
                                                                                                                                                           98 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKWVIL 157
                                                                                                                1 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVIL 60
                                                                                          O; Gaps
                                                                     Length 1416;
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                                                                                          .Indel8
                                                                                                                                                                                                                                                                                                                                                             Human Von Willebrand factor-cleaving protease (vWF-cp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Mature human vWF-cp protein"
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897..952
/note= "Thromspondin type I motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Thromspondin type I motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Thromapondin type I motif"
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/note= "Thromspondin type I motif"
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                                                                     100.0%; Score 773; DB 23; ilarity 100.0%; Pred. No. 7.5e-31; Conservative 0; Mismatches 0;
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/note= "Distintegrin like motif"
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/note= "Cysteine rich region"
554..687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69..75
/note= "Furin cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Catalytical side"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..51
/label=_Signal_peptide
                                                                                                                                                                                                              121 VTQLGGACSPTWSCLITEDTGFDLGVTI 148
                                                                                                                                                                                                                         218 VTQLGGACSPTWSCLITEDTGFDLGVTI 245
                                                                                                                                                                                                                                                                                            AAE24450 standard; Protein; 1427 AA.
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1016..1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224..228
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                                                                        Query Match
Best Local Similarity
Matches 148; Conserv
                                                  1416 AA
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                                                                                                                                                                                                                                                                                                                     AAE24450;
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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New anti-angiogenic intestinal polypeptides, zdint5 polypeptides, which are members of disintegrin proteases, for modulating extracellular matrix interaction, tumour suppression and wound healing -
proteolysis; apoptosis; angiogenesis; infection; cell adhesion; cell fusion; cell asgnalling; tumour; Crohn's disease; melanoma; tinflammatory bowel disease; food poisoning; degenerative disease; inflammation; fertility; gamete maturation; epithelial disorder.
                                                                                                                                                                                                          /note= "potential N-linked glycosylation site"
                                                                                                                                                                                          'note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                           /note= "zinc-binding motif"
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                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 73-74; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2000; 2000US-0501806.
                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2001; 2001WO-US04198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holloway JL, Sheppard PO;
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Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-522477/57.
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                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated or substantially pure Von Willebrand factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for purifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal wWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for producing a preparation of prophylaxis and therapy of thrombosis and thrombombombolic disease such as thrombocic thrombocytopaenia or haemolytic unramic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp contin. vWF-cp gene is located on chromosome 9.
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extracellular matrix interaction; tumour suppression; gamete maturation;
immunologic recognition; gastrointestinal irradiation; chemotherapy;
                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGURQVRG 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 7.7e-31;
Matches 148; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                  B, Gerritsen HE, Furlan M, Turecek P, Schwarz H; .nger F, Antoine G, Kerschbaumer R, Tagliavacca L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a human zdint5 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 5; 93pp; English
                                                                                     20-NOV-2001; 2001WO-EP13391.
                                                                                                                           22-NOV-2000; 2000US-0721254.
12-APR-2001; 2001US-0833328.
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                                                                                                                                                                                                                                                      Scheiflinger F, Antoine
Zimmermann K, Voelkel D;
                                                                                                                                                                                                                                                                                                                     WPI; 2002-479950/51.
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                                                                                                                                                                                        BAXT ) BAXTER AG.
                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD39332.
  WO200242441-A2.
                                                                                                                                                                                                                                  Laemmle B, G
Scheiflinger
                                           30-MAY-2002.
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The present sequence represents a human zdint5 polypeptide. The zdint5 polypeptide is an anti-angiogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is useful as a tool for identifying new family members of polypeptide is useful as a tool for identifying new family members of polypeptides. Zdint5 polypeptides are used to to clone 5' non-coding regions of zdint5 gene. Zdint5 polypeptides are used for tumour suppression, gamete matrix intesting in isolation or in and growth and differentiation either working in isolation or in certis and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery after gastrointestinal irradiation, chemotherapy or antibody use, and extracellular matrix repair and remodeling. The polypeptides are also useful for modulating proteolysis, wepoptosis, angiogenesis, infection, cell adhesion, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, Crohn's degenerative diseases, disorders related to immunity, inflammation, is also the maturation, immunology, trauma and epithelial
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The present sequence represents a human zdint5 polypeptide. The zdint5 polypeptide is an anti-angiogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is polypeptide is useful as a tool for identifying new family members of polypeptides. Zdint5 polymucleotides are useful as probes or primers to clone 5, non-coding regions of zdint5 gene. Zdint5 polypeptides are used for tumour suppression, gamete maturation, immunologic recognition, and growth and differentiation either working in isolation or in conjunction with other molecules in colon, small intestine, fetal lung, testis and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery
                                                                                                                                                                                                                                           extracellular matrix interaction; tumour suppression; gamete maturation; immunologic recognition; gastrointestinal irradiation; chemotherapy; proteolysis; apoptosis; anglogenesis; infection; cell adhesion; cell signalling; tumour; Crohn's disease; melanoma; trauma; inflammatory bowel disease; food poisoning; degenerative disease; inflammatory inflammatory, ford poisoning; degenerative disease; inflammation; fertility; gamete maturation; epithelial disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which
                                                                                                                                                                                                                          Human; zdints; anti-angiogenic; intestinal polypeptide; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti-angiogenic intestinal polypeptides, zdint5 polypeptides, ware members of disintegrin proteases, for modulating extracellular matrix interaction, tumour suppression and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "potential N-linked glycosylation site"
560
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635
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential N-linked glycosylation site"
176
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                                                                                                                                                                                           Amino acid seguence of a human zdint5 polypeptide.
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122 VTQLGGACSPTWSCLITEDTGFDLGVTI 149
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                                                                                      AAG63829 standard; Protein; 1120
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                                                                                                                                                            (first entry)
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595
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N-PSDB; AAH74765.
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                                                                                                                           AAG63829;
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after gastrointestinal irradiation, chemotherapy or antibody use, as anti-infectives, and extracellular matrix repair and remodeling. The polypeptides are also useful for modulating proteolysis, apoptosis, and ection, cell adhesion, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, Crohn's disease, inflammatory bowel disease, food poisoning, melanoma, degenerative diseases, disorders related to immunity, inflammation, fertility, gamete maturation, immunology, trauma and epithelial
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Best Local Similarity 99.3%; Pred. No. 6.1e-31;
Matches 147; Conservative 1; Mismatches O. 7-2-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VTQLGGACSPTWSCLITEDTGFDLGVTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 VIQLGGACSPTWSCLITEDTGFBLGVTI 252
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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N-PSDB; AAC76877.
                                                                                                                                                                                              Sequence 1120 AA;
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                                                                                                                                                                disorders
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cycostatic; hepatoriopic; vulnerary; antiparkinsonian; nootropic; neuroprotective; csteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antidingla antisheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus cryclinal or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocurnal haemoglobinuria, antiniflammatory disease, to enhance
                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation, to inhibit thrombosis, and as a contraceptive
                                                                                                                                           Claim 11; Page 4050; 5507pp; English.
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118 AA; Seguence

ö Gaps ö 68.4%; Score 529; DB 21; Length 118; 97.1%; Pred. No. 1.7e-20; ive 0; Mismatches 3; Indels ( 106 RFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTI Conservative Similarity 1001 Query Match Best Local 9 Matches 61 ò a 요

Human titin (connectin) protein sequence. AAU05396 standard; Protein; 26926 (first entry) 24-OCT-2001 AAU05396; AAU05396 

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Human; titin; connectin; pickwick mutation; cardiac specific exon; N2B; titin-related disease; zebrafish; heart failure; heart disease.

Homo sapiens

WO200151666-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US01212 12-JAN-2000; 2000US-0175787

(GEHO ) GEN HOSPITAL CORP.

Fishman MC;

730 HIKTTDQKGMHISSQIKKTTDLTTERLVHVDKRPRTASPHFTVSKISVPKTEHGYEASIA 789

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WPI; 2001-451869/48. N-PSDB; AAS05390.

the described suppose that the subject of the subject of the subject of the subject of the subject has or is at risk of developing a titin-related disease or condition. The method compiles analysing a titin-related a sample from the subject and detecting the presence of a mutation (e.g. the pickwick mutation in the cardiac specific exon N2B) in the titin gene, which indicates that the subject has or is at risk of developing a titin-related disease. The zebrafish which has a phenotype similar to mammalian heart failure is used as a model. The method is useful for detecting an increased likelihood of heart disease, such as heart failure, in a patient, so that appropriate intervention can be instituted before any symptoms occur. The method may also be used to carlitrate determination of etiology of an existing heart condition, such as heart failure, to identify compounds that can be used to treat or prevent heart conditions, in prenatal genetic screening, e.g. to identify parents who may be carriers of a recessive titin mutation. Compounds identified using the methods may be used to treat patients. The have or are at risk of developing heart disease, e.g. heart Gaps 490 ELKSRTKEIITTKQEQMHVTHEQIRKETEKTFVPKVVISAAKAKEQETRISEEITKKQKQ 549 190 ELLVOGEEEVPAKKTKTIVSTAQISESRQTRIEKKIEAHFDARSIATVEMVIDGAAGQQL 249 309 370 IRTEERWEGRYGVQEQVTISGAAGAAASVSASASYAAEAVATGAKEVKQDADKSAAVATV 429 430 VAAVDMARVREPVISAVEQTAQRTTTTAVHIQPAQEQVRKEAEKTAVTKVVVAADKAKEQ 489 550 VTQEAIMKETRKTVVPKVIVATPKVKEQDLVSRGREGITTKREGVQITQEKMRKEAEKTA 609 18 610 LSTIAVATAKAKEQETILRTRETMATRQEQIQVTHGKVDVGKKAEAVATVVAAVDQARVR 669 13 **EPREPGHLEESYAQQTTLEYGYKERISAAKVAEPPQRPASEPHVVPKAVKPRVIQAPSET** 12 ------250 PHKTPPRIPPKPKSRSPTPPSIAAKAQLARQQSPSPIRHSPSPVRHVRAPTPSPVRSVSP Determining if a subject has or is at risk of developing a titin-related disease or condition, particularly heart failures, comprises detecting the presence of a mutation in the titin gene Indels 24887; 35.2%; Score 272; DB 22; Length 26926; 8 sequence representing human titin (also known 23; ilarity 0.4%; Pred. No. 0.45; Conservative 16; Mismatches Disclosure; Page 57-111; 114pp; English. 26926 AA; Local Similarity 19 -----12 -----Best Local Simi Matches 101; Sequence Query Match 19 19 13 요 g d g ద ઠે ò ò ò ò g ઠે ઠે 유 임 ò ò

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80	49	18	606	30	696	30	1029	30	1089	òe	1149	30	1209		1269	30	1329	30	1389	30	1449	30	1509	36	1569		1629		1689		1749		1809		1869	
1	YKSEAG 8									-										-		:				36		36 36		36		38		38		38
•	PADTPDT		PTLVSGL	AHOED	REAFAED		WMTDTSL		TTGYRYK		SOOEMLY		QEFHISS		LEGMGVTE		TAFASNIF		SPARMSP		RPMPETFV		VILTVEAN		KIRIEGTK		PRGTYRAK		ECRLTPIS		YGTDHTSA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IVLYPEPV		KSYDTGEV	
	SPTPLPQF		APVEI PVTI		SGIARLM		CRFVESRD		WKKSGVPI		ADYELLM		VVRTYVED		LRIKNYRI		'LPEDEGIY		TRMSPARM		RFDLKWG		RAGRSSIS		ІІУРНКҮР		EPERKLII		KRFGPAHF		ITCRATNK		окекокрр		нугріурс	
	PSETRVRAI		TETARVP	F	SIDFQITFO		PEKFTTEE		SGNPKPHV		ASASLLEE		KKMAKDTV		EAVESGF		ASLRIPW		PRSVSRSF		KCLEGQTA		EWTVVAQN		IVWLKNSD	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VEVEFAEP		KKLTSLRL		AYSRDSGI	-GA	 ALTGVTTD		FRVRYDGI	
	GSAIATLQKELSATSSAQKITKSVKAPTVKPSETRVRAEPTPLPQFPFADTPDTYKSEAG		VEVKKEVGVSITGTTVREERFEVLHGREAKVTETARVPAPVEIPVTPPTLVSGLKNVTVI	-VAHOEDTERVA-	REDYQIES		SAVNEAGTVSTSCYLAVQVSEEFFKETTAVTEKFTTEEKRFVESRDVVMTDTSLTEEQAG		PGEPAAPYFITKPVVQKLVEGGSVVFGCQVGGNPKPHVYWKKSGVPLTTGYRYKVSYNKQ		TGECKLVISMTFADDAGEYTIVVRNKHGETSASASLLEEADYELLMKSQQEMLYQTQVTA		FVQEPEVGETAPGFVYSEYEKEYEKEQALIRKKMAKDTVVVRTYVEDQEFHISSFEERLI		KEIEYRIIKTTLEELLEEDGEEKMAVDISESEAVESGFDLRIKNYRILEGMGVTFHCKMS		GYPLPKIAWYKDGKRIKHGERYQMDFLQDGRASLRIPVVLPEDEGIYTAFASNIKGNAIC		SGKLYVEPAAPLGAPTYIPTLEPVSRIRSLSPRSVSRSPIRMSPARMSPARMSPARMSPA	1	RMSPGRRLEETDESQLERLYKPVFVLKPVSFKCLEGQTARFDLKVVGRPMPETFWFHDGQ		QIVNDYTHKVVIKEDGTQSLIIVPATPSDSGEWTVVAQNRAGRSSISVILTVEAVEHQVK		PMFVEKLKUVNIKEGSRLEMKVRATGNPNPDIVWLKNSDIIVPHKYPKIRIEGTKGEAAL		KIDSTVSQDSAMYTATAINKAGRDTTRCKVNVEVEFAEPEPERKLIIPRGTYRAKEIAAP		ELEPLHLRYGGEQWEEGDLYDKEKQQKPFFKKKLTSLRLKRFGPAHFECRLTPISDPTMV	1 1 1	VEWLHDGKPLEAANRLRMINEFGYCSLDYGVAYSRDSGIITCRATNKYGTDHTSATLIVK	9	DEKSLVEESQLPEGRKGLQRIEELERMAHEGALTGVTTDQKEKQKPDIVLYPEPVRVLEG		ETARFRCRVTGYPQPKVNWYLNGQLIRKSKRFRVRYDGIHYLDIVDCKSYDTGEVKVTAE	
	SAQKITK		VREERFE		SPTVTWY		AVQVSEE		'QKLVEGG		AGEYTIVA	. !	YSEYEKEY		LEEDGEEN	1	IKHGERYC	1	TYIPTLEE		LERLYKPV		GTQSLIIV		SRLEMKVR		TAINKAGR		EGDLYDKE		LRMINEFG		KGLQRIEE		KVNWYLNG	
	QKELSATS		GVSITGT	1	ECHISGYE		TVSTSCYL		YFITKPVV		ISMTFADD		GETAPGFV		IKTTLEEL		AWYKDGKR		PAAPLGAP	1 1 1	LEETDESQ		нкууткер	-LTNLNI	KNVNIKEG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ODSAWYTA		RYGOEOWE		KPLEAANR		ESQLPEGR		RVTGYPQP	
1	GSAIATL		VEVKKEV		EGESVTL		SAVNEAG		PGEPAAP		TGECKLV	1	FVQEPEV		KEIEYRI		GYPLPKI		SGKLYVE		RMSPGRR		QIVNDYT		PMFVEKL	1	KIDSTVS		ELEPLHLI	1 1 1 1 1 1	VEWLHDG		DEKSLVE		ETARFRCI	
19	790	19	850	19	910	31	970	31	1030	31	1090	31	1150	31	1210	31	1270	31	1330	31	1390	31	1450	31	1510	37	1570	37	1630	37	1690	37	1750	39	1810	39
ò	g	ò	Q	ò	đ	ò	Q	ò	qq	ò	g	ò	g	ઠે	Q	ò	QQ	ò	g	ò	g	ò	q	ò	g	ò	g	ò	qq	ò	qq	ò	g	ò	g	ò

g G	1870 NPEGVIEHKVKLEIQQREDFRSVLRRAPEPRPEFHVHEPGKLQFEVQKVDRPVDTTETKE	1929
ò	39ELLR	42
q	1930 VVKLKRAERITHEKVPEESEELRSKFKRRTEEGYYEAITAVELKSRKKDESYEELLRKTK	1989
ò	, 43	42
qq	1990 DELLHWTKELTEEEKKALAEEGKITIPTFKPDKIELSPSMEAPKIFERIOSQTVGGGSDA	2049
ò	43	- 45
q	2050 HFRVRVVGKPDPECEMYKNGVKIERSDRIYWYMPEDNVCELVIRDVTAEDSASIMVKAIN	2109
ò	46	45
QQ	2110 IAGETSSHAFLLVQAKQLITFTQELQDVVAKEKDTMATFECETSEPFVKVKWYKDGMEVH	2169
ò	46	45
QQ	2170 EGDKYRMHSDRKVHFLSILTIDTSDAEDYSCVLVEDENVKTTAKLIVEGAVVEFVKELQD	2229
ò	46	2
g	2230 IEVPESYSGELECIVSPENIEGKWYHNDVELKSNGKYTITSRRGRQNLTVKDVTKEDQGE	2289
ò	46	45
q	2290 YSFVIDGKKTTCKLKMKPRPIAILQGLSDQKVCEGDIVQLEVKVSLESVEGVWMKDGQEV	2349
ò	46	45
qq	2350 QPSDRVHIVIDKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSGRVSVYSVDVITPLKDVN	2409
ò	46	45
QQ	2410 VIEGTKAVLECKVSVPDVTSVKMYLNDEQIKPDDRVQAIVKGTKQRLVINRTHASDEGPY	2469
ò	46	45
đ	2470 KLIVGRVETNCNLSVEKIKIIRGLRDLTCTETQNVVFEVELSHSGIDVLWNFKDKEIKPS	2529
ò	94	45
q	2530 SKYKIEAHGKIYKLTVLNMMKDDEGKYTFYAGENMTSGKLTVAGGAISKPLTDQTVAESQ	2589
ò	- 46	2.
q	2590 EAVFECEVANPDSKGEWLRDGKHLPLTNNIRSESDGHKRRLIIAATKLDD <b>LG</b> EYTYKVAT	2649
ò	46	45
q	2650 SKTSAKLKVEAVKIKKTLKNLTVTETQDAVFTVELTHPNVKGVQWIKNGVVLESNEKYAI	2709
ò	46	28
qq	2710 SVKGTIYSLRIKNCAIVDESVYGFRLGRLGASARLHVETVKIIKKPKDVTALENATVAFE	2769
ò	29	58
q	. 2770 VSVSHDTVPVKWFHKSVEIKPSDKHRLVSERKVHKLMLQNISPSDAGEYTAVVGQLECKA	2829
ò		28
QQ	2830 KLFVETLHITKTMKNIEVPETKTASFECEVSHFNVPSMMLKNGVEIEMSEKFKIVVQGKL	2889
ò		58
qq	2890 HQLIIMNTSTEDSAEYTFVCGNDQVSATLTVTPIMITSMLKDINAEEKDTITFEVTVNYE	2949
ò		58

g G	2950	GISYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGDAADYTFVAGKATSTATLYVEA	3009
ò	. 65		58
Q Q	3010	RHIEFRKHIKDIKVLEKKRAMFECEVSEPDITVQWMKDDQELQITDRIKIQKEKYVHRLL	3069
ò	. 65		58
g	3070	I PSTRMSDAGKYTVVAGGNVSTAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDV	3129
ò	. 65		58
g	3130	DAHWYKDGIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYTFVAGRNRSSVTLYVNA	3189
ò	29	3	58
8	3190	PEPPQVLQELQPVTVQSGKPARFCAMISGRPQPKISWYKEEQLLSTGFKCKFLHDGQEYT	3249
ò	59		58
q	3250 1	LLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEVPEVVSPDQEMPVYPPAIITPLQDTV	3309
ò	23		58
g	3310	TSEGQPARFQCRVSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLE1AEAYPEDEGTYT	3369
à	29		58
g	3370	FVANNAVGQVSSTANLSLEAPESILHERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLS	3429
ઠે	59		58
qq	3430	KINETLELLSESPVYPTKFDSEKEGTGP1F1KEVSNAD1SMGDVATLSVTVIG1PKPKIQ	3489
ò	59		58
g	3490	WFFNGVLLTPSADYKFVFDGDDHSLIILFTKLEDEGEYTCMASNDYGKTICSAYLKINSK	3549
ò	59		58
qq	3550	GEGHKDTETESAVAKSLEKLGGPCPPHFLKELKPIRCAQGLPAIFEYTVVGEPAPTVTWF	3609
ò	59		58
g	3610	KENKQLCTSVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENMLGESTCAAELLVLLED	3669
ò	29		58
පු	3670	TDMTDTPCKAKSTPEAPEDFPQTPLKGPAVEALDSEQEIATFVKDTILKAALITEENQOL	3729
ò	59		. 28
g	3730	SYEHIAKANELSSOLPLGAQELQSILEQDKLTPESTREFLCINGSIHFQPLKEPSPNLQL	3789
ò	83	-D343L/11	
q	3790	QIVQSQKTFSKEGILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPLKTLLAEPEGN	3849
ò	99		65
셤	3850	YPQSSIEPPMHSYLTSVAEEVLSLKEKTVSDTNREQRVTLQKQEAQSALILSQSLAEGHV	3909
ò	99		65
g	3910	ESLQSPDVMISQVNYEPLVPSEHSCTEGGKILIESANPLENAGQDSAVRIEEGKSLRFPL	3969
ò	99		65
g	3970	ALEEKQVLLKEEHSDNVVMPPDQIIESKREPVAIKKVQEVQGRDLLSKESLLSGIPEEQR	4029
ò	99		65
g	4030	LNLKIQICRALQAAVASEQPGLFSEWLRNIEKVEVEAVNITQEPRHIMCMYLVTSAKSVT	4089

ò	99	A9
qq	4090	EEVTIIIEDVDPQMANLKMELRDALCAIIYEEIDILTAEGPRIQQGAKTSLQEEMDSFSG 4149
ò	99	59
QQ	4150	SQKVEPITEPEVESKYLISTEEVSYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKP 4209
ò	99	59
QQ	4210	SEEKEESSSESGTEEVATVKIQEAEGGLIKEDGPMIHTPLVDTVSEEGDIVHLTTSITNA 4269
ò	99	59
QQ	4270	KEVNWYFENKLVPSDEKFKCLQDQNTYTLVIDKVNTEDHQGEYVCEALNDSGKTATSAKL 4329
ò	99	69
q	4330	TVVKRAAPVIKRKIEPLEVALGHLAKFTCEIQSAPNVRFGWFKAGREIYESDKCSIRSSK 4389
ò	70	69
q	4390	YISSLEILRTQVVDCGEYTCKASNEYGSVSCTATLTVTVPGGEKKVRKLLPERKPEPKEE 4449
ò	70	69
QQ	4450	VVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPPRPVEEVEVPTVTKRERKIPEPTK 4509
ò	70	69
Q	4510	VPEIKPAIPLPAPEPKPKPEAEVKTIKPPPVEPEPTPIAAPVTVPVVGKKAEAKAPKEEA 4569
ò	70	69
g	4570	AKPKGPIKGVPKKTPSPIEAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDIIL 4629
ò	70	69
qq	4630	TESEFVGSSAIFECLVSPSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAG 4689
ò	70	69
qq	4690	EYTCVLRLGNKEKTSTAKLVVEELPVRFVKTLEEEVTVVKGQPLYLSCELNKERDVVWRK 4749
ò	70	69
q	4750	DGKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYTVTVENANNLECSSCVKVVEVIRD 4809
ò	70	69
g	4810	WLVKPIRDQHVKPKGTAIFACDIAKDTPNIKWFKGYDBIPAEPNDKTEILRDGNHLYLKI 4869
ò	70	69
qq	4870	KNAMPEDIAEYAVEIEGKRYPAKLTLGEREVELLKPIEDVTIYEKESASFDAEISEADIP 4929
ò	7.0	69
qq	4930	GQWKLKGELLRPSPTCEIKAEGGKRFLTLHKVKLDQAGEVLYQALNAITTAILTVKEIEL 4989
ઠે	70	69
QQ	4990	DFAVPLKDVTVPERRQARFECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILVINDS 5049
ò	70	69
QQ	5050	QFDDEGVYTAEVEGKKTSARLFVTGIRLKFMSPLEDQTVKEGETATFVCELSHEKMHVVW 5109
ò	70	69
đ	5110	FKNDAKLHTSRTVLISSEGKTHKLEMKEVTLDDISQIKAQVKELSSTAQLKVLEADPYFT 5169

è	7.0	69	i	
5	2	0002 VIGAVIVITATION CONTRACTOR	g D	6250 EKKSVIFWCRVIN
đ	5170 VR	5170 VKLHDKTAVEKDEITLKCEVSKDVPVKMFKDGEEIVPSPRISIRADGERATLATATATATATATATATATATATATATATATATATAT	ò	04
ò	70		q	6310 AGQDKSVAELLI
셤	5230 DK	5230 DKGEYVCDCGTDKTKANVTVEARLIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLK 5289	ò	70
ò	04	. 69	q	6370 KYKFEKDGSIHRI
ପ୍ଧ	5290 GC	5290 GQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIFITPL 5349	ò	70
ò	70	69	đ	6430 ADVVFLAELNKDI
q	5350 SI	SDVKVFEKDEAKFECEVSREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDE 5409	ò	70 07
ò	70	69	qa	6490 DKEARAKLELAA
q	5410 A	5410 AKYMFEAEDKHTSGKLIIEGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQ 5469	ò	70
ò	70	69	අ	6550 TTAEQTSFRILE
đ	5470 RI	5470 RLHTTRSVSMQDEGKTHSITFKDLSIDDTSOIRVEAMGMSSEAKLTVLEGDPYFTGKLQD 5529	ò	04
ò	70 -	69	දු	6610 SLAWEEPLTDGG
Q	5530 Y'	5530 YTGVEKDEVILQCEISKADAPVKWFKDGKEIKPSKNAVIKTDGKKRMLILKKALKSDIGQ 5589	ò	70
ò	70 -	69	മ	6670 RNRVGTGEPVET
g	5590 Y	5590 YTCDCGTDKTSGKLDIEDREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEAL 5649	ò	04
ò	- 0/	69	qo	6730 IELRDKTSIRWD
	2650 L	5650 LQTPDCEIKEEGKIHSLVLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVT 5709	ò	70TANL
ò	- 04	69	. අ <u>ප</u>	   6790 DPIERPSPPVNL
셤	5710 V	5710 VTAGETATFDCELSYEDIPVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVQ 5769	ò	77
ò	- 04	69	q	6850 PELTYKVTGLEK
g	5770 L	5770 LTAKDFKTHANLFVKEPPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILK 5829	ò	77
ò	- 07	69	셤	6910 IVPNPITILVPS
đ	5830 S	5830 SKKYEIVADGRVRKLVIHDCTPEDIKTYTCDAKDFKTSCNLNVVPPHVEFLRPLTDLQVR 5889	ò	77
ò	70 -	69	q C	6970 LKLENRVKTISG
a	5890 E	5890 EKEMARFECELSRENAKVKWFKDGAEIKKGKKYDIISKGAVRILVINKCLLDDEAEYSCE 5949	ò	44
ò	- 04	69	qa	7030 REVSRKTWTKVM
g	5950	5950 VRTARTSGMLTVLEEEAVFTKNLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIETG 6009	ò	82
ò	- 04	69	QD	7090 VPDPPENVKWRI
q	6010 F	6010 RYEILTEGRKRILVIQNAHLEDAGNYNCRLPSSRTDGKVKVHELAAEFISKPQNLEILEG 6069	ò	82
ò	- 04	69	q	7150 EVTGLEEGKWY
ద	6070	6070 EKAEFVCSISKESFPVQWKRDDKTLESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVG 6129	ò	82
ò	- 01	69	qa	7210 KIELPATVTGK
셤	6130 /	6130 AARAAAHLTVIEKLRIVVPLKDTRVKEQQEVVFNCEVNTBGAKAKWFRNEEAIFDSSKYI 6189	6	82
ò	70	69	අ	7270 NVCGRATAVVE
q	6190	6190 ILQKDLVYTLRIRDAHLDDQANYNVSLTNHRGENVKSAANLIVEEEDLRIVEPLKDIETM 6249	ò	82
ò	70	69	_	

g	6250	EKKSVTFWCKVNRLNVTLKWTKNGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDEGEYIVT 6309
ò	70	69
엄	6310	AGQDKSVAELLIIEAPTEFVEHLEDQTVTEFDDAVFSCQLSREKANVKWYRNGREIKEGK 6369
ò	70	69
g	6370	KYKFEKDGSIHRLIIKDCRLDDECEYACGVEDRKSRARLFVEEIPVEIIRPPODILEAPG 6429
ò	70	69
đ	6430	ADVVFLAELNKDKVEVQWLRNNMVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIAK 6489
ò	70	69
qq	6490	DKEARAKLELAAAPKIKTADQDLVVDVGKPLTMVVPYDAYPKAEAEWFKENEPLSTKTID
ò	70	
qq	6550	TTAEQTSFRILEAKKGDKGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNLEVTETFDGEV
ò	. 70	69
q	6610	SLAWEEPLTDGGSKIIGYVVERRDIKRKTWVLATDRAESCEFTVTGLQKGGVEYLFRVSA
ò	70	
q	6670	RNRVGTGEPVETDNPVEARSKYDVPGPPLNVT1TDVNRFGVSLTWEPPEYDGGAE1TNYV
ò	7.0	69
q	6730	IELRDKTSIRWDTAMTVRAEDLSATVTDVVEGQEYSFRVRAONRIGVGKPSAATPFVKVA 6789
ò	70	76TANLT3S7
අු	6790	   DPIERPSPPVNLTSSDQTQSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLV 6849
ò	77	92
q	6850	PELTYKVTGLEKGNKYLYRVSAENKAGVSDPSEILGPLTADDAFVEPTMDLSAFKDGLEV 6909
ò	77	94
· ස	6910	JVPNPITILVPSTGYPRPTATWCFGDKVLETGDRVKMKTLSAYAELVISPSERSDKGIYT 6969
ò	77	
: a	6970	) LKLENRVKTISGEIDVNVIARPSAPKELKFGDITKDSVHLTWEPPDDDGG&RLTGYVVEK 7029
ò	77	
음	7030	
ò	82	91
ු දු	7090	) VPDPPENVKWRDRTANSIFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKM 7149
ò	82	2 81
g	7150	D EVTGLEEGKWYAYRVKTLNROGASKPSRPTEEIQAVDTQEAPEIFLDVKLLAGLTVKAGT 7209
ò	82	2 81
qq	7210	0 KIELPATVTGKPEPKITWTKADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYIIEAV 7269
ò	82	
g	7270	0 NVCGRATAVVEVNVLDKPGPPAAFDITDVTNESCLLTWNPPRDDGGSKITNYVVERRATD 7329
6	82	2

7330	SEVWHKLSSTVKDTNFKATKLIPNKEYIFRVAAENMYGAGEPVQASPITAKYQPDPGPP 7	7389
		•
82		18
7390	TRLEPSDITKDAVTLTWCEPDDDGGSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKG 7	7449
82		81
7450	LTNKKKYRFRVLAENLAGPGKPSKSTEPILIKDPIDPPWPPGKPTVKDVGKTSVRLNWTK	7509
82	8	81
7510	PEHDGGAKI ESYVI EMLKTGTDEWVRVAEGVPTTQHLLPGLMEGQEYSFRVRAVNKAGES	7569
82	•	81
7570	EPSEPSDPVLCREKLYPPSPPRWLEVINITKNTADLKWTVPEKDGGSPITNYIVEKRDVR	7629
82		81
7630	RKGWQTVDTTVKDTKCTVTPLTEGSLYVFRVAAENAIGQSDYTEIEDSVLAKDTFTTPGP	7689
82		81
7690	PYALAVVDVTKRHVDLKWEPPKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNFRVT	7749
82		81
7750	DVIEGTEVOFQVRAENEAGVGHPSEPTEILSIEDPTSPPSPPLDLHVTDAGRKHIAIAWK	7809
82		81
7810	PPEKNGGSPIIGYHVEMCPVGTEKWMRVNSRPIKDLKFKVEEGVVPDKEYVLRVRAVNAI	7869
82		81
7870	GVSEPSEISENVVAKDPDCKPTIDLETHDIIVIEGEKLSIPVPFRAVPVPTVSWHKDGKE	7929
82		81
7930	VKASDRLTMKNDHISAHLEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDI	7989
82		81
7990	KASDITKSSCKLTWEPPEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWTVKDLIPN	8049
82		81
8050	GEYFFRVKAVNKVGGGEYIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYD	8109
82		81
8110	GGSKIMGYIIEKIAKGEERWKRCNEHLVPILTYTAKGLEEGKEYQFRVRAENAAGISEPS	8169
82		81
8170	RATPPTKAVDPIDAPKVILRTSLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEEIK	8229
82		81
8230	KRAAPLVRRRKGEVQEEEPFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVEND	8289
82		81
8290	HGIAKAPCTVSVLDTPGPPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKP	8349
82		81
8350	DSEWIVVTSTLRHCKYSVTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAP	8409
82		81
8410	DKPIVEDVTSNSMLVKWNEPKDNGSPILGYWLEKREVNSTHWSRVNKSLLNALKANVDGL	8469

ò	95	SAN TANADA CODE OD TO DE VANTA EL EMEDDA	81 8529
8	8470 1		
ò	82	80	81
q	8530 1	FNGGGEIVGYFVDKQLVGTNKWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGP 8	8589
ò	83	00	81
QQ	8590 1	PGETQPVTVAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELD 8	8649
ò	82	8	81
qq	8650 1	KDRVVIDNVGTKSELIIKDALRKDHGRYVITATNSCGSKFAAARVEVFDVPGPVLDLKPV 8	8709
ò	82	8	81
Q	.8710	VTNRKMCLLNWSDPEDDGGSEITGFIIERKDAKWHTWRQPIETERSKCDITGLLEGGEYK 0	8769
ò	82	8	81
g	8770	FRVIAKNKFGCGPPVEIGPILAVDPLGPPTSPERLTYTERQRSTITLDWKEPRSNGGSPI 8	8829
ò	82	8	81
ପ୍	8830	OGYIIEKRRHDKPDFERVNKRLCPTTSFLVENLDEHQMYEFRVKAVNEIGESEPSLPLNV 0	6888
ò	82	8	18
qq	8890	VIQDDEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDAL 0	8949
ò	82		81
qq	8950	Q1TKEEVSRSEAKTELSI PKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPPRNLAV 9	6006
ò	82		81
qq	9010	TDIKAESCYLTWDAPLDNGGSEITHYVIDKRDASRKKAEWEEVTNTAVEKRYGIWKLIPN 9	6906
ò	82		81
qq	9070	GOYEFRVRAVNKYGISDECKSDKVVIQDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNG 9	9129
ò	82		81
QQ	9130	GSPITGYWLEKREEGSPYWSRVSRAPITKVGLKGVEFNVPRLLEGVKYQFRAMAINAAGI ʻ	9189
ò	82	MS	83
qq	9190		9249
ò	84		83
q	9250	GTTDWKRVNEPDKLITTCECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIQE	9309
ò	84		83
q	9310	EPEVFIDIGAQDCLVCKAGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQ	9369
ò	84		83
QQ	9370	LETAENSSVIIIPECKRSHTGKYSITAKNKĄGQKTANCRVKVMDVPGPPKDLKVSDITRG	9429
ò	84		83
g	9430	SCRLSWKMPDDDGGDRIKGYVIEKRTIDGKAWTKVNPDCGSTTFVVPDLLSEQQYFFRVR	9489
ò	84		83
qq	9490	AENRFGIGPPVETIQRTTARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHY	9549

ò	84		83
g	9550 IVECLAWDPTG	IVECLAWDPTGTKKEAWRQCNKRDVEELQFTVEDLVEGGEYEFRVKAVNAAGVSKPSATV	6096
ò	84		83
g	9610 GPCDCQRPDMP	GPCDCQRPDMPPSIDLKEFMEVEEGTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLY	6996
ò	84		83
g	9670 DTHVNKLVVDD	DTHVNKLVVDDTCTLVIPQSRRSDTGLYTITAVNNLGTASKEMRLNVLGRPGPPVGPIKF	9729
ò	84		83
g	9730 ESVSADQMTLS	ESVSADOMTLSWFPPKDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTIPKLLEGHE	9789
ò	84	NILOS	88
g	9790 YVFRIMAQNKY	YVFRIMAQNKYGIGEPLDSEPETARNLFSVPGAPDKPTVSSVTRNSMTVNWEEPEYDGGS	9849
ò	68		88
q	9850 PVTGYWLEMKD	PVTGYWLEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPA	6066
ò	68		88
g	9910 SLPSDPATARD	SLPSDPATARDPIAPPGPPFPKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEE	6966
ò	68		88
g	9970 WEKGKDKEVRG	WEKGKDKEVRGTKLVVTGLKEGAFYKFRVSAVNIAGIGEPGEVTDVIEMKDRLVSPDLQL	10029
ò	68		88
q	10030 DASVRDRIVVH	DASVRDRIVVHAGGVIRIIAYVSGKPPPTVTWNNNERTLPQEATIETTAISSSMVIKNCO	10089
ઠે	68	PEDD	92
g	10090 RSHQGVYSLLA	RSHQGVYSLLAKNEAGERKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGS	10149
ò	93		
g	10150 PITNYVIEKRE	PITNYVIEKRESDRRAWTPVTYTVTRQNATVQGLIQGKAYFFRIAAENSIGMGPFVETSE	10209
ò	93		92
q	10210 ALVIREPITVE	ALVIREPITVPERPEDLEVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIGTEKFHKV	10269
ò	93		92
g	10270 TNDNLLSRKYT	TNDNLLSRKYTVKGLKEGDTYEYRVSAVNIVGQGKPSFCTKPITCKDELAPPTLHLDFRD	10329
ò	93		92
g	10330 KLTIRVGEAFP	KLTIRVGEAFALTGRYSGKPKPKVSWFKDEADVLEDDRTHIKTTPATLALEKIKAKRSDS	10389
ò	93		92
g	10390 GKYCVVVENS1	GKYCVVVENSTGSRKGFCQVNVVDHPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKITN	10449
ò	86		92
Q	10450 YIIEKKEVGKI	YIIEKKEVGKDVAMPVTSASAKTTCKVSKLLEGKDYIFRIHAENLYGISDPLVSDSMKAK	10509
ò	93		92
g	10510 DRFRVPDAPD(	DRFRVPDAPDQPIVTEVTKDSALVTWNKPHDGGKPITNYILEKRETMSKRWARVTKDPIH	10569
ò	93		92
Dp	10570 PYTKFRVPDL	PYTKFRVPDLLEGCQYEFRVSAENEIGIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTC	10629
ò	93		92

q	10630	NSVDLTWQPPRHDGGSKILGYIVEYQKVGDEEWRRANHTPESCPETKYKVTGLRDGQTYK 10689
ò	93	76TDqdH
d d	10690	:
δ	86	26
q	10750	FPKVTWKKEDRDAPTKARIDVTPVGSKLEIRNAAHEDGGIYSLTVENPAGSKTVSVKVLV 10809
ò	98	16
đ	10810	LDKPGPPRDLEVSEIRKDSCYLTWKEPLDDGGSVITNYVVERRDVASAQMSPLSATSKKK 10869
ò	96	46 81
qq	10870	SHFAKHLNEGNQYLFRVAAENQYGRGPFVETPKPIKALDPLHPPGPPKDLHHVDVDKTEV 10929
ò	98	26
Q	10930	SLVWNKPDRDGGSPITGYLVEYQEEGTQDWIKFKTVTNLECVVTGLQQGKTYRFRVKAEN 10989
8	98	16
g	10990	IVGLGLPDTTIPIECQEKLVPPSVELDVKLIEGLVVKAGTTVRFPAIIRGVPVPTAKWTT 11049
ò	96	46
g	11050	DGSEIKTDEHYTVETDNFSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGP 11109
ò	98	46
đ	11110	PTGPINILDVTPEHMTISWQPPKDDGGSPVINYIVEKQDTRKDTWGVVSSGSSKTKLKIP 11169
ò	98	26
q	11170	HLQKGCEYVFRVRAENKIGVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAATVSWTL 11229
ò	96	46
qq	11230	PKSDGGSPITGYYMERREVTGKWYRVNKTPIADLKFRVTGLYEGNTYEFRVFAENLAGLS 11289
ò	98	ADDLV101
g	11290	KPSPSSDPIKACRPIKPPGPPINPKLKDKSRETADLVWTKPLSDGGSPILGYVVECQKPG 11349
ò	102	101
QQ	11350	TAQMNRINKDELIRQCAFRVPGLIEGNEYRFRIKAANIVGEGEPRELAESYJAKDILHPP 11409
ò	102	101
g	11410	EVELDVTCRDVITVRVGQTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVEL 11469
ò	102	101
g	11470	QIKEAVRADHGKYIISAKNSSGHAQGSAIVNVLDRPGPCQNLKVTNVTKENCTISWENPL 11529
ò	102	101
g	11530	DNGGSEITNFIVEYRKPNQKGWSIVASDVTKRLIKANLLANNEYYFRVCAENKVGVGPTI 11589
ò	102	101
g	11590	ETKTPILAINPIDRPGEPENLHIADKGKTFVYLKWRRPDYDGGSPNLSYHVERRLKGSDD 11649
ò	102	101
qq	11650	) WERVHKGSIKETHYMVDRCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQKPVLDLK 11709
ò	102	101

g	11710	LSGVLTVKAGDTIRLEAGVRGKPFPEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKA	11769
ò	102		101
Q	11770	KRSDGGKYVVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGC	11829
ò	102		101
qq	11830	EIQNYILEKCETKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESKP	11889
ઠે	102		101
Вр	11890	VIAKTKYDKPGRPDPPEVTKVSKEEMTVVWNPPEYDGGKSITGYFLEKKEKHSTRWVPVN	11949
ò	102	,	101
g	11950	KSAI PERRMKVONLLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEPPGPPTNFRVV	12009
ò	102		101
qq	12010	DTTKHSITLGWGKPVYDGGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTS	12069
ò	102		101
g	12070	LDENQEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRL	12129
ò	102		101
g	12130	FAIVRGRPAPKVTWRKVGIDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLVNPAGE	12189
ò	102		101
q	12190	KAVFVNVRVLDTPGPVSDLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWS	12249
ò	102		101
q	12250	TVTPEVKKTSFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLE	12309
ò	102		101
g	12310	ATEMTKNSATLAWLPPLRDGGAKIDGYIISYREEEQPADRWTEYSVVKDLSLVVTGLKEG	12369
ò	102		101
g	12370	KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKILMPEQITIKAGKKLRIEAHVYGKP	12429
ò	102		101
g	12430	HPTCKWKKGEDEVVTSSHLAVHKADSSSILIIKDVTRKDSGYYSLTAENSSGTDTQKIKV	12489
ò	102		101
g	12490	VVMDAPGPPQPPFD1SD1DADACSLSWH1PLEDGGSN1TNY1VEKCDVSRGDWTALASV	12549
ò	102		101
g	12550	TKTSCRVGKLI PGQEYI FRVRAENR FGI SEPLTSPKMVAQFPFGVPSEPKNARVTKVNKD	12609
ò	102		101
q	12610	C1FVAWDRPDSDGGSP11GYLIERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFR1	12669
ò	102		101
q	12670	YALNKAGSSPPSKPTEYVTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFV	12729
ò	102		101
g	12730	EACKLPGDKWVRCNTAPHQI PQEEYTATGLEEKAQYQFRAIARTAVNISPPSEPSDPVTI	12789
ò	102		101
QQ	12790	LAENVPPRIDLSVAMKSLLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAM	12849

ò	102	TOT
Q	12850	QRNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAM 12909
ò	102	101
Q	12910	LSWEPPLEDGGSEITNYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYQFRICAEN 12969
ò	102	101
QQ	12970	KYGVGDPVFTEPAIAKNPYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEK 13029
ò	102	101
g	13030	RETQAVNWTKVNRKPIIERTLKATGLQEGTEYEFRVTAINKAGPGKPSDASKAAYARDPQ 13089
ò	102	101
q	13090	YPPAPPAFPKVYDTTRSSVSLSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPONLOK 13149
ò	102	101
Q	13150	TRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPDKHYPKDILIPPEGEHDADLRKTLILR 13209
ò	102	101
q	13210	AGVTMRLYVPVKGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYIL 13269
ò	102	101
qq	13270	TLENSCGKKEYTIVVKVLDTPGPPINVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKR 13329
ò	102	101
q	13330	DAERKSWSTVTTECSKTSFRVPNLEEGKSYFFRVFAENEYGIGDPGETRDAVKASQTPGP 13389
ò	102	101
qq	13390	VVDLKVRSVSKSSCSIGWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLT 13449
ò	102	101
qq	13450	EGKEYTFRVSAENENGEGTPSEITVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPI 13509
ò	102	101
Q	13510	KGKPAPSVSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGKYTITLKNVAGTKEG 13569
ò	102	101
qq	13570	TISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTC 13629
ò	102	101
qq	13630	ASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPPNIVD 13689
ò	102	101
qq	13690	VRHDSVSLTWTDPKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEY 13749
ò	102	101
g	13750	EFRVMAINLAGVGKPSLPSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLT 13809
ò	102	101
qq	13810	GYIVEKRDLPSKSWMKANHVNVPECAFTVTDLVEGGKYEFRIRAKNTAGAISAPSESTET 13869
ò	102	101
QQ	13870	IICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDIT 13929

ò	102	101	
g	13930	QITSTPISSMLIIKYATRKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSA 13989	
ò	102	101	
q	13990	EKATLTWTPPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRV 14049	-
ò	102	101	
q	14050	SAVNHYGKGEPVQSEPVKMYDRFGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSEITGY 14109	•
ò	102	101	
Q	14110	HVERREKKSLRHVRAIKTPVSDLRCKVTGLQEGSTYEFRVSAENRAGIGPPSEASDSVLM 14169	
ò	102	101	
QQ	14170	KDAAYPPGPPSNPHVTDTTKKSASLAMGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGT 14229	
ò	102	-LYITRF 107	
Q	14230	:     ALRITOFVVPDLQTKEKYNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTL 14289	
ò	108	, 101	
Op	14290	VVRAGLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFV 14349	
ò	108	107	
g	14350	MTIENPAGKKSGFVNVRVLDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEK 14409	
ò	108	107	
qq	14410	REATRKSYSTATTKCHKCTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASEAPS 14469	
ઠે	108	107	
g	14470	PPDSLNIMDITKSTVSLAMPKPKHDGGSKITGYVIEAQRKGSDQWTHITTVKGLECVVRN 14529	
ò	108	107	
qq	14530	LTEGEEYTFQVMAVNSAGRSAPRESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE 14589	
ò	108	107	
QQ	14590	IPVLGRPKPTVTWKKGDQILKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGE 14649	
ò	108	107	
qq	14650	VGDVITIQVHDIPGPPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTW 14709	
ò	108	107	
qq	14710	VELATTVIRTTYKATRLTTGLEYQFRVKAQNRYGVGPGITSAWIVANYPFKVPGPPGTPQ 14769	
ò	108	107	
QQ	14770	VTAVTKDSMTISWHEPLSDGGSPILGYHVERKERNGILWQTVSKALVPGNIFKSSGLTDG 14829	
ઠે	108	107	
q	14830	I AYEFRVIAENMAGKSKPSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGF 14889	**
ò	108	107	
g	14890	KITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEP 14949	
ò	108	107	
g	14950	) SDAITCRODVEAPKIKVDVKFKDTVILKAGEAFRLEADVSGRPPPTMEWSKDGKELEGTA 15009	·
è	108	107	_

qq	15010	KLEIKIADFSTNLVNKDSTRRDSGAYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTE 15	6909
ò	108	10	07
qq	15070	VTSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYI 15	15129
ò	108	10	107
g	15130	FRVMAVNKYGVGEPLESEPVLAVNPYGPPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEI	15189
ò	108	10	107
Q	15190	INYIVERRDKAGQRWIKCNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPF	15249
ઠે	108	10	101
QQ	15250	YKACDTVFKPGPPGNPRVLDTSRSSISIAMNKPIYDGGSEITGYMVEIALPEEDEWQIVT	15309
ò	108		107
q	15310	PPAGLKATSYTITGLTENQEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADL	15369
ò	108		107
qa	15370	RKVVTIRACCTLRLFVPIKGRPDPEVKWARDHGESLDKASIESASSYTLLIVGNVNRFDS	15429
ò	108		107
qq	15430	GKYILTVENSSGSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTWDPPLLDGGSKIKNY	15489
ò	108		107
g	15490	IVEKRESTRKAYSTVATNCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKAS 1	5549
ò	108		107
QQ	15550	ERPLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEA	15609
ò	108		101
Ω	15610	TITGLIQGEEYSFRVSAQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLK	15669
ò	108		107
Q	15670	VDVPFIGRPTPAVTWHKDNVPLKQTTRVNAESTENNSLLTIKDACREDVGHYVVKLTNSA .1	5729
ò	108		107
g	15730	GEAIETLNVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGGSSINN <b>VL</b> VEKRDTSTT	15789
ò	108		107
đ	15790	TWOIVSATVARTTIKACRLKTGCEYOFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGT	15849
ò	108	1	.07
q	15850	PVVTLSSRDSMEVQWNEPISDGGSRVIGYHLERKERNSILWVKLNKTPIPOTKFKTTGLE 1	60651
ò	108		107
С	15910	EGVEYEFRVSAENIVGIGKPSKVSECYVARDPCDPPGRPEAIIVTRNSVTLQWKKPTYDG	15969
ò	108		101
đ	15970	GSKITGYIVEKKELPEGRWMKASFTNIIDTHFEVTGLVEDHRYEFRVIARNAAGVFSEPS	16029
ò	108		107
q	16030	ESTGAITARDEVDPPRISMDPKYKDTIVVHAGESFKVDADIYGKPIPTIQMIKGDQELSN	16089
ò	108		107

ò

ဂ္ဂ	16090	TARLEIKSTDFATSLSVKDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVI	16149
⋩	108		107
g	16150	SGVTAEKCTLAWKPPLQDGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNE	16209
à	108		107
g	16210	YTFRIMAVNKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGS	16269
3	108		107
g	16270	EILGYVLEKRDKEGIRWTRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPS	16329
à	108		107
ą	16330	AYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPIYDGGCEIQGYIVEKCDVNVGEWTM	16389
à	108	JG.	109
g	16390	CTPPTGINKTNIEVEKLLEKHEYNFRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLDL	16449
ે	110	BL	111
6	16450		16509
ò	112		111
6	16510	DSGKYTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIK	16569
ò	112		111
გ	16570	NYIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIK	16629
ò	112		111
8	16630	VAEVPQPPGKITVDDVTRNSVSLSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSL	16689
ò	112		111
a	16690	QAVITNLTQGEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDVKPAFSSYSVQVGQD	16749
ò	112		111
a	16750	LKIEVPISGRPKPTITWTKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN	16809
ò	112		111
a	16810	VVGQKTAS1E1VTLDKPDPPKGPVKFDDVSAES1TLSWNPPLYTGGCQ1TNYIVQKRDTT	16869
ò	112		111
엄	16870	TTVWDVVSATVARTTLKVTKLKTGTEYQFRI FAENRYGQSFALESDPIVAQYPYKEPGPP	16929
ઠે	112		111
g	16930	GTPFATAISKDSMVIQWHEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTQFKAQN	16989
ò	112		111
a	16990	LEEGI EYEFRUYAENI VGVGKASKNSECYVARDPCDPPGTPEPIMVKRNEITLQWTKPVY	17049
ò	112		111
g	17050	DGGSMITGYIVEKRDLPDGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISK	17109
ò	112		111
g	17110	PSDSTGPITAKDEVELPRISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEI	17169
ò	112		116
g	17170	EESARCEIKNTDFKALLIVKDAIRIDGGQYILRASNVAGSKSFPVNVKVLDRPGPPEGPV	17229

ò	117 0	QVRGVTQLGGQURGVT	126
g	17230 0	O'TGVTSEKCSLTWSPPLÓDGGSDISHYVVEKRETSRLAWTVVASEVVTNSLKVTKLLEG	17289
ò	127 -		126
qq	17290 N	NEYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDG	17349
ò	127 -		126
g	17350 G	GSE11GY1VEKRDRSG1RW1KCNKRR1TDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSP	17409
ò	127 -	ACSP	130
g	17410 A		17469
ò	131 -		130
Q	17470	<b>QIVTPQTGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDL</b>	17529
ò	131 -	TWS	133
qq	17530 D	DSELRKGIVVRAGGSARIHIPFKGRPMPEITWSREEGEFTDKVQIEKGVNYTQLSIDNCD	17589
ઠે	134 -		133
g	17590 F	RNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAK	17649
ઠે	134 -		133
q	17650 \	VKNYVI DKRESTRKAYANVSSKCSKTSFKVENLTEGAI YY FRVMAENEFGVGVPVETVDA	17709
ò	134 -		133
g	17710	VKAAEPPSPPGKVTLTDVSQTSASLMWEKPEHDGGSRVLGYVVEMOPKGTEKWSIVAESK	17769
ò	134 -		133
g	17770	VCNAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAG	17829
ò	134		133
đ	17830 E	EDLKI EI PVIGR PRPNI SWVKDGE PLKQTTRVNVE ETATSTVLHI KEGNKDD FGKYTVTA	17889
ò	134		133
a	17890 1	TNSAGTATENLSVIVLEKPGPPVGPVRFDEVSADFVVISWEPPAYTGGCQISNYIVEKRD	17949
ò	134		133
g	17950 7	TTTTWHMVSATVARTT1K1TKLKTGTEYQFR1FAENRYGKSAPLDSKAVIVQYPFKEPG	18009
ò	134		133
g	18010	PPGTPFVTS1SKDQMLVQWHEPVNDGGTK1IGYHLEQKEKNSILWVKLNKTPIQDTKFKT	18069
ò	134		133
g	18070	TGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKP	18129
ò	134		133
엄	18130	AYDGGSKITGYIVEKKDLPDGRWMKASFTNVLETEFTVSGLVEDORYEFRVIARNAAGNF	18189
ò	134		133
g	18190	SEPSDSSGAITARDEIDAPNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGK	18249
ò	134		133
q	18250	ELEETAARMEIKSTIQKTTLVVKDCIRTDGGQYILKLSNVGGTKSIPITVKVLDRPGSPE	18309

ò	134 133	Db 19390 AGPLEINGLTAEKCSLSWGRPQEDGGADIDYYHRKKRETSHLAWTICEGELOMTSCKVTK 19449
qq	18310 GPLKVTGVTAEKCYLAMNPPLQDGGANISHYIIEKRETSRLSWTQVSTEVQALNYKVTKL 18369	134
ò	134 133	1 5
q	18370 LPGNEYIFRVMAVNKYGIGEPLESGPVTACNPYKPPGPPSTPEVSAITKDSMVVTWARPV 18429	
ò	134 133	Db 19510 ESDGGSEISGYIIERREKNSLRWVRVNKKPVYDLRVKSTGLREGCEYEYRVYAENAAGLS 19569
a	18430 DDGGTEIEGYILEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENAAGVGE 18489	Qy 134 133
à	134 133	Db 19570 LPSETSPLIRAEDPVFLPSPPSKPKIVDSGKTTITIAWVKPLFDGGAPITGYTVEYKKSD 19629
g	18490 PSEPSVFYRACDALYPPGPPSNBKVTDTSRSSVSLAMSKPIYDGGAPVKGYVVEVKEAAA 18549	Qy 134 133
ò		Db 19630 DTDWKTSIQSLRGTEYTISGLTTGAEYVFRVKSVNKVGASDPSDSSDPQIAKEREEFPLF 19689
qq	18550 DEWTTCTPPTGLQGKQFTVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPE 18609	Qy 134
ò	134 133	Db 19690 DIDSEMRKTLIVKAGASFTMTVPFRGRPVPNVLWSKPDTDLRTRAYVDTTDSRTSLTIEN 19749
ద	18610 IELDADLRKVVVLRASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEVTSSFTMLVID 18669	Qy 134 133
ò	134 133	Db 19750 ANRNDSGKYTLTIQNVLSAASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVPENDGG 19809
g	18670 NVTRFDSGRYNLTLENNSGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDG 18729	Qy 134 133
ò		Db 19810 APVKNYHIEKREASKKAWVSVTNNCNRLSYKVTNLQEGAIYYFRVSGENEFGVGIPAETK 19869
Q	18730 GAKITNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAET 18789	Qy 134 133
ò	134 133	Db 19870 EGVKITEKPSPPEKLGVTSISKDSVSLTWLKPEHDGGSRIVHYVVEALEKGQKNWVKCAV 19929
qq	18790 TEPVKVSEPPLPPGRVTLVDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEKWSTCT 18849	Oy 134 133
ò	134 133	Db 19930 AKSTHHVVSGLRENSEYPFRVFAENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTV 19989
đ	18850 QVKTLEATISGLTAGEEYVFRVAAVNEKGRSDPRQLGVPVIARDIEIKPSVELPFHTFNV 18909	Οχ 134
ò	134 133	Db 19990 YVRAGSNLKVDIPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGR 20049
đ	18910 KAREQLKIDVPFKGRPQATVNWRKDGQTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYE 18969	
ò	134 133	Db 20050 YEITAANSSGTTKAFINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSQVTNYI 20109
q	18970 LCVSNSAGSITVPITIIVLDRPGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIVEK 19029	Qy 134 133
ò	134 133	Db 20110 LLKRETSTAVWTEVSATVARTMMKVMKLTTGEEYQFRIKAENRFGISDHIDGACVTVKLP 20169
g	19030 KETTSTTWHIVSQAVARTSIKIVRLTTGSEYQFRVCAENRYGKSSYSESSAVVAEYPFSP 19089	Οχ 134 133
ò	134 133	Db 20170 YTTPGPPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWOKANKLVIRT 20229
Q	19090 PGPPGTPKVVHATKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQV 19149	Ογ 134 133
ò	134	Db 20230 THFKVTTISAGLIYEFRVYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSL 20289
a	19150 KVSGLDEGLMYEYRVYAENIAGIGKCSKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWS 19209	Qy 134 133
ò	134 133	Db 20290 SWQQPAFDGGSKITGYIVERRDLPDGRWTKASFTNVTETQFTISGLTQNSQYEFRVFARN 20349
QQ	19210 KPHYDGGAKITGYIVERRELPDGRWLKCNYTNIQETYFEVTELTEDQRYEFRVFARNAAD 19269	ον 134 133
ò	134 133	Db 20350 AVGSISNPSEVVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEW 20409
đ	19270 SVSEPSESTGPIIVKDDVEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKD 19329	Qy 134 133
ò		Db 20410 YKDDKELQTNALVCVENTTDLASILIKDADRLNSGCYELKLRNAMASASATIRVQILDKP 20469
g	19330 GIEIEERARTEIISTDNHTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPP 19389	Oy 134CLIT 137
ò	134	

g	20470	GPPGGP1EFKTVTAEK1TLLWRPPADDGGAK1THY1VEKRETSRVVWSMVSEHLEEC11T	20529
ò	138		137
q	20530	TTKI I KGNEYI FRVRAVNKYGIGEPLESDSVVAKNAFVTPGPPGI PEVTKI TKNSMTVVW	20589
ò	138		137
g	20590	SRPIADGGSDISGYFLEKRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAA	20649
ò	138		137
q	20650	GQGPFSEPSEFYKAADP1DPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIR	20709
ò	138	•	137 ·
QQ	20710	QGEEEEWTTVSTKGEVRTTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDIL	20769
ò	138		137
g G	20770	EAPEIDLDVALRTSVIAKAGEDVQVLIPFKGRPPPTVTWRKDEKNLGSDARYSIENTDSS	20829
ò	138		137
g	20830	SLLTI PQVTRNDTGKY ILTI ENGVGEPKSSTVSVKVLDTPAACQKLQVKHVSRGTVTLLW	20889
ò	138		137
qq	20890	DPPLIDGGSP1INYV1EKRDATKRTWSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENEIG	20949
ò	138		137
g	20950	<pre>IGEPCETTEPVKAAEVPAPIRDLSMKDSTKTSVILSWTKPDFDGGSVITEYVVERKGKGE</pre>	21009
ò	138		137
a	21010	QTWSHAGISKTCEIEVSQLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELIITPEVDLS	21069
ò	138		137
g	21070	D1PGAQVTVRIGHNVHLELPYKGKPKPS1SWLKDGLPLKESEFVRFSKTENKITLSIKNA	21129
ò	138		137
đ	21130	KKEHGGKYTVILDNAVCRIAVPITVITLGPPSKPKGPIRFDEIKADSVILSWDVPEDNGG	21189
ò	138		137
g	21190	GEITCYSIEKRETSQTNWKMVCSSVARTTFKVPNLVKDAEYQFRVRAENRYGVSQPLVSS	21249
ò	138		137
g	21250	IIVAKHQFRIPGPPGKPVIYNVTSDGMSLTWDAPVYDGGSEVTGFHVEKKERNSILWQKV	21309
ò	138		137
g	21310	NTSPISGREYRATGLVEGLDYQFRVYAENSAGLSSPSDPSKFTLAVSPVDPPGTPDYIDV	21369
ò	138		137 ′
g	21370	TRETITLKWNPPLRDGGSKIVGYSIEKRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEF	21429
ò	138		137
g	21430	RIIARNAVGTISPPSQSSGIIMTRDENVPPIVEFGPEYFDGLIIKSGESLRIKALVQGRP	21489
ò	138		137
q	21490	VPRVTWFKDGVE1EKRMNMEITNVLGSTSLFVRDATRDHRGVYTVEAKNASGSAKAEIKV	21549
ò	138		137
엄	21550	KVQDTPGKVVGPIRFTNITGEKMTLWWDAPLNDGCAPITHYIIEKRETSRLAWALIEDKC	21609

ò	138 -		137
д	21610 E	EAQSYTAIKLINGNEYQFRVSAVNKFGVGRPLDSDPVVAQIQYTVPDAPGIPEPSNITGN 2	21669
ò	138 -		137
QΩ	21670 S	SITLTWARPESDGGSEIQQYILERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEFH ;	21729
ò	138 -		137
đ	21730 V	VMAENAAGVGPASGISRLIKCREPVNPPGPPTVVKVTDTSKTTVSLEWSKPVFDGGMEII ;	21789
ò	138 -		137
ą	21790 0	GYIIEMCKTDLGDWHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGAGKGDSCEVTGTI ;	21849
ò	138 -		137
đ	21850 A	KAVDRLTAPELDIDANFKQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHT ;	21909
ò	138 -		137
QQ	21910 1	TDSFSTLTVENCNRNDAGKYTLTVENNSGSKSITFTVKVLDTPGPPGPITFKDVTRGSAT ;	21969
ò	138 -		137
q	21970 I	LMWDAPLLDGGARIHHYVVEKREASRRSWQVISEKCTRQIFKVNDLAEGVPYYFRVSAVN ;	22029
ò	138 -		137
<b>업</b>	22030 E	EYGVGEPYEMPEPIVATEQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQ ;	22089
ò	138		137
qq	22090 F	KGSDLWVEACHTKOLTFTVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVIIKEPQIEPT ;	22149
ò	138		137
qq	22150 A	ADLIGITNQLITCKAGSPFTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTLT ;	22209
ò	138 -		137
g	22210 \	VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGPVTGPIEVSSVSAESCVLSWGEPK ;	22269
ò	138		137
g	22270	DGGGTEITNYIVEKRESGTTAMQLVNSSVKRTQIKVTHLTKYMEYSFRVSSENRFGVSKP ;	22329
ò	138 .	*	137
g	22330 1	LESAPIIAEHPFVPPSAPTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTIL :	22389
ò	138		137
Q	22390	WVKENKVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPE	22449
δ	138		137
đ	22450	VTDVTRSTVSLIWSAPAYDGGSKVVGYIIERKPVSEVGDGRWLKCNYTIVSDNFFTVTAL	22509
ò	138		137
q	22510	SEGDTYEFRVLAKNAAGVISKGSESTGPVTCRDEYAPPKAELDARLHGDLVTIRAGSDLV	22569
ò	138		137
qq	22570	LDAAVGGKPEPKIIWTKGDKELDLCEKVSLQYTGKRATAVIKFCDRSDSGKYTLTVKNAS	22629
ò	138		137
q	22630	GTKAVSVMVKVLDSPGPCGKLTVSRVTQEKCTLAWSLPQEDGGAEITHYIVERRETSRLN	22689

ò	138		137
a	22690 WVIVEGE	WVIVEGECPTLSYVVTRLIKNNEYIFRVRAVNKYGPGVPVESEPIVARNSFTIPSPPGIP	22749
ò	138		137
q	22750 EEVGTGK	EEVGTGKEHIIJQWTKPESDGGNEISNYLVDKREKESLRWTRVNKDYVVYDTRLKVTSLM	22809
ò	138		137
g	22810 EGCDYQF	EGCDYQFRVTAVNAAGNSEPSERSNF1SCREPSYTPGPPSAPRVVDTTKHS1SLAWTKPM	22869
ò	138		137
g	22870 YDGGTD1	YDGGTDIVGYVLEMQEKDTDQWYRVHTNATIRNTEFTVPDLKMGQKYSFRVAAVNVKGMS	22929
ò	138		137
a	22930 EYSESIA	EYSESIAEIEPVERIEIPDLELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQGID	22989
ò	138		137
g	22990 LASRAII	LASRAIIDTTESYSLLIVDKVNRYDAGKYTIEAENQSGKKSATVLVKVYDTPGPCPSVKV	23049
ò	138		137
g	23050 KEVSRD	KEVSRDSVTITWE1PTIDGGAPINNYIVEKREAAMRAFKTVTTKCSKTLYRISGLVEGTM	23109
ò	138		137
g	23110 HYFRVL	HYFRVLPENIYGIGEPCETSDAVLVSEVPLVPAKLEVVDVTKSTVTLAWEKPLYDGGSRL	23169
ò	138		137
පු	23170 TGYVLE	TGYVLEACKAGTERWMKVVTLKPTVLEHTVTSLNEGEQYLFR1RAQNEKGVSEPRETVTA	23229
ò	138		137
g	23230 VTVQDL	VTVQDLRVLPTIDLSTMPQKTIHVPAGRPVELVIPIAGRPPPAASWFFAGSKLRESERVT	23289
ò	138	EDTGEDTG	141
g	23290 VETHTK	 VETHTKVAKLTIRETTIRDTGEYTLELKNVTGTTSETIKVIILDKPGPPTGPIKIDEIDA	23349
ò	142		141
Q	23350 TSITIS	TSITISWEPPELDGGAPLSGYVVEQRDAHRPGWLPVSESVTRSTFKFTRLTEGNEYVFRV	23409
ò	142		141 .
qq	23410 AATNRF	AATNRFGIGSYLQSEVIECRSSIRIPGPPETLQIFDVSRDGMTLTWYPPEDDGGSQVTGY	23469
ò	142		141
g	23470 IVERKE	IVERKEVRADRWVRVNKVPVTMTRYRSTGLTEGLEYEHRVTAINARGSGKPSRPSKPIVA	23529
ò	142		141
g	23530 MDPIAP	MDPIAPPGKPQNPRVTDTTRISVSLAMSVPEDEGGSKVTGYLIEMQKVDQHEWTKCNTTP	23589
ò	142		141
g	23590 TKIREY	TKI REYTLTHLPQGAEYRFRVLACNAGGPGEPAEVPGTVKVTEMLEYPDYELDERYQEGI	23649
ò	142		141
g	23650 FVRQGG	FVROGGVIRLTIPIKGKPFPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYD	23709
ò	142		141
g	23710 LVLEN	LVLENKCGKKAVYIKVRVIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDCGADILGYILE	23769
ć	140		141

පු	23770	RREVPKAAWYTIDSRVRGTSLVVKGLKENVEYHFRVSAENQFGISKPLKSEEPVTPKTPL 23829
ò	142	141
đ	23830	NPPEPPSNPPEVLDVTKSSVSLSWSRPKDDGGSRVTGYYIERKETSTDKWVRHNKTQITT 23889
ò	142	141
g	23890	TMYTVTGLVPDAEYQFRIIAQNDVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKDS 23949
ò	142	141
qq	23950	VTLQWEKPECDGGKEILGYWVEYRQSGDSAWKKSNKERIKDKQFTIGGLLEATEYEFRVF 24009
ò	142	141
đ	24010	AENETGLSRPRRTAMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKW 24069
ò	142	141
q	24070	YRFGKELIQSRKYKMSSDGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATP 24129
ò	142	
d d	24130	QFHPGYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHL 24189
ò	142	141
g	24190	VMKNVQRKTHAGKYKVQLSNVFGTVDAILDVEIQDKPDKPTGPIVIEALLKNSAVISWKP 24249
ò	142	141
g	24250	PADDGGSWITNYVVEKCEAKEGAEWQLVSSAISVTTCRIVNLTENAGYYFRVSAQNTFGI 24309
ò	142	
q	24310	SDPLEVSSVVIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDGGAKIRNYYLEKREK 24369
ò	142	
QQ	24370	KQNKWISVTTEEIRETVFSVKNLIEGLEYEFRVKCENLGGESEWSEISEPITPKSDVPIQ 24429
ò	142	141
අු	24430	APHFKEELRNLNVRYQSNATLVCKVTGHPKPIVKWYRQGKEIIADGLKYRIQEFKGGYHQ 24489
ò	142	141
QQ	24490	) LIIASVTDDDATVYQVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAWHALRGEVVS 24549
ò	142	141
g	24550	) IKIPFSGKPDPVITWQKGQDLIDNNGHYQVIVTRSFTSLVFPNGVERKDAGFYVVCAKNR 24609
ò	142	141
g	24610	) FGIDQKTVELDVADVPDPPRGVKVSDASRDSVNLTWTEPASDGGSKITNYIVEKCATTAE 24669
ò	142	141
đ	24670	) RWLRVGOARETRYTVINLFGKTSYQFRVIAENKFGLSKPSEPSEPTITKEDKTRAMNYDE 24729
ò	142	141
g	24730	D EVDETREVSMTKASHSSTKELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKG 24789
ò	142	2 141
셤	24790	0 TDQVLVKKEISILNIARHRNILHLHESFESMEELVMIFEFISGLDIFERINTSAFELNER 24849
ò	143	2

32;

145 EINSYVHQVCEALQFLHSHNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKFGDNFRL 24 14910 LFTAPEYYAPEVAQFHANNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKFGDNFRL 24 14910 LFTAPEYYAPEVAQHDVVSTATDWMSLGTLVYVLLSGINPFLAETWQJIENIMANEYFF 24 14910 DEEAFKEISIEAMDFVDRLLVKERKSRMTASSALQHPWLKQKIERVSTKVIRTLKHRRYY 25 14910 DEEAFKEISIEAMDFVDRLLVKERKSRMTASSALQHPWLKQKIERVSTKVIRTLKHRRYY 25 14910 OF VCKIENYDGSTQVTWYFCORQLENSEKYEITYEDGVAILIYVKDITKLDDGTYRCKVVND 25 145

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2158 AMDTGRLSALSPDLIVINSVAQYFPSREYLABVVEALVRIPGVRRIFFGDMRTYATHKDF 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : |
2218 LVARAVHTNGSKVTRSKVQQEVARLEELEEELLVDPAFFTSLKESLSEEIEHVEILPKNM 2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2698 EESTIQKILEKEQTTPFNLASEPGFRLALLKTGEDEHILSTVMHHAISDGWSVDIFQQEI 2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2758 GQFYSAILRGHDPLAQIAPLSIQYRDFATWQRQIFQVAEHRRQLAYWTKQLADNKPAELL 2817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2878 TIGTPIANRNRPELEGLIGFFVNTQCMRITVDVEDSFETLVHQVRETTLAAHANQDVPFE 2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2938 QIVSNILPGSSDTSRNPLVQLMFALHSQQNLGKVRLEGIEEEIISIAETTRFDIEFHLYQ 2997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2998 EAERLNGSIVYAADLFVPETIQSVITIFQGILQKGLGEPDMPVASMALDGGLESLRSTGL 3057
                                                                                                                                                                                                                                                                   ||| :|
2098 AAGHVLEIGTGTGMVLFNLGQAGLKSYIGLEPSQSAVQFVNKAAQTFPGLEGKAQVHVGT 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2278 KVNNELSSYRYGAVLHIRNHNQNQSRSIHKINAESWIDFASSQMDRQGLARLLKENKDAE 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2338 SIAVFNIPYSKTIVERHIAKSLADDHDGDDTHSSIDGVAWISAAREKASQCPSLDVHDLV 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2398 QLAEDAGFRVEVSWARQRSQNGALDVFFHHFQPTENESRALVDFPTDYKGQQARSLTNRP 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2458 LQRVESRRIEAQVREQLQVLLPAYMIPARIVVLQNMPLNTSGKVDRKELTLRAKVTAART 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2518 PSSELVAPRDSIEAIICKEFKDVLGVEVGITDNPFNVGGHSLLATKLAARLSRQLNAQIA 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2578 VKDIFDRPVIADLAATIQQDTTEHNPILPTSYTGPVEQSFAQGRLWFLDQLNVGATWYLM 2637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2818 IDFKRPPMLSGRAGEIPVVVDGLIYEKLQDFCRIRQVTAFTVLLAAFRAAHYRMTGTEDA 2877
                                                                                                                                                                                  Gabs
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to a recombinant host. This allows effective production of antibiotic cyclosporin or its derivatives.
                                                                                                                                                                               21; Indels 12475;
                                                                                                                           Query Match

34.2%; Score 264; DB 15; Length 15281;
Best Local Similarity 0.8%; Pred. No. 0.3;
Matches 102; Conservative 24; Mismatches 21; Indels 12475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 -----
                                                                                                                                                                                                                                      1 AAGGIL------
                                                                                   Sequence 15281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 -----
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>	12		18
. 4	3058	LHPQQTDYPCDASVVQIFKQQVAVNPDVIAVRDESTRLSYADLDRKSDQVACWLSRRGIA	3117
⋩	19		18
ð	3118	PETFVAILAPRSCETIVAILGVLKANLAYLPLDVNVPASRLEAILSEVSGSMLVLVGAET	3177
≿	19		18
ą	3178	PIPEGMAEAETIRITEILADAKTDDINGLAASQPTAASLAYVIFTSGSTGRPKGVMVEHR	3237
à	19		18
ą	3238	GIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLLESTAL	3297
ጵ	19		18
ရ	3298	EKVFFDQRVNVALLPPALLKQCLDNSPALVKTLSVLYIGGDRLDASDAAKARGLVQTQAF	3357
ጵ	19		18
ą	3358	NAYGPTENTVMSTIYPIAEDPFINGVPIGHAVSNSGAFVMDQNQQITPPGAMGELIVTGD	3417
à	19		18
g	3418	GLARGYTTSSLNTGRFINVDIDGEQVRAYRTGDRVRYRPKDLQIEFFGRIDHQVKIRGHR	3477
à	19		18
ą	3478	I EPAEVEYALLSHDLVTDAAVVTHSQENQDLEMVGFVAARVADVREDESSNQVQEWQTHF	3537
à	19		18
ą	3538	DSIAYADITTIDQQSLGRDFMSWTSMYDGSLIKKSQMQEWLDDTMRSLLDSQPPGHVLEV	3597
ጽ	19		18
ą	3598	GTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGLEDRIRVEVGTATDIDRL	3657
à	19		18
g	3658	GDDLHAGLVVVNSVAQYFPSQDYLAQLVRDLTKVPGVERIFFGDMRSHAINRDFLVARAV	3717
ठे	19		18
q	3718	HALGDKATKAEIQREVVRMEESEDELLVDPAFFTSLTTQVENIKHVEILPKRMRATNELS	3777
ò	19		18
g	3778	SYRYAAVLHVNDLAKPAHKVSPGAWVDFAATKMDRDALIRLLRGTKISDHIAIANIPNSK	3837
ò	19		18
q	3838	TIVERTICESVYDLGGDAKDSNDRVSWLSAARSNAVKVASLSAIDLVDIAQEAGFRVEIS	3897
ò	19		18
QQ	3898	I CARQWSQNGALDAVFHHLGPSPQSSHVLIDFLTDHQGRPEEALTNHPLHRAQSRRVERQI	3957
ò	19		18
qq	3958	I RERLÇTLLPAYMIPAQIMVLDKLPLNANGKVDRKQLTQRAQTVPKAKQVSAPVAPRTEIE	4017
ò	19		18
Q	4018	RVLCQEFSDVLGVDIGIMENFFDLGGHSLMATKLAARISRRLETHVSVKEIFDHPRVCDL	4077
ò	19		
g	4078	3 VLIVQQGSAPHDPIVSTKYTGPVPQSFAQGRLWFLDQLNFGATWYLMPLAVRLRGAMNVH	4137
ò	19		18

QQ	4138 A	altaallalerrhellrttfyeqngvgmqkvnpvytetlriidlsngdgdylptlkkeqt	4197
ò	19 -		18
qq	4198 A	APFHLETEPGWRVALLRLGPGDYILSVVWHHIISDGWSVDVLFQELGQFYSTAVKGHDPL	4257
ò	19 -		18
g	4258 S	SQTTPLPIHYRDFALWQKKPTQESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGQAG	4317
ô	19 -		18
g	4318 E	EMSVTI EGALYKNLEEFCRVHRVTSFVVLLAALRAAHYRLTGSEDATIGTPI ANRNRPEL	4377
ò	19 -		18
qq	4378 E	EQIIGFFVNTQCIRITVNEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDAS	4437
ò	19 -		18
QC	4438 R	RNPLVQLMFAVHSQKNLGELKLENAHSEVVPTEITTRFDLEFHLFQQDDKLEGSILYSTD	4497
ò	19 -		18
g	4498 I	LFEAVSVQSLLSVFQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSV	4557
ò	19 -		18
Q	4558 \	VDVFHEQVSINPDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCE	4617
ò	19		18
QQ	4618 1	IIAFLGILKANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVP	4677
ò	19 .		18
g	4678 1	IRDTFTTLTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMVQHRNIVRLVKNSNVV	4737
ò	19	POAHO	23
q	4738 7	akopaaariahisnlafdassweiyapllnggaivcadyfttidpqalqetfoeheirga	4797
ò	24 -		23
q	4798 N	MLPPSLLKQCLVQAPDMISRLDILFAAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILS	4857
ò	24		23
qq	4858 7	TIYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDOKARGYMDPKL	4917
ò	24		23
g	4918	DADRFIQLTVNGSEQVRAYRTGDRVRYRPKDFQIEFFGRMDQQIKIRGHRIEFAEVEQAF	4977
ò	24		23
Dp	4978	LNDGFVEDVAIVIRTPENQEPEMVAFVTAKGDNSAREEEATTQIEGWEAHFEGGAYANIE	5037
ò	24	EDT	56
පු	5038	EIESEALGYDFMGWTSMYDGTEIDKDEMREWLNDTMRSLLDGKPAGRVLEVGTGTGMIMF	5097
ò	27	ERYV	30
QQ	5098	NLGRSQGLERYIGLEPAPSAAEFVNNAAKSFPGLAGRAEVHVGTAADVGTLQGLTSDMAV	5157
ò	31		30
g	5158	INSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAMNRDFAAARAAYSLADNASKD	5217
ò	31		30

Ω	5218	RVRQKMMELEEKEEELLVDPAFFTALASQLQDRIQHVEILPKRMKATNELSSYRYAAVLH	5277
>-	31		30
۵	5278	ISDEPLPIYKIDPEAWINFEGSRLTREALAQVLKENENAESVAISNIPYSKTVVERHIVR	5337
>-	31		30
Ω	5338	SLDQEDANAPEESMDGSDWISAVRTRAQQCHTLSASDLFDIAEDAGFRVEVSWARQHSQH	5397
>	31	XL7	33
۵	5398	GALDAVFHHLKPATEDSRVLIKFPTDHQGRPLKSLTNQPLLPAQSRRAELLIREGLQTLL	5457
>-	34		3,3
۵	5458	PPYMIPSQITLIDRMPLNANGKVDRRELARRAKITQKSKPVEDIVPPRNSVEATVCKGFT	5517
>	34		33
Ω	5518	DVLGVEVGITDNFFNLGGHSLMATKLAARLGRQLNTRISVRDVFDQPVVADLAAVIQRNS	5577
>	34	LNIGA	38
a	5578	APHEPIKPADYTGPVPQSFAQGRLWFLDQLNVGATWYLMPLGIRLHGSLRVDALATAISA	5637
>	39		38
Q	5638	LEQRHEPLRTTFHEEDGVGVQVVQDHRPKDLR11DLSTQPKDAYLAVLKHEQTTLFDLAT	5697
>	39		38
Д	5698	EPGWRVALIRLGEEEHILSIVWHHIISDGWSVEVLFDEMHRFYSSALRQQDPWEQILPLP	5757
>	39		38
۵	5758	IQYRDFAAWQKTEEQVAEHQRQLDYWTEHLADSTPAELLTDLPRPSILSGRANELPLTIE	5817
>	39		38
Ω	5818	GRLHDKLRAFCRVHQATPFV1LLAALRAAHYRLTGAEDATLGTP1ANRNRPELENMIGFF	5877
>	39		38
Ω	5878	<b>UNTQCMRIAIEENDNFESLVRRVRSTATSAFANQDVPFESIVSSLLPGSRDASRNPLVQV</b>	5937
>	39		38
Ω	5938	1LAVHSQQDLGKLTLEGLRDEAVDSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLRTI	5997
>	39		38
Д	5998	ESVVSVFLETLRRALDQPLTPLAVLPLTDGVGE1ASKGLLDVPRTDYPRDANIVEVFQQH	6057
>	39		38
Ω	6058	VRATPDAIAVKDATSILTYAQLDQQSDRLAIWLSRRHMMPETLVGVLAPRSCETIIAMFG	6117
<u>&gt;</u> -	39		38
۵	6118	IMKANLAYLPLDINSPAARLRSILSAVDGNKLVLLGSGVTAPEQENPEVEAVGIQEILAG	6177
>	39		38
مِ	6118	TGLDKTQGSNARPSATSLAYVI FTSGSTGKPKGVMVEHRSVTRLAKPSNVI SKLPQGARV	6237
≽	39		38
۵	6238	AHLANIAFDASIWEIATTLLNGATLVCLDYHTVLDCRTLKEVFERESITVVTLMPALLKQ	6297
≥-	39		38
ည	6298	CVAEIPETLAHLDLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTVISTIYEVDADE	6357

ò	39	97
qq	6358	MFVNGVPIGKTVSNSGAYVMDRNQQLVPSGVVGELVVTGDGLARGYTDPSLNKNRFIYIT 6417
ò	39	38
đ	6418	VNGESIRAYRTGDRVRYRPHDLQIEFFGRMDQQVKIRGHRIEPGEVESALLSHNSVQDAA 6477
ò	39	38
QΩ	6478	VVICAPADQDSGAEMVAFVAARNTEDEDTQEEEAVDQVQGWETHFETAAYSEVKDIRQSE 6537
ò	39	38
qq	6538	VGNDFMGWTSMYDGSEIDKTDMHEWLNDTMRMILDAREPGHVLEIGTGTGMVMFNLAKCP 6597
ò	39	38
qq	6598	GLQGYVGFEPSKSAAQFVNDAAQSFPALKDGRSIVHVGTATDINKAGPIQPRLVVINSVA 6657
ò	39	38
qq	6658	QYFPTPEYLFRVVEALVQIPSVERIVFGDMRTNAINRDFVASRALHTLGQKANKRLVRQM 6717
ò	39	11 11.
q	6718	
ò	46	45
Q	6778	EQSTIHQVSPNAWIDFAADGLDRQTLINLLKEHKDAGTVAIGNIPYSKTIVERFVNKSLS 6837
ò	46	45
Q	6838	EDDMEEGGNSLDGSAWVAAVRMAAQSCPSLDAMDVKEIAQEAGYQVEVSWARQWSONGAL 6897
ò	46	49
qq	6898	DAIFHHFEPPKEGARTLIEFPTDYEGRNVNTLTNRPLNSIQSRRLÄTÖIREKLQTLLPPY 6957
ò	20	64 48
qq	6958	MIPSRIMVLDQMPVANNGKIDRKELVRRAIVAPKPRSAATRVAPRNEIEAILRDEFEDVL 7017
ò	20	64
q	7018	GTEVSVLDNFFDLGGHSLMATKLAARVSRRLDAHISIKDVFDQPVLADLAASIQRESAPH 7077
ò	20	46
ф	7078	EPIPQRPYTGPAEQSFAQGRLWFLDQLNLGATWYLMPLAIRIRGQLRVAALSAALFALER 7137
ò	80	64
qq	7138	RHETLRTTFEESDGVGVQIVGEARNSDLRVHDVSTGDDGEYLEVLRREQTVPFDLSSEPG 7197
ò	20	PRVHLVK 56
qq	7198	:        WRVCLVKTGEEDHVLSIVMHHIIYDGWSVDILRGELGQFYSAALRGQDPLLHANPLPIQY 7257
ò	57	95
අ	7258	RDFAAWQREAKQVEEHQRQLGYWSKQLVDSTPAELLTDLPRPSILSGRAGSVDVTIEGSV 7317
ò	57	MVILT 61
q	7318	YGALQSFCRTRSVTTFVVLLTVFRIAHFRLTAVDDATIGTPIANRNRPELETLVGCFVNT 7377
ò	62	61
ć	9,44	OCMPTETIVE TANDOLD NO OLD TANDOLD PER TVS ALV PGSRNTSRNPLVOLMFA 7437

9 20	.2 61
Db 7438	18 VQSVEDYDQVRLEGLESVMMPGEASTRFDMEFHLVPGDQKLTGSVLYSSDLFEQGTIQNF 7497
0,	62 61
Db 7498	8 VDIFQECLRSVLDQPLTPISVLPFSNAISNLESLDLLEMPTSDYPRDRTVVDLFREQAAI 7557
0,7	62 61
8557 da	8 CPDSIAVKDSSSQLTYAQLDEQSDRVAAWLHERHMPAESLVGVLSPRSCETIIAYFGIMK 7617
oy 6	62 61
Db 7618	8 ANLAYLPLDVYAPDARLAAILDTVEGERLLLLGAGVPQPGIQIPRLSTAYIAEALSHATT 7677
0,	62BPEG
Db 7678	  8 VDVTSIPQPSATSLAYVIFTSGSTGKPKGVMIEHRGIVRLVRDTNVNVFPESGSALPVSH 7737
0,	99
Db 7738	18 FSNLAWDAATWEIYTAVLNGGTVVCIDRDTMLDIAALNSTFRKENVRAAFFTPAFLKQCL 7797
0,	66APNITANL 73
Db 7798	:     38 AETPELVANLEILHTAGDRLDPGDANLAGKTAKGGIFNVLGHTENTAYSTFYPVVGEETF 7857
۰ ۷	74
Db 7858	58 'VNGVPVGRGISNSHAYIIDRHQKLVPAGVMGELILTGDGVARGYTDSALNKDRFVYIDIN 7917
0y 1	74 73
Db 7918	18 GKSTWSYRTGDKARYRPRDGQLEFFGRMDQMVKIRGVRIEPGEVELTLLDHKSVLAATVV 7977
7 م	74 73
Db 7978	78 VRRPPNGDPEMIAFITIDAEDDVQTHKAIYKHLQGILPAYMIPSHLVILDQMPVTDNGKV 8037
0y 7	74 73
Db 8038	38 DRKDLALRAQTVQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEVGITDGFFDLGGHSLLA 8097
ر ۷۷	74
8608 qa	98 TKLAARLSRQLNTRVSVKDVFDQPILADLADIIRRGSHRHDPIPATPYTGPVEQSFAQGR 8157
7 ر	74
Db 8158	58 LWFLEQLNLGASWYLMPFAIRMRGPLQTKALAVALNALVHRHEALRTTFEDHDGVGVQVI 8217
, ,	74
Db 8218	18 OPKSSQDLRIIDLSDAVDDTAYLAALKREQTTAFDLTSEPGWRVSLLRLGDDDYILSIVM 8277
, ,	74 73
Db 8278	78 HHIISDGWTVDVLRQELGQFYSAAIRGQEPLSQAKSLPIQYRDFAVWQRQENQIKEQAKQ 8337
ò	74
DP 833	338 LKYWSQQLADSTPCEFLTDLPRPSILSGEADAVPMVIDGTVYQLLTDFCRTHQVTSFSVL 8397
ò	74 73
Db 835	398 LAAFRTAHYRLTGTLDATVGTPIANRNRPELEGLIGFFVNTQCMRMAISETETFESLVQQ 8457
ò	74 73
Db 849	58 VRLTTTEAFANQDVPFEQIVSTLLPGSRDTSRNPLVQVMFALQSQQDLGRIQLEGMTDEA 8517
· ò	74 73

1	82	à
9597	9538 ARRAQVVAKRKAVSARVAPRNDTEIVLCEEYADILGTEVGITDNFFDMGGHSLMATKLAA	qq
81	82	ò
9537	9478 GROLRTLINRPLQRAQSRRIESQVFEALQTALPAYMIPSRIIVLPQMPTNANGKVDRKQL	qq
81	82	ò
9477	9418 TSFDAPALTQLAKEEGFRVELSWARQRSQNGALDAVFHRLATDANCERSRVLVHFPTDHQ	q
81	82	ò
9417	9358 QGLRNLLQQGRDDVMIAVGNIPYSKTIVERHIMNSLDQDHVNSLDGTSWISDARSAAAIĊ	qq
18	ONS	ò
9357	9298 QLPNIKHVEVLPKLMKATNELSSYRYAAVLHISHNEEEQLLIQDIDPTAWVDFAATQKDS	g
9.4	62	ò
9297	9238 RVFFGDIRSQALNRDFLAARAVRALGDNASKEQIREKIAELEESEEELLVQPAFFVSLRS	Q
7.8		ò
9237	9178 LPSLAGKARVLVGTALDIGSLDKNEIQPELVVINSVAQYFPTSBYLIKVVKAVVEVPSVK	q
78		ò
9177	9118 WLDETTASLLDNRPPGHILEIGAGTGMILSNLGKVDGLQKYVGLDPAPSAAIFVNEAVKS	qq
78	74TSSTT	ò
9117	9058 EDETIEQHESNKQVQGWGEHFDVSRYADIKDLDTSTFGHDFLGWTSMYDGVDIPVNEMKE	qq
73	74	ò
9057	8998 DFEIEFFGRMDQQVKIRGHRIEPAEVEHALLGHDLVHDAAVVLRKPANQEPEMIAFITSO	qq
73	14	ò
8997	8938 GNQQLVSPGVMGEIVVTGDGLARGYTDSALDEDRFVHVTIDGEENIKAYRTGDRVRYRPK	gg
73	74	ò
8937	8878 LDAHDAVAASGLIQDAVYNAYGPTENGMQSTMYKVDVNEPFVNGVPIGRSITNSGAYVMD	qq
73	74	ò
8877	8818 GGTLVCLDYLTLLDSKILYNVFVEAQVNAAMFTPVLLKQCLGNMPAIISRLSVLFNVGDR	đ
73	74	ò
8817	8758 MFTSGSTGKPKGVMIDHRSIIRLVKNSDVVATLPTPVRMANVSNLAFDISVQEIYTALLN	q
73	74	ò
8757	8698 ILSAVPGHKLVLVQAHGPELGLTMADTELVQIDEALASSSSGDHEQIHASGPTATSLAYV	g
73	74	ò
8697	8638 DGQSNKLAHWLCQRNMAPETLVAVFAPRSCLTIVAFLGVLKANLAYLPLDVNAPAARIEA	q
73	74	ò
8637	8578 MAMPITDGITKLRDQGLLTVAKPAYPRESSVIDLFRQQVAAAPDAIAVMDSSSTLTYADL	qq
73	74	ò
8577	8518 LETPLSTRLDLEVHLFQEVGKLSGSLLYSTDLFEVETIRGIVDVFLEILRRGLEQPKORL	QQ

ð	9598	RLSRRLDTRVTVKEVFDKPVLADLAASIEQGSTPHLPIASSVYSGPVEQSYAQGRLWFLD	9657
≿	82		81
۾	9658	OFNLNATWYHMSLAMRLLGPLNMDALDVALRALEQRHETLRTTFEAQKDIGVQVVHEAGM	9717
≿	82		81
ð	9718	KRLKVLDLSDKNEKEHMAVLENEQMRPFTLASEPGWKGHLARLGPTEYILSLVMHHMFSD	7777
≿	82	GWS	84
ð	9778	 GWSVDILRQELGQFYSAALRGRDPLSQVKPLPIQYRDFAAWQKEAAQVAEHERQLAYWEN	9837
≿	85	,	84
ą	9838	QLADSTPGELLTDFPRPQFLSGKAGVIPVT1EGPVYEKLLKFSKERQVTLFSVLLTAFRA	9897
≿	85		84
ည္	9898	THFRLTGAEDATIGTPIANRNRPELEHIIGFFVNTQCMRLLLDTGSTFESLVQHVRSVAT	9957
≿	85		84
ð	9958	DAYSNQDIPPERIVSALLPGSRDASRSPLIQLMFALHSQPDLGNITLEGLEHERLPTSVA	10017
≿	85	NITO	88
ą	10018	TRFDMEFHLFQEPNKLSGSILFADELFQPETINSVVTVFQEILRRGLDQPQVSISTMPLT	. 77001
>	8		88
ą	10078	DGLIDLEKLGLLEIESSNFPRDYSVVDVFRQQVAANPNAPAVVDSETSMSYTSLDQKSEQ	10137
≿	89	Md.	06
ð	10138		10197
⋩	91		. 06
ą	10198	GKRLVLLGSGIDMPQSDRMDVETARIQDILTNTKVERSDPMSRPSATSLAYVIFTSGSTG	10257
جَ	. 91		06
a	10258	RPKGVMIEHRNILRLVKQSNVTSQLPQDLRMAHISNLAFDASIWEIFTAILNGGALICID	10317
⋧	91		06
ð	10318	YFTLLDSQALRTTFEKARVNATLFAPALLKECLNHAPTLFEDLKVLYIGGDRLDATDAAK	10377
⋩	16		06
ą	10378	IQALVKGTVYNAYGPTENTVMSTIYRLTDGESYANGVPIGNAVSSSGAYIMDQKQRLVPP	10437
ጵ	91		06
ထူ	10438	GVMGELVVSGDGLARGYTNSTLNADRFVDIVINDQKARAYRTGDRTRYRPKDGSIEFFGR	10497
ጵ	91		06
ą	10498	MDQQVKIRGHRVEPAEVEQAMLGNKAIHDAAVVVQAVDGQETEMIGFVSMASDRFSEGEE	10557
⋩	91	LOG	93
ą	10558	EITNQVQEWEDHFESTAYAGIEAIDQATLGRDFTSWTSMYNGNLIDKAEMEEWLDDTMQS	10617
à	94		93
a	10618	LLDKEDARPCAEIGTGTGMVLFNLPKNDGLESYVGIEPSRSAALFVDKAAQDFPGLQGKT	10677
8	94		93
ą	10678	I QILVGTAEDIKLVKDFHPDVVVINSVAQYFPSRSYLVQIASELIHMTSVKTIFFGDMRSW	10737

ò	94		92
පු	10738	ATNRDFLVSRALYTLGDKATKDQIRQEVARLEENEDELLVDPAFFTSLTSQWPGKVKHVE	10797
ć	96		95
đ	10798	ILPKRMRTSNELSSYRYAAVLHICRDGEGRNRYGRRVHSVEENAWIDFASSGMDRHALVO	10857
ò	96		95
Q	10858	MLDERRDAKTVAIGNI PHSNTINERHFTTSLDTEGEGIAQDSLDGSAWQSATKAMAARCP	10917
ò	96		95
QQ	10918	CLSVTELVEIGQAAGFRVEVSWARQRSQHGALDVVFHHLEDDRVGRVLINFPTDFERLPP	10977
ò	96		95
g	10978	STGLTSRPLQRIQNRRFESQIREQLQTLLPPYMVPSRIVVLERMPLNANSKVDRKELARK	11037
ò	96	H5	76
q	11038	ARTLQTIKPSATRVAPRNDIEAVLCDEFQAVLGVTVGVMDNFFELGĠHSLMATKLAARLS	11097
ò	86	ADLV	101
QC	11098	RRLDTRVSVKDIFNQPILQDLADVVQTGSAPHEAIPSTPYSGPVEQSFSGGRLWFLDQLN	11157
ò	.102		101
QΩ	11158	LNASWYHMPLASRLRGPLRIEALQSALATIEARHESLRTTFEEQDGVPVQIVRAARNKOL	11211
ò	102		101
q	11218	RIIDVSGTEDAYLAALKQEQDAAFDLTAEPGWRVALLRLGPDDHVLSIVMHHIISDGWSV	11277
ò	102	LY.	103
QQ	11278	   ILRQELGGLYSNASSQPAPLPIQYRDFAIWQKQDSQIAEHQKQLNYWKRQLVNSKPAEL	11337
ò	104		103
QQ	11338	LADFTRPKALSGDADVI PIEIDDQVYQNLRSFCRARHVTSFVALLAAFRAAHYRLTGAED	11397
ò	104		103
đ	11398	ATIGSPIANRNRPELEGLIGCFVNTQCLRIPVKSEDTFDTLVKQARETATEAQDNQDVPF	11457
ò	104	TIRRIDIEL	111
g	11458	ERIVSSMVASSRDTSRNPLVQVMFAVHSQHDLGNIRLEGVEGKPVSMAASTRFDAËMHLF	11517
ò	112		111
d	11518	EDQGMLGGNVVFSKDLFESETIRSVVAVFQETLRRGLANPHANLATLPLTDGLPSLRSLC	11577
ò	112	- Od	113
q	11578	   LQVNQPDYPRDASVIDVFREQVASIPKSIAVIDASSQLTYTELDERSSQLATWLRRQVTV	11637
ò	114	GNRQV	118
Q	11638	PEELVGVLAPRSCETIIAFLGIIKANLAYLPLDVNAPAGRIETILSSLPGNRLILLGSDT	11697
ò	119	ec —	119
Q	11698	QAVKLHANSVRFTRISDALVESGSPPTEELSTRPTAQSLAYVMFTSGSTGVPKGVMVEHR	11757
ò	120	GVT	122
g	11758	:   GITRLVKNSNVVAKQPAAAIAHLSNIAFDASSWEIYAPLLNGGTVVCIDYYTTIDIKAL	11817

ઠે	123		i	
g	11818	EAVFKQHHIRGAMLPPALLKQCLVSAPTMISSLEILFAAGDRLSSQDAILARRAVGSGVY 11877	gg '	12898 FSI
8	123	122	ò	
i			q	12958 GP7
2		NAYGFTENTVLSTIHNIGENEAFSNGVPIGNAVSNSGAFVMDQNQQLVSAGVIGELVVIG 1133/	ò	123
ò	123	122	q	13018 ARC
g	11938	DGLARGYTDSKLRVDRFIYITLDGNRVRAYRTGDRVRHRPKDGQIEFFGRMDQQIKIRGH 11997	ò	123
ò	123	122	쉽	13078 PA
g	11998	RIEPAEVEQALARDPAISDSAVIJOLTDEEEPELVAFFSLKGNANGTNGVNGVSDQEKID 12057	ò	123
ò	123	122	;	13138 TA
q	12058 (	GDEQHALLMENKIRHNLQALLPTYMIPSRIIHVDQLPVNANGKIDRNELAVRAQATPRTS 12117	<u> </u>	
ò	123	122	5 2	200
d d	12118	SVSTYVAPRNDIETIICKEFADILSVRVGITDNFFDLGGHSLIATKLAARLSRRLDTRVS 12177	3 8	
ò	123	122	<b>5</b>	
g	12178	VRDVFDTPVVGQLAASIQQGSTPHEAIPALSHSGPVQQSFAQGRLWFLDRFNLNAAWYIM 12237	Q O	•
Š		122	ò	
3 6		PEGVELRGPLRYDALOTALRALEERHELLRTTEEODGYGMOIVHSPRWRDICVVDISGA 12297	đ	13318 GSI
3 8			ò	123
3	571		QO	13378 RY
සු	12298	NEDLAKLKEEQQAPFNLSTEVAWRVALFKAGENHHILSIVMHHIISDGWSVDIFQQELAQ	ò	123
ò	123		QQ	13438 AV
g	12358	FYSVAVRGHDPLSQVKPLPIHYRDFAVWQRQDKQVAVHESQLQYWIEQLADSTPAEILSD 12417	ò	123
ò	123		i qu	13498 IG
g	12418	FNRPEVLSGEAGTVPIVIEDEVYEKLSLFCRNHQVTSFVVLLAAFRVAHYRLTGAEDATI 12477	ò	
ò	123	122	i i	. משטרו
q	12478	GTPIANRNRPELEDLIGFFVNTQCMRIALEEHDNFLSVVRRVRSTAASAFENQDVPFERL 12537	3 8	
ò	123	122	5 t	
q	12538	12538 VSALLPGSRDASRNPLVQLMFVVHSQRNLGKLQLEGLEGEPTPYTATTRFDVEFHLFEQD 12597	3 8	0 0 0
ઠે	123	122	à á	17 77 7
g	12598	12598 KGLAGNVVPAADLFEAATIRSVVEVFHEILRRGLDQPDIAISTMPLVDGLAALNSRNLPA 12657	3 8	
ò	123	122	ें दे	
q	12658	12658 VEDIEPDFATEASVVDVFQTQVVANPDALAVTDTSTKLTYAELDQQSDHVAAWLSKQKLP 12717	2 (	13. 00. CT
ò	123	122	ŝ	
: 6		AESIVAVIAPRSSETIVACIGILKANLAYLPMDSNVPEARROAILSEIPGEKFVLLGAGV 12777	셤	13798 DA
3 8			ò	133
s 8	777	OGDGINKIP VG GAMA YANK TOO KAA MAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	q	13858 FY
9	12778	PI PDNKTADVKMYF I SDI VASKI DKS I SPG I KPSASS DA I VI F I SGS I GRFRGVMV ERRG	ò	133
ò	123		qq	13918 YT
අ	12838	VISLVKQNASRIPQSLRMAHVSNLAFDASVWEIFTTLLNGGTLFCISYFTVLDSKALSAA	ò	133
ò	123	122		

qq	12898	FSDHRINITLLPPALLKQCLADAPSVLSSLESLYIGGDRLDGADATKVKDLVKGKAYNAY 12	2957
ò	123	12	22
g	12958	GPTENSVMSTIYTIEHETFANGVPIGTSLGPKSKAYIMDQDQQLVPAGVMGELVVAGDGL 13	13017
ò	123	12	122
q	13018	ARGYTDPSLNTGRFIHITIDGKQVQAYRTGDRVRYRPRDYQIEFFGRLDQQIKIRGHRIE 13	13077
ò	123	12	122
Q	13078	PAEVEGALLSDSSINDAVVVSAQNKEGLEMVGYITTQAAQSVDKEEASNKVQEWEAHFDS 13	13137
ò	123	12	122
qq	13138	TAYANIGGIDRDALGQDFLSWTSMYDGSLIPREEMQEWLNDTWRSLLDNQPPGKVLEIGT 13	13197
ò	123	12	122
Ор	13198	GTGMVLFNLGKVEGLQSYAGLEPSRSVTAWVNKAIETFPSLAGSARVHVGTAEDISSIDG 11	13257
ò	123	27	122
Ω	13258	LRSDLVVINSVAQYFPSREYLAELTANLIRLPGVKRIFFGDMRTYATNKDFLVARAVHTL 13	13317
ò	123	77	122
q	13318	GSNASKAMVRQQVAKLEDDEEELLVDPAFFTSLSDQFPDEIKHVEILPKRMAATNELSSY 13	13377
ò	123	27	122
QQ	13378	RYAAVIHVGGHQMPNGEDEDKQWAVKDINPKAWVDFAGTRMDRQALLQLLQDRQRGDDVV 13	13437
ò	123	21	122
QQ	13438	AVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAWISRTGSRAKECPALSVADLIEIGKG 13	13497
ò	123	12	122
đ	13498	IGFEVEASWARQHSQRGGLDAVFHRFEPPRHSGHVMFRFPTEHKGRSSSSLTNRPLHLLØ 13	13557
ò	123	21	122
d	13558	SRRLEAKVRERLQSLLPPYMIPSRITLLDQMPLTSNGKVDRKKLARQARVIPRSAASTLD 1	13617
ò	123	0570	126
đ	13618	FVAPRTEIEVVLCEEFTDLLGVKVGITDNFFELGGHSLLATKLSARLSRRADAGITVKQV 1	13677
ò	127		126
qq	13678	FDQPVLADLAASILQGSSRHRSIPSLPYEGPVEQSFAQGRLWFLDQFNIDALWYLIPFAL 1.	13737
ò	127	7	126
g	13738	RMRGPLQVDALAAALVALEERHESLRTTFEERDGVGIQVVQPLRTTKDIRIIDVSGMRDD 1	13797
ò	127	1	132
qq	13798	DAYLEPLQKEQQTPFDLASEPGWRVALLKLGKDDHILSIVMHHIISDGWSTEVLQRELGQ 1.	13857
ò	133	1	132
ф	13858	FYLAAKSGKAPLSQVAPLPIQYRDFAVWQRQEEQVAESQRQLDYWKKQLADSSPAELLAD	13917
ò	133	1	132
đ	13918	YTRPNVLSGEAGSVSFVINDSVYKSLVSFCRSRQVTTFTTLLAAFRAAHYRMTGSDDATI	13977
è	1,3,3	T. I. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. T. S. C. T. S.	136

g	13978 GTPIANRNRPELENLIGCFVNTQCMRITIGDDETFESLVQQVRSTTATAFENQDVPFERI 14037
ò	137 144
g	14038 VSTLSAGSRDTSRNPLVQLLFAVHSQQGLGRIQLDGVVDEPVLSTVSTRFDLEFHAFQEA 14097
ò	145 144
g	14098 DRLNGSVMFATDLFQPETIQGFVAVVEEVLQRGLEQPQSPIATMPLAEGIAQLRDAGALQ 14157
ઠે	145 144
g	14158 MPKSDYPRNASLVDVFQQQAMASPSTVAVTDSTSKLTYAELDRLSDQAASYLRRQQLPAE 14217
ò	145
a	14218 TMVAVLAPRSCETIIAFLAILKANLAYMPLDVNTPSARMEAIISSVPGRRLILVGSGVRH 14277
ò	145 144
QQ	14278 ADINVPNAKTMLISDTVTGTDAIGTPEPLVVRPSATSLAYVIFTSGSTGKPKGVMVEHRA 14337
ò	145 144
g	14338 IMRLVKDSNVVTHMPPATRMAHVTNIAFDVSLFEMCATLLNGGTLVCIDYLTLLDSTMLR 14397
ò	145 144
g	14398 ETFEREQVRAAIFPPALLRQCLVNMPDAIGMLEAVYVAGDRFHSRDARATQALAGPRVYN 14457
ò	145 144
qq	14458 AYGPTENAILSTIYNIDKHDPYVNGVPIGSAVSNSGAYVMDRNQQLLPPGVMGELVVTGE 14517
ò	145
Op	14518 GVARGYTDASLDTDRFVTVTIDGQRQRAYRTGDRVRYRPKGFQIEFFGRLDQQAKIRGHR 14577
ò	145 144
ద	14578 VELGEVEHALLSENSVTDAAVVLRTMEEEDPQLVAFVTTDHEYRSGSSNEEEDPYATQAA 14637
ò	145 144
g	14638 GDMRKRLRSLLPYYMVPSRVTILRQMPLNANGKVDRKDLARRAQMTPTASSSGPVHVARR 14697
ò	145GVT 147.
g	14698 NETEAAICDEFETILGVKVGIT 14719
AXX XXX XXX	AB841379 AB841379 Standard, Protein; 1784 AA. XX AC AAB41379; XX AC AAB41379; XX AC AAB41379;
X E	ORF1143 p
XX	Human: open reading frame: ORFX; detection; cytostatic; hepatotropic;
33	outpeary; antipecratic; antiparkinsonian; nootropic; neuroprotective;
3 3 3	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
3 3 2 2	hypotensive; dermatological; immunosuppressive; antiliniammatory; antiviral; antibacterial; antifungal; antirheumatic; antihyroid;
¥ ¥	y; cancer; proliferative disorder; hypertension of the control of
<u> </u>	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection;
ž ž	severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allerov: aplastic ansemia; nocturnal haemoglobinuria; burn; wound;

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AAC 74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatocropic; vulnerary; artiporiatic; antiporhatic; neuroprotective; coreopathic; anticonvulsant; antiarthritic; immunosuppressant; coreopathic; anticonvulsant; antiarthritic; immunosuppressant; cartifiabetic; hypotensive; dermatological; immunosuppressive; artifiabetic; hypotensive; dermatological; immunosuppressive; antiantensement. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the proteins associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders ostcoarthritis, coretters of disorders, neurodegenerative disorders ostcoarthritis, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, altergies, aplastic anaemia, burns, wounds, bone and cartilage damage, cadaman, untinflammatory disease; to enhance consulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 RGGLGRAHIRAHTPACHLLGEVQDPELEGGLAAISACDGLKGVFÖLSNEDYFIEPLDSAP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels 1067; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AGGSFLSYELWPRALRKRDVSVRRDAPYELQYRGRELRFNLTANQHLLAPGFVSETRR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 ARPGHAQPHVVYKRQAPERLAQRGDSSAPSTCSASVPRAGVSTGALGAAAAVAAATARRL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 238; DB 21; Length 1784; S.8%; Pred. No. 0.038; tive 25; Mismatches 51; Indels 1067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11, Page 1678-1682; 5507pp; English
                                                                                                                                                                                                           31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127626.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                         31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.8
Best Local Similarity 5.8*
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                   Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 1784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC75588
                                                                                                 WO200058473-A2
                                                             Homo sapiens.
                                                                                                                                       05-OCT-2000.
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ADAMTS-N; disintegrin; metalloprotesse; thrombospondin type I motif; tumour cachexis; inflammation; dermatosparaxis; EDS-VIIC; angiogenesis; Eblers-Danlos syndrome type VIIC; articular cartilage erosion; human; metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.

WO200111074-A2 Homo sapiens.

Human ADAMTS-7 amino acid sequence.

14-MAY-2001 (first entry)

AAB72283;

ò	57 MVILTEPEGAPNITANLTSSLL		102
g	297 LVLLEDEEEDLKITHHADNTLK		356
ò	103		102
qq	357 CETLGLSHVAGMCQPHRSCSIN	CETLGLSHVAGMCQPHRSCSINEDTGLPLAFTVAHELGHSFGIQHDGSGNDCEPVGKRPF	416
ò	103		107
g	417 IMSPQLLYDAAPLTWSRCSRQY	IMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDPPAKDIIDFPSVPPGVLYDVSHQ	476
ò	108		107
₫.	477 CRLQYGAYSAFCEDMDNVCHTL	CRLQYGAYSAFCEDMDNVCHTLMCSVGTTCHSKLDAAVDGTRCGENKWCLSGECVPVGFR	536
ઠે	108		107
q	537 PEAVDGGWSGWSAWSICSRSCC	PEAVDGGWSGWSAWSICSRSCGMGVQSAERQCTQPTPKYKGRYCVGERKRFRLCNLQACP	296
ò	108		107
g	597. AGRPSFRHVQCSHFDAMLYKGC	AGRPSFRHVQCSHFDAMLYKGQLHTWVPVVNDVNPCELHCRPANEYFAKKLRDAVVDGTP	929
ò	108	- DLE	110
g	657 CYQVRASRDLCINGICKNVGCD	CYQVRASRDLCINGICKNVGCDFEIDSGAMEDRCGVCHGNGSTCHTVSGTFXRRPRVXGY	716
ò	111LPDGNRQVR		
qq	:      ::  717 VDVGLIPAGAREIRIQEVAEA		776
ò	120	GVTOGVTO	123
q	777 RGNWENLTSPGPTKEPVWIQVE	RGNWENLTSPGPTKEPVWIQVPASRGPGGGSRGGVPRPSTLHGRSRPGGVSPGSVTEPGS	836
ò	124		126
g	837 EPGPPAAASTSVSPSLKWPNLV	EPGPPAAASTSVSPSLKWPNLVAAVHRGGWGQAPLGLGGWRRHLVLMGPRLPTQLLFQES	968
ò	127		126
qq	897 NPGVHYEYTIHREAGGHDEVP	NPGVHYEYTIHREAGGHDEVPPVFSWHYGPWTKCTVTCGRGVQRQNVYCLERQAGPVDE	956
, <b>ò</b>	127		130
g	957 EHCDPLGRPDDQQRKCSEQPC	EHCDPLGRPDDQQRKCSEQPCPARWWAGEWQLCSSSCGPGGLSRRAVLCIRSVGLDEQSA	1016
ò	131	TWTWTW	142
a	1017 LEPPACEHLPRPPTETPCNRHV	LEPPACEHLPRPPTETPCNRHVPCPATWAVGNWSQCSVTCGEGTQRRNVLCTNDTGVPCD	1076
ò	143		142
q	1077 EAQQPASEVTCSLPLCRWPLG	EAQQPASEVTCSLPLCRWPLGTLGPEGSGSGSSSHELFNEADFIPHHLAPRPSPASSPKP	1136
ò	143		142
g	1137 GTMGNAIEEEAPELDLPGPVF	GTMGNAIEEERAPELDLPGPVFVDDFYYDYNFINFHEDLSYGPSEEPDLDLAGTGDRTPPP	1196
ò	143		142
Q	1197 HSHPAAPSTGSPVPATEPPAA	HSHPAAPSTGSPVPATEPPAAKEEGVLGPWSPSPWPSQAGRSPPPPSEQTPGNPLINFLP	1256
ò	143DLGV 146		
a a	1257 EEDTPIGAPDLGL 1269		
REST AAB	RESULT 13 AAB72283 ID AAB72283 standard, Protein; XX	; 997 AA.	

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This invention relates to murine and human ADAMTS-N (A disintegrin-like and metalloprotease domain with thrombospondin type I motifs) proteins, designated ADAMTS-S, 6, 7, 8, 9, 10 and Rl. Also included in the convention are cDNA sequences encoding the proteins, and antibodies invention are cDNA sequences encoding the proteins, and antibodies conspecific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate ADAMTS-N expression. Disorders that may be treated to using the nucleic acids, proteins and antibodies include, for example themore cachexia, inflammation, dermatosparaxis in cartile or Enters-Danlos tumour cachexia, inflammatory and non-inflammatory) disease, and they may also be used for angiogenesis tumour growth and metastases, and they may also be used for controlling embryogenesis and implantation of fertilised, eggs. The present sequence represents human ADAMTS-7 gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AGGSFLSYELWPRALRKRDVSVRRDAPAFYELQYRGRELRFNLTANQHLLAPGFVSETRR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 RGGLGRAHIRAHTPACHLLGEVQDPELEGGLAAISACDGLKGVFGLSNEDYFIEPLDSAP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 ARPGHAQPHVVYKRQAPERLAQRGDSSAPSTCGVQVYPELESRRERWEGRQGWRRPRLRR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGGILHLEL-----LVAVG----- 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TERYVLTNLNIGAELLRDPSLGAOFRVHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 -----VFQAHQED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.7%; Score 237; DB 22; Length 997; 18.2%; Pred. No. 0.01; ive 24; Mismatches 62; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirohata S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Fig 4; 181pp; English
                                                                                                                                                                                                                                                                                                                                        (CLEV-) CLEVELAND CLINIC FOUND. (APTE/) APTE S S. (HURS/) HURSKAINEN T L. (HIRO/) HIROHATA S.
                                                                                                                                                                                                                                                                                                             99US-0369364.
                                                                                                                                                                                                                                                                             03-AUG-2000; 2000WO-US21223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 18.2
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Apte SS, Hurskainen TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159978/16.
N-PSDB; AAF63440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         997 AA;
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                                                                                                                                                                                                                                            15-FEB-2001
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3 GGIL------
                                                      Conservative
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1505 AA;
                                      Local Similarity
nes 57; Conserv
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Sequence
                          Query Match
                                                      Matches
                                                                                                                                                                                               16
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                                                                                                                                                                                                                                                                                                                                                                                                449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition
                                                                                                                                                                                                                                                                                                           vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypotensive; neuroleptic; neuroprotective; anabolic; antimiflammatory; asparryl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72910 represent human protease amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                        351
233 LHQRSVSKEKWCETLVVADAKMVEYHGQPQVESYVLTIMNMVAGLFHDPSIGNPIHITIV 292
                                                                                                                                                                                                                                                                                                   primer; cytostatic; immunomodulator; cardiant;
                          KMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGN
                                             Caenepeel S;
                                                                                                                                                                                                                                                                      Human metalloprotease partial protein sequence #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manning G,
                                                                                                    116 R--QVRGVTQLGGACSPTWSCLITEDTGFDLGVTI 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Figure 2F; 232pp; English.
                                                                                                                                                                                   AAU72897 standard; Protein; 1505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sudarsanam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000; 2000US-201879P
                                                                                                                                                                                                                                           26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whyte D,
                                                                                                                                                                                                                                                                                                  Human; protease; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-041502/05.
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Payne V;
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989 SRESYCMNNFGHRLADNECQELSRVTRENCNEFSCPSWAASEWSECLVTCGKGTKORQVW 1048
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                                                                                                                                                                          149 ĠĠĿIGTFKGQNGEYFLEPIMKADGNEYEDGHNKPHLIYRQDLNNSFLOTLKYCSVSESQI 208
                                                                                                                                                                                                                                                                                        268
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                     209 KETSLPFHTYSNMNEDLNVMKERVLGHTSKNVPLKDERRHSRKKRLISYPRYIEIMVTAD
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                                                                                                                                                                                                                                                                                                                                            PDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 INEEKGLISAFTIAHELGHTLGVQHDDNPRCKEMKVTKYHVMAPALSFHMSPWSWSNCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Indels 830;
30.7%; Score 237; DB 23; Length 1505; 5.9%; Pred. No. 0.029; ive 30; Mismatches 51; Indels 830.
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time : 70 secs

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 LHQRSVSKEKMVETLVVADAKMVEYHGQPQVESYVLTIMNMVAGLFHDPSIGNPIHITIV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 ARPGHAQPHVVYKRQAPERLAQRGDSSAPSTCGVQVYPELESRRERWEQRQWRRPRLKR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 RLVLLEDEEEDLKITHHADNTLKSFCKWQKSINMKGDAHPLHHDTAILLTRKDL-CAAMN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 AGGSFLSYELWPRALRKRDVSVRRDAPAFYELQYRGRELRFNLTANQHLLAPGFVSETRR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 RGGLGRAHIRAHTPACHLLGEVQDPELEGGLAAISACDGLKGVFÖLSNEDYFIEPLDSAP 172
                                                                                                                               Human; a disintegrin and metalloprotease type metal protease; MDTS1;
MDTS2; MDTS3; ADAM type metal protease; cytostatic; antiarthritic;
cancer; arthritis; arthrosis, deformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.7%; Score 237; DB 22; Length 1686; Best Local Similarity 18.2%; Pred. No. 0.038; Matches 61; Conservative 24; Mismatches 62; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAGGILHLEL-----LVAVG----- 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             New metal protease and metal protease gene, for use as a drug for cancers, arthritis and arthrosis deformans
                                                                                                 Human ADAM type metal protease MDTS1 protein SEQ ID NO:1.
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AAB74944 standard; Protein; 1686 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 12-17; 31pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                         99JP-0180973
                                                                 02-JUL-2001 (first entry)
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N-PSDB; AAF82149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1686 AA;
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                                                                                                                                                                                                      Homo sapiens.
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                               AAB74944;
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Search completed: March 20, 2003, 12:37:50

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March 20, 2003, 12:31:32 ; Search time 49.6216 Seconds (without alignments) 564.722 Million cell updates/sec
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716
1 AVGPDVFQAHQEDTERYVLT.....SPTWSCLITEDTGFDLGVTI 136
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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3: sp\_fungi::
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7: sp\_mammal::
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8: sp\_organelle:\*
9: sp\_phage:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match	* Query Match Length DB	a ID		Description	u,
100.0 1427	. 4	4 09	096L37	mod 75130	homo sapien
28.1 2165	S	5 01	019791		caenorhabdi
27.1 1054	ហ	5	29W493	Q9w493 dro	drosophila
24.2 950	4	4 08	)8TE58	Q8te58 homo	no sapien
_	4	4 08	28TEY8	Овсеув ношо	no sapien
21.6 1223	4	4 08	SBWXSB	Овихвв рошо	no sapien
	4	80	28TE55	<b>Q8te55</b> homo	no sapien
		80	28TE56	Q8te56 homo	no sapien
		80	28TE57		no sapien
	-	90	28TE59	Q8te59 hom	homo sapien
	10	9	29W1Z6		drosophila
	ın	80	28T458	-	drosophila
	4	4	28TE60	_	homo sapien
	S	5	Q9VF61	_	drosophila
17.9 1688	S	2 08	28SXB0	_	drosophila
	u	5	722580	022580 cae	caenorhabdi

100.0%; Score 716; DB 4; Length 1427; 100.0%; Pred. No. 2.6e-69;

Query Match Best Local Similarity

17	85	11.9	1062	ហ	Q19204	
18	81.5	11.4	541	16	Q9F3J1	
6.	16	10.6	802	Ξ	091703	Q91y03 mue mueculu
200	75.5	20.0	152	0	004205	004205 arabidopsis
212	75.5	10.5	209	S	09NDL4	
22	75.5	10.5	503	ഗ	020930	
	7.4	10.3	755	ហ	09VF30	Q9v£30 drosophila
2.5	73.5	10.3	1444	S	017591	
25	72.5	10.1	355	4	Оэнелз	
26	72	10.1	531	4	<u>о</u> 90нз2	
27	72	10.1	1190	'n	O9V7E5	
28	71.5	10.0	518	10	091,722	091j22 oryza Bativ
29	71.5	10.0	723	4	Q9UF23	Q9ufz3 homo sapien
30	71.5	10.0	963	4	Q9P202	O9p202 homo sapien
31	71	9.	236	16	Q9101V5	O9knvs vibrio chol
32	7.1	6.6	254	æ	Q94X42	Q94x42 bemisia tab
33	71	6.6	443	16	Q9HT65	O9ht65 pseudomonas
34	71	6.6	726	4	097416	Q9y416 homo sapien
35	71	6.	906	4	Q8WVS2	Q8wvs2 homo sapien
36	7.1	6.	1104	4	Q9BSJ8	Q9bsj8 homo sapien
3.7	70.5	9.8	227	~	Q9L8E8	Q918e8 vibrio harv
38	70.5	9.	266	17	057843	O57843 pyrococcus
33	70.5	9.8	275	S	Q9VP95	
40	70.5	9.8	388	16	Q9RK22	a
41	70.5	9 8	539	٣	P78832	8
42	70.5	9.	593	7	Q925M0	
43	70.5	8	785	16	Q98KF6	
44	70.5	8.6	793	11	Q91X21	Ogixzi mus musculu
45	70	в. В.	358	7	Q9X5K8	Q9x5k8 streptomyce
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RESULT 1						
096L37 1D 096	L37	PRELIF	PRELIMINARY;		PRT; 1427 AA.	
	096L37;		•			
	1000-040	(TYEM	Af,re]	19	Created)	

TRESOLITION OF CLANDER OF THE LIMINARY; PRT; 1427 AA.

(096137) PRELIMINARY; PRT; 1427 AA.

(106127) O56127

(106127) O1001 (TrEMBLrel. 19, Created)

(106127) O1002001 (TrEMBLrel. 19, Last sequence update)

(107) O1002002 (TrEMBLrel. 19, Last sequence update)

(108) O1002002 (TrEMBLrel. 21, Last annotation update)

(108) O2002 (TrEMBLrel. 21, Last annotation update)

(109) O2002002 (TrEMBLrel. 21, Last annotation update)

(119) O2002002 (TrEMBLrel. 21, Last annotation update)

(120) O2002002 (TrEMBLrel. 21, Last annotation update)

(200) O2002002 (TrEMBLrel. 21, Last annotation update)

(201) O2002002 (TrEMBLrel. 21, Last annotation update)

(202) O2002002 (TrEMBLrel. 21, Last annotation update)

(202) O2002002 (TrEMBLrel. 21, Last annotation update)

(202) O2002002 (TrEMBLrel. 21, Last annotation update)

(202) O2002002 (TrEMBLrel. 21, Last annotation update)

(202) O20020 (TrEMBLrel. 21, Last annotation update)

(202) O20020 (TrEMBLrel. 21, Last annotation update)

(202) O20020 (TrEMBLrel. 21, Last annotation update)

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(202) O20020 (TrEMBLrel. 21, Last annotation update)

(202) O20020 (TrEMBLRELEL 21, Last annotation update)

(202) O20020 (TrEMBLRELEL 21, Last annotation update)

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(202) O20020 (TrEMBLRELEL 21, Last annotation update)

(202) O20020 (TrEMBLRELEL 21,

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RAMEDINE=ZOUSHOUG; PUDAGGG=JU7J1124;

RAMEDINE=ZOUSHOUG; PUDAGGG=JU7J1124;

RA Adams M.D. Celniker S.E., 11 P.W. Hooking R.A., Galle R.F.,

RA Adams G.G., Scherer S.E., 11 P.W. Hooking R.A., Galle R.F.,

RA Adamonatides P.G., Scherer S.E., 11 P.W. Hooking R.A., Galle R.F.,

RA Bardon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RAMENCH, Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,

RA Ballew R.W. Basu A., Baxendal J., Bayrakaroglu L., Beasley E.M.,

RA Besson K.Y., Bence P.V., Barman B.P., Bhandari D., Beasley E.M.,

RA Burtis R.C., Busam D.A., Buller H. Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Burtis R.C., Gabrieliara C.C., Ferriac C., Ferriac S., Busam D.A.,

RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houseron K.A., Howland T.J., Weil M.-H., Ibeyam C.,

RA Hartis N.L., Levitsky A.A., Li J., Will Y., Rocherone D.L.,

RA Hartis N.L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Matteria B., Marnoh T.J., Warny D., Lai Z.,

Liu X., Matteria B., Marnoh T.J., Hernandez J.,

RA Bazzolo M., Pittema G.S., Pen S., Pollard J., Puri V., Reese M.G.,

RA Bazzolo M., Pittema G.S., Pen S., Pollard J., Puri V., Reese M.G.,

RA Bazzolo M., Pittema G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Bazzolo M., Pittema G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Bazzolo M., Pittema G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Bazzolo M., Pittema G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Stupgsti M.P., Smith H.O.,

RA Spier E., Spradling A.C., Stapleton M., Shuges A.,

RA H
                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
66 LSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLIT 125
                                352 QDFCRWQQYYNDPDDSSVQHHDVAILLTRKDICRSQGKCDTLGLAELGTWCDMQKSCAII 411
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                         PRT; 1054 AA.
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InterPro, IPR002870; Pep_M12B_prop
InterPro, IPR001890; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
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HSSP; P15167; 1ATL.
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                  412 EDNGLSAAFTI 422
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                                                                                                     EDTGFDLGVTI
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                                                                                                                                                  292 MYEYHGRSLEDYVLTLFSTVASIYRHQSLRASINVVVVKLIVLKTENAGFRITQNAQOTL 351
                                                                                0; Gaps
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          Gaps
                                                          1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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InterPro; IPR00130; Zn MTpeptdse.
InterPro; IPR00130; Zn MTpeptdse.
Pfam; PF00421; Reprolysin; 1.
SMART; SM0209; tSp 1; 14.
SMART; SM0209; TSP; 18.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS500142; ISP1; 6
PROSITE; PS500142; ZINT PROTEASE; UNKNOWN 1.
SEQUENCE 2165 AA; 244397 MW; FCC3DABAAA9C4888 CRC64;
          Indels
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Last annotation update)
          ö
          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                019791; 027524;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                SCLITEDTGFDLGVTI 222
                                                                                                                                                                                                                                                       SCLITEDTGFDLGVTI 136
            Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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RESULT 2

207 121

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MEDLINE-21839041; PubMed-11741898; Colige A., Van Beeumen J., Colige A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J., Li State A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J., Cloning and Cheretization of ADAMTS-14, a Novel ADAMTS Displaying High Homology with ADAMTS-2 and ADAMTS-3."; J. Biol. Chem. 277:5756-5766(2002).

EMBL, AR366351; AAL79814.1; SEQUENCE 1159 AA; 127336 MW; ASB130149BF7FF34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 VDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESLGVHINIALVRLIMVGYRQSLSLIERG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 NLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VGPDVFQAH-QEDTERXVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAMTS14.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
A digintegrin-like and metalloprotesse with thrombospondin type
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MEDLINE=21638061; PubMed=11779638;
A Bolz H., Ramirez A., von Brederlow B., Kubisch C.;
B Characterization of ADAMTS14, a novel member of the metalloproceinase family.";
L Biochim. Biophys. Acta 152:221-225(2001).
R EMBL, AF158666; AALGA0229.1;
R InterPro; IPR0018970; Pep M12B propep.
R InterPro; IPR0018970; Pep M12B propep.
R Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01421; Reprolysin; 1.
                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.3%; Score 160; DB 4; Best Local Similarity 29.9%; Pred. No. 1.7e-08; Matches 41; Conservative 25; Mismatches 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1223 AA.
                     21,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 RSCALNHEDGFSSAFVI 332
              01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
ADAMTS14.
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                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=9606;
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QBWXSB
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                                                                                                                                                                                                                                                                                                                                                                                                             392 NAQKNLDRFCSWQHKLNKGSEKDPHHHDVAILITR--KNICANNCMTLGLANVGGMCKPK 449
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      2 VGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEG--APNITA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAMTS15.

Homo sapiens (Human).

Evkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                             Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 15 with thrombospondin domains.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF00421; Reprolysin; 1.
Pfam; PF00040; tsp_1; 2.
SWART; SM00209; TSP_1; 2.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS500142; ZINC_PROTEASE; UNKNOWN 1.
SRQUENCE 1054 AA; 118616 MW; DC1545555CB6212 CRC64;
                                                                                                                                                                                                         27.1%; Score 194; DB 5; 32.1%; Pred. No. 2.8e-12; ive 21; Mismatches 68
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                                                                                                                                                                                                  Query Match
Best Local Similarity 32.1%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 OSCSVNEDNGIMLSHTI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 WSCLITEDTGFDLGVTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 31.09
Matches 39; Conservative
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Q8TES8;
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QBTEYB
ID QBTEYB
AC QBTEYB;
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OBTE58
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 VDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESLGVHINIALVRLIMVGYRQSLSLIERG 326
                                                                              NLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPT 119
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           Gaps
                                 VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs a family of meralloproteinases with distincerin and thrombospondin-1 domains."; Gene 283:49-62(2002).

EMBL, AJ345098; CAC87943.1; --
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Euteleostomi;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 17, with thrombospondin domains.
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
           63; Indels
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D585B6593977ED15 CRC64;
                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 21.6%; Score 154.5; DB 4; Local Similarity 30.7%; Pred. No. 7.2e-08; les 42; Conservative 23; Mismatches 63;
30.7%; Pred. No. 7.2e-08; tive 23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1095 AA.
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01-JUN-2002 (TrEMBLrel. 21, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Metalloprocease-disintegrin protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1223 AA; 133925 MW;
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                                                                                                                             WSCLITEDTGFDLGVTI 136
                                                                                                                                                380 RSCALNHEDGESSAFVI 396
              Conservative
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                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ntegrin; Protease.
 Local Similarity
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-FETAL LUNG;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
              42;
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Q8TESS;
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              Matches
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Q0TESS
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61 LTSSLLSVCGWSQTINPEDDTDPGHADLV--LYITRFDLELPDGNRQVRGVTQLGGACSP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 VDKKMMQNHGHENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISHH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 DMVQYHGAEAAQRFILTVMNMVYNMFQHQSLGIKINIQVTKLVLLRQRPAKLSIGHHGER 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 SLLSVCGW-----SQTINPEDDTDPGHADLVLYITRFDLEL-PDGNRQVRGVTQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 SLESFCHWQNEEYGGARYLGNNQVPGGKDDPPLVDAAVFVTRTDFCVHKDEPCDTVGIAY 362
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUN-2002 (TrEMBLrel. 21, Last seguence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type I motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, expression analysis, and structural characterization seven novel human ADANTSs, a family of metalloproteinasms with disintegrin and thrombospondin-1 domains.";

Gene 283:49-62(2002).
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                                                       Lopez-Otin C.; "Cloning, expression analysis, and structural characterization seven novel human ADAMTSS, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002) EMBL; AJ315735; CAC86016.1; -.
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                                                                                                                                                                                                                                                                                                                   Query Match
21.4%; Score 153.5; DB 4; Length 1095;
Best Local Similarity 28.3%; Pred. No. 8e-08;
Matches 41; Conservative 24; Mismatches 67; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
                           Quesada V.,
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Integrin; Protease.
SEQUENCE 1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
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MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C.,
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1 Similarity 31.2%; Pred. No. 3.5e-07;
43; Conservative 22; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 LGGVCSAKRKCVLAEDNGLNLAFTI 387
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                                                                                                                                                                                                                                               Integrin; Protease.
SEQUENCE 1095 AA;
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RA Dodgon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferrac C., Ferraca S., Fleischmann W., RA Globek A., Gorgelian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Harrey D., Heiman T.J., Hernandez J.R., Houck J., RA Jush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z., Liang Y., Lin X., Mattei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B.E., Molningh T.C., McLeod M.P., McPherson D., Markulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheria D.L., Ranchor S.M., Moy M., Mirphy B., Murphy L., Mizny D.M., Nelson D.L., Ranchor K., Sunders R., Palazolo M., Pitchan G.S., Pan S., Pollard J., Port V., Reese M.G., Ranchor K., Saunders R.D.C., Scheeler F., Shen H., Ranger E., Spradling A.C., Staplecon M., Stupski M.P., Smith T., Ranger E., Spradling A.C., Staplecon M., Stupski M.P., Smith T., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao Q., Zheng K., Then R., Zhong W., Zhong W., Zhong K., Zhao M., Zhong K., Zhan M., Zhong K., Zhan M., Zhong K., Zhan M., Zhong K., Zhan M., Zhong S., Yao Q., Zheng R., Ribin G., Shan, Shong S., Yao Q., Zheng R., The genome sequence of Encophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Mooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 VDSDLY-AHMOKNPPTNTESKVVSFLLAMIN-GVQLLYHHPTLGRRINFVLKRLEIWKSW 351
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Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stableton M., Brokstein P., Hong L., Agbayani A., Carfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
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19.3%; Score 138; DB 5; Length 1091;
Best Local Similarity 31.0%; Pred. No. 4e-06;
Matches 45; Conservative 25; Mismatches 57; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FiyBase; FEGN0014778; CG3622.
InterPro; IPR001590; Reprolysin.
InterPro; IPR00130; Zn Mrpeptdse.
Pfam: PF01421; Reprolysin. 1.
PROSITE; PS50215; ADAM MRPRO; I.
PROSITE; PS0142; ZINC_PROTEASE; UNKNOWN 1.
SEQUENCE 109142; ZINC_PROTEASE; UNKNOWN 1.
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EMBL, AE003458; AAF46905.1;
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01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG3622 protein.
CG3622.
CG3622.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Archropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 SSLLSVCGW-----SQTINPEDDTDPGH----ADLVLYITRFDLEL-PDGNRQVRGVT 110
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                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization eeven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62 (2002).
EMBL, AJ311904; CAC84565.1; -.
SEQUENCE 1207 AA; 134061 MW; AF36F6BF5886FDE2 CRC64;
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ches 70; Indels
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                                                                  1207
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                     PRELIMINARY;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                           17 YVLTNLNIGAELL-RDPSLGAQFRVHLVKMVILT--EPEGAPNITANLTSSLLSVCGWSQ 73
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
                                                                                                                                       Length 790;
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Best Local Similarity 32.2%; Pred. No. 3.4e-06;
Matches 39; Conservative 21; Mismatches 53; Indels
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                (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                   EMBL, AY089340; AAL90078.1; -.
SEQUENCE 790 AA; 89226 MW; DF8ADB792D78E794 CRC64;
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Drosophila melanogaster (Fruit fly)
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Lopez-Otin C.;
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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30.2%; Pred. No. 5.1e-05;
tive 24; Mismatches 58; Indels
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SEQUENCE 1229 AA; 138136 MW; C1293180AB198700 CRC64;
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InterPro, IPR002870, Pep_M128_propep.
InterPro, IPR001590, Reprolysin.
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PROSITE; PS5021s; ADAM MEPRO; 2.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR000130; Zn MTpeptdae.
Bfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 2.
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470 SS-SCSIVQDTGLPTAFTM 487

118 PTWSCLITEDTGFDLGVTI 136

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2;
                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GH16393p.
GG6107.
Drosophila melanogaster (Fruft. fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidee; Drosophila.
1011 TaxID=7227;
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                                                                                                                                                                                                                                                                                                       STRAINBERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.M., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY094716; AAM1169.1; -.
SEQUENCE 1688 AA; 189867 MW; 48FBBDD4DEOCA4DZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.9%; Score 128.5; DB 5; Length 1688; Best Local Similarity 30.2%; Pred. No. 7.7e-05; Matches 42; Conservative 24; Mismatches 58; Indels 15;
                                   PRT; 1688 AA
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RESULT 15
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 AVGPDVFQAHQEDTERXVLT.....SPTWSCLITEDTGFDLGVTI 136
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3: /SIDSI/gegdata/geneseqp-embl/AA1982.DAT:*

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAU79217
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Gapop 10.0 , Gapext 0.5
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212.5 29.7 1686 22 AAB74944 Huma 212.5 29.7 1686 22 AAE00313 Huma 212.5 29.7 1686 22 AAE00314 Huma 212.5 29.7 1784 21 AAB41379 Huma 212.0 29.3 1505 23 AAB65949 Huma 206.5 28.8 1690 22 AAB65949 Huma 201 28.1 2150 21 AAY53898 Amin 201 28.1 2165 22 AAB960410 Huma 9 194 27.1 1054 22 AAB960410 Huma 187.5 26.5 1673 21 AAB21264 Huma 187.5 26.2 1602 23 ABG30702 Huma 187.5 26.2 1602 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma 187.5 26.2 1629 23 AAG30703 Huma	87.5 18.5 18.4 28.5 28.5 28.5 28.5 28.5 24.9 28.5 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24.6 176 24.6 24	ULT 1 AAE24448 standard; Protein; 148 AA. AAE24448; 04-OCT-2002 (first entry) Human Von Willebrand factor-cleaving protease fragment #1. Human; Von Willebrand factor-cleaving protease; vWF-cp; therapy; enzyme; transgenic animal; immunisation; thromboembolic disease; preeclampsia; thromboctic thrombocytic purpura; TTP; Henoch-Schonlein purpura; thrombocic thrombocytic purpura; TTP; Henoch-Schonlein purpura; transgenic; anticoagulant.  Homo sapiens.  30-MAY-2002.  20-NOV-2001; 2000US-0721254.  22-NOV-2001; 2001US-0833328:  (BAXT ) BAXTER AG.  Laemmle B, Gerritsen HE, Furlan M, Turecek P, Schwarz H; Schwarz H; Scheiflinger F, Ancoine G, Kerschbaumer R, Tagliavacca L; Zimmermann K, Voelkel D;
111111111111111111111111111111111111111	8	RESULT 1 AAE24448 ID AAE24448 XX AAE2 XXX DT 04-0 XXX DE HUMB XX HUMB

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N-PSDB; ABK52579
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                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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                                                                                                  The invention relates to an isolated or substantially pure Von Willebrand factor-cleaving procease (VWF-cp) polypeptide. VWF-cp is useful for purifying VWF which involves providing VWF-cp as a ligand, concacting a solution comprising VWF with the polypeptide ligand under conditions where VWF is bound to the ligand and recovering from the ligand purified where VWF-cp is useful for producing anti-VWF cp polypeptide antibodies which involves immunising an animal with VWF-cp and isolating the anti-VWF cp polypeptide antibodies from the animal. VWF-cp is useful for two polypeptide antibodies from the animal. VWF-cp is useful for thromboembolic disease such as thrombot, thrombocytic purpura (TTP), thench-Schonlein purpura, preclampsia, neonatal thrombocytopaenia or heamolytic-uraemic syndrome. VWF-cp can also be used for processing plasmatic or recombinantly produced VWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human VWF-cp
                                                                                                                                                                                                                                                                                                                                                     ö
                                    Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
                                                                                                                                                                                                                                                                                                                                                                                                                     1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aggrecanase; osteopathic; antiarthritic; antiinflammatory; human;
cartilage; osteoarthritis; inflammatory disease; enzyme.
                                                                                                                                                                                                                                                                                                                             100.0%; Score 716; DB 23; Length 148; 100.0%; Pred. No. 3e-78; Live 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agostino MJ, Wolfman NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU97641 standard, Protein, 242
                                                                                    Claim 1; Fig 3; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001; 2001WO-US32458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2000; 2000US-241469P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human aggrecanase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SCLITEDTGFDLGVTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 SCLITEDIGFDLGVTI 148
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Twine NC,
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       2002-479950/51
                                                                                                                                                                                                                                                                                                           148 AA;
                N-PSDB; AAD39331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200233093-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU97641;
                                                                                                                                                                                                                                                                                                             Seguence
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This invention relates to the CDNA and protein sequences of a novel
human aggrecanase polypeptide. The protein of the invention may be
used to inhibit the proteolytic activity of aggrecanase, or to inhibit
the aggrecanase-mediated cleavage of aggrecan in cartilage. The
protein of the invention is useful for developing inhibitors of
aggrecanase protein. The CDNA sequence encoding the aggrecanase protein
of the invention is useful for designing probes for obtaining DNA
of the invention is useful for designing probes for obtaining DNA
cof the invention is useful for describing probes for obtaining DNA
cof the invention is useful for designing probes for obtaining DNA
cof the invention is useful for detecting or disposing genetic disorders
convolving the aggrecanase, or disporders involving cellular, organ or
tissue disorders in which aggrecanase is irregularly transcribed or
tissue disorders in which aggrecanase is irregularly transcribed or
tissue disorders in which aggrecanase is irregularly transcribed or
thereting conditions characterised by degradation of articular
in treating conditions characterised by degradation of articular
cartilage, by blocking the enzyme's proteolytic activity
aggrecanase protein inhibitor and a method for inhibition of its activity
aggrecanase protein inhibitor and a method for inhibition of its
including osteoarthritis and other inflammatory diseases. The
including osteoarthritis and other inflammatory diseases. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity
Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide, which are useful for treating aggrecanase-associated condition such as osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVLLTEPEGAPNITAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAOFRVHLVKMVILTEPEGAPNITAN 60
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                                                                                                                                                                                        Claim 11; Page 33-34; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU79217 standard; Protein; 933 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136
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Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 AA;
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Xiao Y;

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The invention relates to an isolated or substantially pure von Willebrand factor-cleaving protease (wWF-cp) polypeptide. wWF-cp is useful for purifying wWF which involves providing wWF-cp as a ligand, contacting a solution comprising wWF with the polypeptide ligand under conditions where wWF is bound to the ligand and recovering from the ligand purified comprising wwF with the polypeptide ligand under conditions where wWF is useful for producing anti-wWF or polypeptide antibodies from the animal. wWF-cp and isolating the anti-crow wWF or polypeptide antibodies from the animal. wWF-cp is useful for thromboembolic disease such as thrombott thrombocytopaenia or thromboembolic disease such as thrombott thrombocytopaenia or haemolytic-uraemic syndrome. wWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated or substantially purified Von Willebrand factor-clea protease, useful for producing preparation for therapy of thrombosiand thromboembolic disease such as thrombotic thrombocytic purpura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1353;
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Tagliavacca
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100.0%; Score 716; DB 23;
Best Local Similarity 100.0%; Pred. No. 7.6e-77;
Matches 136; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                           Furlan M, Turecek
Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB04153 standard; protein; 1416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 64-68; 93pp; English.
                                                                                                                                                                                                                                           Laemmle B, Gerritsen HE, Fi
Scheiflinger F, Antoine G,
Zimmermann K, Voelkel D;
                                                                        20-NOV-2001, 2001WO-EP13391
                                                                                                                    22-NOV-2000; 2000US-0721254.
12-APR-2001; 2001US-0833328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1353 AA;
                                                                                                                                                                                             (BAXT ) BAXTER AG.
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                    30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human ADAM-TS-like protein and the polynucleotide encoding it. The protein of the invention is useful for treating cardiovascular disorders including diseases of the heart and vascular system, such as congestive heart failure, myocardial infarction, ischaemic heart diseases (e.g., stable angina, unstable angina), atrial chromboat arrhythmia, hypertensive vascular diseases (e.g., all kinds of secondary arterial hypertension), and peripheral vascular diseases (e.g., all chrombosis and embolism, inflammatory vascular disease, acute arterial thrombosis and embolism, inflammatory vascular disease. The sequences are useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutetions in the nucleic acid sequences which encode the protein. The sequences are also useful for modulating ADAM-TS-like protein activity in a disease condition. This sequence represents the human ADAM-TS-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVVRMVLLTEPEGAPNITAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                               New purified human ADAM-TS-like protein, useful for identifying modulators of protein activity for treating cardiovascular or liver disorder or chronic obstructive pulmonary disease
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Fig 2; 106pp; English
                                              28-SEP-2000; 2000US-235881P.
25-JUL-2001; 2001US-307393P.
  26-SEP-2001; 2001WO-EP11124
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Best Local Similarity 100.7
Matches 136; Conservative
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                                                                                                                         (FARB ) BAYER
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The present sequence represents a ADAMTS protein, designated ADAMTS-M, that exhibits the characteristics of the ADAM (A Disintegrin And that exhibits the characteristics of the ADAM (A Disintegrin And the ADAM (A Disintegrin And the ADAM (A Disintegrin ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISINTEGRIN ADAM (A DISIN
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                                                                                                                                                                                                                                                                                   /note= "The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain"
Parkinson's; migraine; pain; depression; multiple sclerosis; burn; infertility; diabetic shock; gene therapy; ADAMTS-M; A Disintegrin And Metalloprotease; thrombospondin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buckbinder L, Mitchell PG, Wachtmann TS, Walsh RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1099..1156
/label= Thrombospondin_submotif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Thrombospondin_submotif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Heparin-binding_domain
                                                                                                                                                                                                                                                                                                                                                                             98..311
/label= Metalloprotease_domain
                                                                                                                                                                                                                                            4..97
label= Furin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              324..394
/label= Disintegrin_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-binding_motif
                                                                                                                                  Location/Qualifiers
                                                                                                                                                           ..97
|label= Prodomain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001; 2001EP-0303706
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/label= Zi
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N-PSDB; ABA02549.
                                                                                                                                                                                                                                                 Cleavage-Bite
                                                                                              Ното варіеля
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diabetic shock. The polynucleotide and polypeptide are also useful for diagnosing the diseases above. The polynucleotide is particularly useful in gene therapy for treating the diseases cited above.
                                                                                                                                                     LTSSLLSVCGWSQTINPEDDTDEGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                        Gaps
                                                                                                            1 AVGPDVFQAHQEDTERYVLINLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
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                                                                   Length 1416;
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                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                               Human Von Willebrand factor-cleaving protease (vWF-cp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Mature human vWF-cp protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88..743
note= "Thromspondin type I motif"
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/note= "Thromspondin type I motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Thromspondin type I motif"
                                                                  100.0%; Score 716; DB 23;
100.0%; Pred. No. 8.1e-77;
ive 0; Mismatches 0;
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te= "Cysteine rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Thromspondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Catalytical side"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .51
label= Signal_peptide
                                                                                                                                                                                                                                                                                AAE24450 standard; Protein; 1427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Met turn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Spacer"
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                                                                                                                                                                                                                  230 SCLITEDIGFDLGVT1 245
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                                                                                          Matches 136; Conservative
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                                                 1416 AA;
                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                       AAE24450;
                                                  Sequence
                                                                       Query Match
Best Local
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09-FEB-2001; 2001WO-US04198
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                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                       151..161
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                                                                                                                                                                                              W0200159112-A1
                                                                                         Key
Modified-site
                                                                                                                              Modified-site
                                                                Homo sapiens
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Best Local Simi
Matches 135;
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                                                                                                                                                                                                                                                                                                            The invention relates to an isolated or substantially pure Von Willebrand factor-cleaving protease (wWF-cp) polypeptide. wWF-cp is useful for purifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for producing a preparation of prophylaxis and therapy of thrombosis and thrombombombolic disease such as thrombosic thrombosic purpure (TTP), Henoch-Schonlein purpure, precelampsia, neonatal thrombosytopaenia or haemolytic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp protein. vWF-cp gene is located on chromosome 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, zdint5; anti-angiogenic; intestinal polypeptide; wound healing;
extracellular matrix interaction; tumour suppression; gamete maturation;
immunologic recognition; gastrointestinal irradiation; chemotherapy;
                                                                                                                                                                                                                                  Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 LTSSLLSVCGMSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 8.2e-77;
Matches 136; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                            P, Schwarz
Tagliavacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a human zdint5 polypeptide.
                                                                                                                                         Laemmle B, Gerritsen HE, Furlan M, Turecek
Scheiflinger F, Antoine G, Kerschbaumer R,
Zimmermann K, Voelkel D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG63826 standard; Protein; 203 AA
                                                                                                                                                                                                                                                                                         Claim 1; Fig 5; 93pp; English
                                                  20-NOV-2001; 2001WO-EP13391.
                                                                           22-NOV-2000; 2000US-0721254.
12-APR-2001; 2001US-0833328.
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                                                                                                                                                                                              WPI; 2002-479950/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1427 AA;
                                                                                                                (BAXT ) BAXTER AG.
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WO200242441-A2
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                        30-MAY-2002
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The present sequence represents a human zdint5 polypeptide. The zdint5 to polypeptide is an anti-anglogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is useful as a tool for identifying new family members of polypeptides. Zdint5 polypeptides are useful as probes or primers to folypeptides. Zdint5 polypeptides are used for tumour suppression, gamere maturation, immunologic recognition, and growth and differentiation either working in isolation or in ceris and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery after gastrointestinal irradiation, chemotherapy or antibody use, as anti-infectives, and extracellular metrix repair and remodeling. The polypeptides are also useful for modulating proteolysis—rapoptosis, angiogenesis, infection, cell adhesion, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, Crohn's degenerative diseases, disorders related to immunity, inflammation, financiallity, gamete maturation, immunology, trauma and epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
proteolysis; apoptosis; angiogenesis; infection; cell adhesion; cell fusion; cell signalling; tumour; Crohn's disease; melanoma; trauma; inflammatory bowel disease; food poisoning; degenerative disease; inflammation; fertility; gamete maturation; epithelial disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKMVILTEPQGAPNITAN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-angiogenic intestinal polypeptides, zdint5 polypeptides, vare members of disintegrin proteases, for modulating extracellular matrix interaction, tumour suppression and wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "potential N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                   'note= "potential N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "zinc-binding motif"
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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WPI; 2000-602362/57.
N-PSDB; AAC76877.
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                                                                                                                                                                                                                                                  Best Local Sim
Matches 135;
                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB42668;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human zdint5 polypeptide. The zdint5 polypeptide is an anti-angiogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is polypeptide is useful as a tool for identifying new family members of polypeptides. Zdint5 polynucleotides are useful as probes or primers to clone 5' non-coding regions of zdint5 gene. Zdint5 polypeptides are used for tumour suppression, gamete maturation, immunologic recognition, and growth and differentiation either working in isolation or in conjunction with other molecules in colon, small intestine, fetal lung, testis and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery
                                                                                                                                                                                                                                                                extracellular matrix interaction, tumour suppression; gamete maturation; immunologic recognition; gastrointestinal irradiation; chemotherapy; proteolysis; apoptosis; anglogenesis; infection; cell adhesion; cell fusion; cell signalling; tumour; Crohn's disease; melanoma; trauma; inflammatory bowel disease; food poisoning; degenerative disease; inflammatory, sowel disease; cod poisoning; degenerative disease; inflammation; fertility; gamete maturation; epithelial disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New anti-angiogenic intestinal polypeptides, zdint5 polypeptides, which are members of disintegrin proteases, for modulating extracellular matrix interaction, tumour suppression and wound healing
                                                                                                                                                                                                                                                      Human; zdint5; anti-angiogenic; intestinal polypeptide; wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "unspecified residue encoded by TTN"
                                                                                                                                                                                                                Amino acid sequence of a human zdint5 polypeptide
                                                                                                AAG63829 standard; Protein; 1120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 84-88; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-2001; 2001WO-US04198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2000; 2000US-0501806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holloway JL, Sheppard PO;
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
      134 SCLITEDTGFDLGVTI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-522477/57.
N-PSDB; AAH74765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  595
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                                                                                                                                          AAG63829;
                                                                RESULT 8
                                                                                      AAG63829
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as anti-infectives, and extracellular matrix repair and remodeling. The polypeptides are also useful for modulating proteolysis, apoptosis, angiogenesis, infection, cell adheaton, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, crown's polypeptides are also useful for treating tumour formation, crohn's disease, inflammatory bowel disease, food polsoning, melanoma, degenerative diseases, disorders related to immunity, inflammation, fertility, gamete maturation, immunology, trauma and epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRPDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX ORF2432 polypeptide sequence SEQ ID NO:4864.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 713; DB 22;
Pred. No. 1.3e-76;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB42668 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%;
ilarity 99.3%;
Conservative 1
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 SCLITEDIGFDLGVTI 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCLITEDIGFDLGVTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leach M;
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 1120 AA;
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AAB74944;
             Apte SS,
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                                                                                            AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; outnerary; antiporiatic; antiporiatic; neuroprotective; coteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidabetic; hypotensive; dermaclogical; immunosuppressant; cartidabetic; hypotensive; dermaclogical; immunosuppressive; antidabetic; hypotensive; dermaclogical; immunosuppressive; antidabetic; hypotensive; dermaclogical; immunosuppressive; antidabetic; hypotensive; dermaclogical; immunosuppressive; cartidabetic; hypotensive; dermaclogical; immunosuppressive; antidabetic; hypotensive; dermaclogical; immunosuppressive; antidabetic; hypotensive; dermaclogical conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, cordinate disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic cordinate disease; cardiovascular disease; disorders, astenma, bacterial or fungal infection, malaria, autoinmune disorders, astenma, allergies, aplastic anemia, burns, wounds, bone and cartilage damage, cocural haemoglobinuria, antidiamatory disease; to enhance contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif; tumour cachexia; inflammation; dermatosparaxis; EDS-VIIC; angiogenesis; Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human; metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 LGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYIT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LGAHFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHADLVLYIT 60
            Novel nucleic acids and peptides derived from open reading frame X.. useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 529; DB 21; Length 118; 97.1%; Pred. No. 8.8e-56; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFDLELPDGNXAVRGVTQLGGACSPTWSCLITEDTGFDLGVTI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTI
                                                                          Claim 11; Page 4050; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ADAMTS-7 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB72283 standard; Protein; 997 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APTE S S.
HURSKAINEN T L.
HIROHATA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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(HURS/)
(HIRO/)
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This invention relates to murine and human ADAWTS-N (A disintegrin-like and metalloprocease domain with thrombospondin type I motifs) proteins, designated ADAWTS-S, 6, 7, 8, 9, 10 and Rl. Also included in the cinvention are cDNA sequences encoding the proteins, and antibodies specific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate ADAMTS-N expression. Disorders that may be treated using the nucleic acids, proteins and antibodies include, for example tumour cachexia, inflammation, dermatosparaxis in cattle or Enters-Danlos syndrome type VIC (EDS-VIC) in humans, erosion of articular cartilage in arthitic (both inflammatory and non-inflammatory) disease.

Controlling embryogenesis and implantation of fertilised eggs. The correct present sequence represents human ADAWTS-7 gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ?
                                                                                                                                                     Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumours, inflammation and arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 WSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITEDT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 QPQVESYVLTIMMWAGCFHDPSIGNPIHITIVRLVLLEDEEEDLKITHHADNTLKSFCK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 WQKSINWKGDAHPLHHDTAILLTRKDL-CAAMNRPCETLGLSHVAGMCQPHRSCSINEDT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 OEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCG 70
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MDTS2; MDTS3; ADAM type metal protease; cytostatic; antiarthritic;
cancer; arthritis; arthrosis deformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ñ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ADAM type metal protease MDTS1 protein SEQ ID NO:1.
Hirohata S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB74944 standard; Protein; 1686 AA
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                                                                                                                                                                                                                                                                                                       Claim 15; Fig 4; 181pp; English.
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Best Local Similarity 37.5%
Matches 48; Conservative
   Hurskainen TL,
                                                                     2001-159978/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            997 AA;
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phosphorylation site'

Matches

11

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/note= "Growth factor and cytokine metalloproteinase family signature 2 domain" 539..544
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605..608
/notes "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569. 571
/notes "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                     /note= "protein kinase C phosphorylation site"
373..376
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                           401..404
//occe-
10aein kinase II phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
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note= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation
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'label= Thrombospondin_domain
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label= zinc_binding_domain
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/label= Disintegrin_domain
                                                           "Casein kinase II
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/note= "Encoded by CRC"
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/note= "N
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/note= "N-
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/note= "N
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                                                                                                                          The present sequence represents a disintegrin and metalloprotease (ADAM) type metal protease designated MDTS1, isolated from human. MDTS proteins have cytostatic and antiarthritic activities. They can be used as a drug for cancers, arthritis and arthrosis deformans.
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                                                      for use as a drug for
                                                                                                                                                                                                                             Match 29.7%; Score 212.5; DB 22; Length 1686; Local Similarity 37.5%; Pred; No. 7.9e-16; nes 48; Conservative 22; Mismatches 55; Indels 3;
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/note= "Protein kinase C phosphorylation site"
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'label= Human_mature_27875_ADAM-TS_protein
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                                                        New metal protease and metal protease gene, cancers, arthritis and arthrosis deformans
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/label= Signal_peptide
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               WPI; 2001-285362/30.
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740747 /note= "Tyrosine kinase phosphorylation site" 765770 /note= "N-myristoylation site" 774779 /note= "N-myristoylation site" /note= "N-glycosylation site"	- Thrombospondin_domain 55 "CAMP- and CGMP-dependent protein 173 174 175 176 176 176 176 176 176 176 176	/note= "Casein kinase II phosphorylation site" 949994  label= Thrombospondin_domain 949988  label= Thrombospondin_domain	950953 /note= "N-glycosylation site" /note= "Casein kinase II phosphorylation site"	962964 /note= "Protein kinase C phosphorylation site" 97197	/noce "Nomyristoylation site"	1006= "Glycosaminoglycan attachment site" 1011.:1014 /note= "Casein kinase II phosphorylation site"	10351037 /notes "Protein kinase C phosphorylation site" 10391044	/noce= "N"myristoylation site" 1192.1195 /noce= "Casein Kinase II phosphorylation site"	12631252   Inotes	/nose= "N-myriscoyiation Bire" 13081311 /note= "Casein kinase II phosphorylation site" 13581363	/note= "N-myristoylation site" /note= "N-myristoylation site" /note= "Protein kinase C phosphorylation site"	13851387 /notes "Protein kinase C phosphorylation site" 1397. 1400	<pre>/note= "Casein kinase II phosphorylation site" 14121415 /note= "N-qlycosylation site"</pre>	14151463 /label= Thrombospondin_domain 1419142	/notes "N-glycosylation site" 14401443	/notes "tagein Ainase II phosphoryiation site /hotes "Protein kinase C phosphorylation site"	1466. 1521 /label= Thrombospondin_domain 1470. 1473	/note= "N-glycosylation site" 14831486	/note= "CaBein Kinase 11 phosphorylation site" 14831485 /note= "Protein kinase C phosphorylation site"
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/note= "Crystallins beta and gamma Greek key motif"
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phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
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'note= "Protein kinase C phosphorylation site"
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110.112
/note= "Protein kinase C phosphorylation site"
                                                                                                               "Protein kinase C phosphorylation site"
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| Jabel = Human_mature_27875_ADAM-TS_protein
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/label= Signal_peptide
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FT	Modified-site	147150 /note= "Casein kinase II phosphorvlation site"	
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t t	re e		
FT		/note= "Casein kinase II phosphorylation site"	
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뀹		244259 /label= Metalloproteinase_domain	
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. E. E	, ,	/note= "Casein kinase II phosphorylation site"	
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4 E-		/notes "N-myristoylation site"	
FT	Domain	539545 /note= "Growth factor and cytokine metalloproteinase	
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F F	Modified-site	539544 /note= "N-myristoylation site"	
FT	Domain	541592	
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F F	4	/label= Thrombospondin_domain	
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FT	Modified-site	5695/1 /note= "Protein kinase C phosphorylation site"	
FT	Modified-site	598600 /notes "Protein kinase C phosphorylation site"	
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FT	4	/note= "N-myristoylation site"	
- L	d-Bire	Notes "N-myristoylation site"	
FT	Binding-site	687692 /note= "Cytochrome C family heme-binding site"	
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FF	Modified - Bite	/note= "N-glycosylation site"	
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FF	Modified-8ite	/lb. /21 /notes "N-myristoylation site"	
F 7	Modified-site	740747 /note= "Tyrosine kinase phosphorylation site"	
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872..875 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site" /notes "Casein kinase II phosphorylation site" | 1035...1037 | hotes "Protein kinase C phosphorylation site" | notes "N-myristoylation site" | 192...1195 notes "Casein kinase II phosphorylation site" 440..1442 Atoces "Protein kinase C phosphorylation site" 466..1521 notes "Casein kinase II phosphorylation site" 412..1415 notes "N-glycosylation site" 12..1463 labels Thrombospondin\_domain note= "Casein kinase II phosphorylation site" note= "Protein kinase C phosphorylation site" 185..1387 note= "Protein kinase C phosphorylation site" 397..1400 .960 ..ce= "Casein kinase II phosphorylation site" 62. 964 note= "Protein kinase C phosphorylation site" note= "Casein kinase II phosphorylation site" 263..1252 308. 1311 note= "Casein kinase II phosphorylation site" 358. 1363 note="N\myristoylation site" 370..1372 and kinase C phosphorylation site" 101...903 'note= "Protein kinase C phosphorylation site" 117..920 note≈ "Casein kinase II phosphorylation site" 006..1009 note= "Glycosaminoglycan attachment site" 011..1014 notes "N myristoylation site" 263..1268 notes "N-myristoylation site" 765..770 /notee "N-myristoylation site" /notes "N-myristoylation site" 774..779 /notes "N-myristoylation site" note= "N-myristoylation site" 419..1422 notes "N-glycosylation site" 440..1443 note= "N-glycosylation site" 125..868 label= Thrombospondin\_domain abel= Thrombospondin\_domain 470..1473 note= "N-glycosylation site" 778..781 /note= "N-glycosylation site" 49..994 label= Thrombospondin\_domain 49..988 label= Thrombospondin\_domain "N-glycosylation site" "N-glycosylation site" /1..974 /note= "N-9 005..1010 950..953 /note= "N notes Addified-site Modified-site Modified-site Modified-site Modified-site Modified-site Andified-site Modified-site Adified-site Modified-site Modified-site Modified-site Modified-site Modified-site Adified-site Modified-site Binding-site Domain Domain Domain Domain Domain

/note= "N-myristoylation site"

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AAU72897;
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                                                                                                                                                                                                                                                                                                                        71 WSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITEDT 128
                                                                                                                                                                                                                                                                                                                                      120 WQKSINWKGDAHPLHHDTAILLTRKDL-CAAMNRPCETLGLSHVAGMCQPHRSCSINEDT 378
                                                                                                                                                                                                                                                                                      260 QPQVESYVLTIMMMVAGLFHDPSIGNPIHITIVRLVLEDEEEDLKITHHADNTLKSFCK 319
                                                                                                                                                                                                                                                                     11 QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCG 70
          /notes "Casein kinase II phosphorylation site"
1528.1530
/notes "Protein kinase C phosphorylation site"
1546.1549
/notes "Casein kinase II phosphorylation site"
1592.1597
/notes "N-myristoylation site"
1599.1601
/notes "Protein kinase C phosphorylation site"
1606.1609
                                                                                                                                                                                                                   29.7%; Score 212.5; DB 22; Length 1686; 37.5%; Pred. No. 7.9e-16; ive 22; Mismatches 55; Indels 3;
                                                                                                                                         note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                      phosphorylation site"
1620. 1622
1620. 1822
1625. 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF1143 polypeptide sequence SEQ ID NO:2286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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  1528..1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis, contraceptive
                                                                                                                                                                                                                                  Best Local Similarity 37.5
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             129 GFDLGVTI 136
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AAB41379
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatoropic; vulnerary; cartiporiatic; antiparkinsonian; mootropic; neuroprotective; cartiporiatic; anticonvulsant; antiarthitic; immunosuppressant; cartiabetic; hypotenative; dermarological; immunosuppressant; antithiamatory; antibacterial; antiviral; antifungal; antitheumatic; antidinflammatory; antibacterial; antiviral; antifungal; antitheumatic; antithiamatory; antibacterial; antiviral; antifungal; antitheumatic; cantinflammatory; antibacterial; antiviral; antichingal; antithreumatic; antithiamatory; antibacterial; antiviral; antifungal; antitheumatic; cantinflammatory; antibacterial; antiviral; antifungal; antitheumatic; cantionic acids can be used for predisposition to, or preventing or treating conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, contained associated disorders, neuroacterial; antions disorders, neuroacterial; antimingal expression; hypothyroidism, cholesterol ester storage, systemic lupus cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, conternal or fungal infection, malaria, autoimmune disorders asthmac, allergies, aplactic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 WSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--OVRGVTQLGGACSPTWSCLITEDT 128
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                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 QEDTERYVLTNILNIGAELLRDPSLGAQFRVHLVKWVILTEPEGAPNITANLTSSLLSVCG
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29.7%; Score 212.5; DB 21; Length 1784;
Best Local Similarity 37.5%; Pred. No. 8.6e-16;
Matches 48; Conservative 22; Mismatches 55; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 1678-1682; 5507pp; English.
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Shimkets RA, Leach M;
                                                                                                2000-602362/57.
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The invention relates to an isolated, enriched, or purified protease polypeptide (1) and polynucleotide (11) encoding (1). (1) may be used to screen for substances (5) that may modulate its activity. Administering (1) shich modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or hammacopoietic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migrafine, pain, escual dysfunction, mood disorders, attention disorders, neurological disorders and substances of the color of the disorders and inflammatory disorders and substances also be useful as a disponsite tool for a disease or disorder such as those above. Adul 2816. Protease amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                  Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 VVSAHGSNLQNYILTLMSIVATIYKDPSIGNLIHIVVVKLVMIHREEGEPVINFDGATTL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLIT 125
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29.3%; Score 210; DB 23; Length 1505;
Best Local Similarity 34.4%; Pred. No. 1.3e-15;
Matches 45; Conservative 23; Mismatches 63; Indels 0; Gaps
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                                                                                                                                                                                                                                                  Manning G, Caenepeel S;
                                                                                                                                                                                                                                                     Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Figure 2F; 232pp; English.
                                                                                                                                   34-MAY-2001; 2001WO-US14431.
                                                                                                                                                                      04-MAY-2000; 2000US-201879P.
                                                                                                                                                                                                                                                     Plowman GD, Whyte D,
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                                                       WO200183782-A2.
                  Homo sapiens.
                                                                                              38-NOV-2001.
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PubMedal1557746;
PubMedal1557746;
Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,
Eujikawa K.;
"Structure of von Willebrand Factor-cleaving Protease (ADAMTS13), a
Metalloprotease Involved in Thrombotic Thrombocytopenic Purpura.";
J. Biol. Chem. 276:41059-41063 (2001).
MEROPS; M12.241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Von Williebrand factor-cleaving protease precursor.
ADAMTS13.
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InterPro; IPR00184; TSP1.
InterPro; IPR00130; Zn MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp 1; 4.
PR0STIE; PS50215; ADAM MEPRO; 1.
PROSTIE; PS50192; TSP1; 1.
PROSTIE; PS01142; ZINC_PROTEASE; UNKNOWN_1.
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08V6J1
08V6J1
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040263
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Best Local Similarity
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SIGNAL 1
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Q93p04 prochloroco
007295 prochloroco
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060416 homo sapien
Q96fv4 homo sapien
068831 bacteroides
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O9y4a8 homo sapien
O9bpu9 homo sapien
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09ug64 homo sapien
096yk1 sulfolobus
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                                                                                                                       March 20, 2003, 12:31:32 ; Search time 4.37838 Seconds (without alignments) 564.722 Million cell updates/sec
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                     GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Q96FV4
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                 BLOSUM62 . . . Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                              1 AAGGILHLELLV 12
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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Match Length
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Perfect score:
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Score

Result

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Matches

RESULT 2 Q9LWH0

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SEQUENCE FROM N.A.

STRAIN=CL-BRENNER;

STRAIN=CL-BRENNER;

Pravia C.A., Boncempl E.;

"A novel ubiquitin-conjugating enzyme of trypanosoma cruzi.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-I. FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER

PROTEINS (BY SIMILARITY).

-I. CATALYIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP +

DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.

-I. PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
10 JUNNOWN (Protein for MGC:4093) (protein for MGC:2435).
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             73.7%; Score 42; DB 4; Length 694; 66.7%; Pred. No. 15; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUBELUNG;
Strausberg M.A.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BCO04444; AAH044441; -.
EMBL; BCO04444; AAH044471; -.
EMBL; BCO04EST ABAGE STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREED STREE
                                                                                                                                                                        PRAMY: KTOA. C. C. BRLZ; 1. SMART; KTOA. C. C. BRLZ; 1. PROSITE; PSO0036; BZIP_BASIC; 1. DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4;
Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative ubiquitin-conjugating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
AF135116; AAF61415.1; -. AF134891; AAF6,404.1; -. AF133059; AAG43275.1; -.
                                                       AF133059; AAG43275.1; -. AB010812; BAA76288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%;
70.0%;
                                                                                                                               InterPro; IPR004827; TF_bZIP. Pfam; PF00170; bZIP; 1.
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Q964Q5;
01-DEC-2001 (TEMBLrel. 19,
01-DEC-2001 (TEMBLrel. 19,
01-MAR-2002 (TEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.73
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGGILHLELLV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AGGLLHLTLL 21
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152 AAGGTVHLEI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGGILHLEL 10
                                                                                     EMBL; AB010812; BA
HSSP; P34707; 1SKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5693;
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                                 EMBL; AF134891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q964Q5
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Q9BPU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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Blank V., Andrews N.C.;
"NRF3, a basic leucine zipper protein interacting with MAFG.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAINSCY. NIPPONBARE; Sabaki T., Mansumoto K.; Matsumoto T., Yamamoto K.; Matsumoto T., Yamamoto K.; Matsumoto T., Yamamoto K.; Matsumoto T., Yamamoto C., PAC Clone:P0675A05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
13.7%; Score 42; DB 10; Length 355;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 8; Conservative 2; Mismatches 2; Indels
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002071; BAA95889.1; -.
Hypothetical protein.
SEQUENCE 355 AA; 37762 MW; C5AD33502A9D3732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stoesz S.P., Liu S., Pickett C.B.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein.
Oryza sativa (Rice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694 AA.
                                                                                                                                                                                                                                                        355 AA.
                0; Mismatches
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TISSUE=BONE MARROW, AND PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                      12; Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
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49 ASGGVLHLVLFV 60
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                                                                       1 AAGGILHLELLV 12
                                                                                                      75 AAGGILHLELLV 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
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RESULT 3

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PRELIMINARY;
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341 AGGGILAAELLV 352
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TISSUE=B-CELL;
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C -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).

- 1- SIMILARITY: BELCHOKS TO THE UBIQUITIN-CONJUCATING ENZYME FAMILY.

R FAEBL; AF284603; AAK82982.1:

R INCEPPO; IPRO00615; BPD_cransp.
InterPro; IPRO00615; BPD_cransp.
InterPro; IPRO00615; BPD_cransp.
R Pfam; PF00179; UBO_conjugat. 1.
R PROSITE; PS00140; BPD_TRANSP INN MEMBR; UNKNOWN 1.
R PROSITE; PS00140; BPD_TRANSP INN MEMBR; UNKNOWN 1.
R PROSITE; PS00127; UBIQUITIN_CONJUGAT_2; 1.
M Ligase; Ubiquitin conjugation.
O SEQUENCE 151 AA; 17473 MW; 11E72C9720E27748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALOSO216; CAB43319.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 38; DB 5; Length 151; 70.0%; *Pred. No. 18; 2; Indels ive 1; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annoration update)
Putative aspartate-semialdehyde dehydrogenase.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 35.2 kDa protein (Fragment).
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Pfam, PF00675, Peptidase M16, I.
Hypothetical protein.
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Best Local Similarity 70.v
Best Local 3; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Best Local Similarity 72.7%; Pred: No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC14079; AAH14079.1; -. InterPro; IPR001431; Peptidase M16. Pfam; PF00675; Peptidase_M16; I. Hypothetical protein. SEQUENCE 384 AA; 43029 MW; 96FF3CIABC7AE912 CRC64; V.
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060416;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-BCG-2001 (TrEMBLrel. 19, Last sequence update)
WUGSC:H_RG276003.2 protein.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 43.0 kDa protein.
Homo sapiens (Human)
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"Cloning, expression, and sequencing of a cell surface antigen containing a leucine-rich repeat motif from Bacteroides forsythus ATCC 43037", "
Intert. Immun. 66:5703-5710(1998).
EMBL, AF054892, AAC82625.1; -...
InterPro; IPR003343; Big_2.
Pfam; PF02368; Big_2.
PRINTS; PR01611; LIMPII.
SEQUENCE 1081 AA; 113908 MW; 6E5E36FA0ACDBDSC CRC64;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                   MEDLINE-99043895; PubMed-9826345;
Sharma A., Sojar H.T., Glurich I., Honma K., Kuramitsu H.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 38; DB 2; Length 1081; 80.0%; Pred. No. 1.4e+02; Ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56616;
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DNA Res. 6:83-101(1999).
EMBL, APO00063; BAARION1.1;
Hypothetical protein; Complete proteome.
SEQUENCE 116 AA; 12506 MW; 2ADE1A5B2B82FABA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Chlorophyll a/b-binding light-harvesting protein Pcb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hyporhetical protein APE1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA.
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Best Local Similarity Bu.v.
B; Conservative
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STRAIN=ATCC43037;
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                                                                                              Genco R.J.;
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Q93P06;
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Matches
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093P06
1D 093P0
AC 093P0
DT 01-DE
DT 01-DE
DT Chlor
DE CRIOR
GN FRAG
GN Proch
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Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                   SEQUENCE FROM N.A.
Rohlfing T., Wohldmann P., Antoniou B., Bauer C., O'Neal D.;
"The sequence of Homo sapiens BAC clone CTA-27603.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 66.7%; Score 38; DB 4; Length 490; Local Similarity 72.7%; Pred. No. 62; less 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 38; DB 4; Length 489; 72.7%; Pred. No. 62; ive 1; Mismatches 2; Indels
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010398; AAH10398.1; -.
MEROPS; M16.975; -.
                                                                                                                                                                                                                            Waterston R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004668; AAC15866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001431; Peptidase_M16.
Pfam, PF00675; Peptidase_M16, 1.
PROSTE; PS00143; INSULINASE; WINSOWN 1.
SEQUENCE 490 AA; 54191 MW; 8999F3F57A4D14E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            79250D016E60CFEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unknown (protein for MGC:13691).
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Last annotation update)
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Pfam; PF00675; Peptidase M16; I.
PROSITE; PS00143; INSULINASE; I.
SEQUENCE 489 AA; 54366 MW; 7925
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Best Local Similarity 72...
Berna 8; Conservative
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TISSUE=SKELETAL MUSCLE;
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243 AAGGVSHDELL 253
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243 AAGGVSHDELL 253
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Matches
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Q96FV4
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322 AA.

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Garczarek L., van der Staay G.W.M., Hess W.R., Le Gall F.,
Pattensky F.;
Barcensky F.;
Barcession and phylogeny of the multiple antenna genes of the low-
light adapted strain Prochlorococcus marinus SS120
(Oxyphocobacteria) ";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP554646; AAK69280.1; -
InterPro; IPR000932; PSIIprot.
InterPro; IPR000408; Reg_chr_condens.
PREM: PF00421; PSII; 1.
PROM: PROM: PSII; 1.
                                                                                                "Expression and phylogeny of the multiple antenna genes of the low-
light adapted strain Prochlorococcus marinus SS120
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Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBI_TaxID=1219;
                                                               STRAIN=SB;
Garczarek L., van der Staay G.W.M., Hees W.R., Le Gall F.,
Partensky F.;
                                                                                                                                                                                                                                                             Query Match 64.9%; Score 37; DB 2; Length 322; Best Local Similarity 72.7%; Pred. No. 62; Matches 9; Conservative 1; Mismatches 2; Indels
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                                                                                                                      Oxyphocoacceria).";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR534645; AAK69279.1;
InterPro; IPR00092; PSIIptot.
InterPro; IPR00092; PSIIptot.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00411; PSII; 1.
PROSITE; PS00626; RCC1_2; UNKNOWN_I.
NON_TER 1 1 322
SEQUENCE 322 AA; 35495 MW; B0762A1DD6279032 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chlorophyll a/b-binding light-harvesting protein Pcb
                                                                                                                                                                                                                                                                                                                                                                                                     322 AA.
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                                                  SEQUENCE FROM N.A.
               Prochlorococcus.
NCBI_TaxID=1219;
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093P05
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A Garcarek L., van der Staay G.W.M., Hess W.R., Le Gall F.,
A Patrensky F.,
T Bayression and phylogeny of the multiple antenna genes of the low-
I light adapted strain Prochlorococcus marinus SS120
(XY) (Oxyphorobacceria) ";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL, AF554647, AAK69281.1;
DR InterPro; IPR000408; Reg_chr_condens.
DR InterPro; IPR0041; PSII, 1.
DR PROSITE; PS00626; RCC1_2; UNKNOWN_1.
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                                                                                                                                         Prochlorococcus marinus.
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annoration update)
Chlorophyll a/b-binding light-harvesting protein Pcb
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Job time : 7.37838 secs
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Matches 8; Conservative
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                             Prochlorococcus.
NCBI_TaxID=1219;
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GenCore version 5.1.4\_p5\_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 12:31:05; Search time 6.24324 Seconds

(without alignments)
256.118 Million cell updates/sec

Sequence: 57

Sequence: 1 AAGGILHLELLV 12

Scoring table: BLOSUM62

Scoring table: BLOSUM62

Searched: 908470 seqg, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

A Geneseq 101002:\*

| SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*
| SIDSI/gcgdata/geneseqg-emb1/AA1981.DAT:\*
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| SIDSI/gcgdata/geneseqge-emb1/AA1999.DAT:\*
| SIDSI/gcgdata/geneseqge-emb1/AA29000.DAT:\*
| SIDSI/gcgdata/geneseqge-emb1/AA2001.DAT:\*
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| SIDSI/gegdata/geneseqge-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Score Match Length DB 1	Query Match Length DB	Length DB	80		ΙD				Description	ion
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57 100.0 12 2	100.0 12 2	12	•	č	AAE24446				Human	/on Willebra
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57 100.0 15	100.0 15	15		23	AAE24454				Human 1	/on Willebra
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                                                                                                  The invention relates to an isolated or substantially pure Von Willebrand factor-cleaving procease (vWF-cp) polypeptide. vWF-cp is useful for purifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified where vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for twe vWF cp polypeptide antibodies from the animal. vWF-cp is useful for thromboembolic disease such as thrombotic thrombocytopaenia or thromboembolic disease such as thrombotic thrombocytopaenia or heamolytic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which construction expression systems and generating transgenic animals which construction expression systems and generating transgenic animals which
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                          Novel isolated or substantially purified Von Willebrand factor-cleaving protesse, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
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Scheiflinger F, Antoine G, Kerschbaumer R, Tagliavacca L;
Zimmermann K, Voelkel D;
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 57; DB 23; Length 12; 100.0%; Pred. No. 0.00083; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE24447 standard; peptide; 15 AA
                                                                                  Claim 1; Page 38; 93pp; English
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12-APR-2001; 2001US-0833328.
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Matches 12, Conservative
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    WPI; 2002-479950/51
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factor cleaving protease (vWF-cp) polypeptide a ligand, contacting a purifying vWF which involves providing vWF-cp as a ligand, contacting a golutifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-conference of polypeptide antibodies from the animal. vWF-cp is useful for vWF cp polypeptide antibodies from the animal. vWF-cp is useful for confering a preparation of prophylaxis and therapy of thromboens and thromboens of thromboens and thromboens of thromboens and thromboens of thromboens of thromboens of thromboens of thromboens of thromboens of thromboens of thromboens of the syndrome. VWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which the present sequence is human vWF-cp
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protease, useful for producing preparation for therapy of thrombosi
and thromboembolic disease such as thrombotic thrombocytic purpura
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Kerschbaumer R, Tagliavacca L;
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                                                                                                                           Claim 1; Page 32; 93pp; English
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Scheiflinger F, Antoine G,
Zimmermann K, Voelkel D;
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            The invention relates to an isolated or substantially pure yon Willebrand factor-cleaving protesse (vWF-cp) polypeptide. vWF-cp is useful for purifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for producing a preparation of prophylaxis and therapy of thrombosis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, Von Willebrand factor-cleaving protease, VWF-cp, therapy, enzyme, transgent animal; immunisation; thromboembolio disease, precolampsia, thromboent chromboetic thromboeytic purpura, TPP, Henoch-Schonlein purpura, thromboetic thromboetic thromboetic thromboetic thromboetic thromboetic thromboetic syndrome;
                                                                                                                                                                                              thromboembolic disease such as thrombotic thrombocytic purpura (TTP), Henoch-Schonlain purpura, precelampaia, neonatal thrombocytopsenia or haemolytic-uraemic syndrome. WHF-cp can also be used for processing plasmatic or recombinantly produced WMF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human VMF-cp N-terminal peptide.
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Tagliavacca L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Von Willebrand factor-cleaving protease fragment #1.
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Scheiflinger F, Antoine G, Kerschbaumer R,
Zimmermann K, Voelkel D;
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purifying wWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for an animal with vWF-cp and isolating the antibodies which involves immunising an animal with vWF-cp and isolating the antiproducing a preparation of prophylaxis and therapy of thrombosis and thromboembolic disease such as thrombocut thrombocytic purpura (TTP), Henoch-Schonlein purpura, preeclampsia, neonatal thrombocytopaenia or haemolyvic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; zdints; anti-angiogenic; intestinal polypeptide; wound healing; extracellular matrix interaction; tumour suppression; gamete maturation; immunologic recognition; gastrointestinal irradiation; chemotherapy; proteolysis; apoptosis; angiogenesis; infection; cell adhesion; cell fusion; cell signalling; tumour; Crohn's disease; melanoma; trauma; inflammatory bowel disease; food poisoning; degenerative disease; inflammation; fertility; gamete maturation; epithelial disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid seguence of a human zdint5 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG63826 standard; Protein; 203 AA.
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N-PSDB; AAH74759.
                                                                                                                                                                                                                                                                                         148 AA;
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The invention relates to a human ADAM-TS-like protein and the
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                     The present sequence represents a human zdint5 polypeptide. The zdint5 polypeptide is an anti-angiogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is useful as a tool for identifying new family members of polypeptides is useful as a tool for identifying new family members of polypeptides. Zdint5 polypeptides are to clone 5' non-coding regions of zdint5 gene. Zdint5 polypeptides are to clone 5' non-coding regions of zdint5 gene. Zdint5 polypeptides are and growth and differentiation either working in isolation or in and growth and differentiation either working in isolation or in conjunction with other molecules in colon, small intestine, fetal lung, testis and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery after gastrointestinal irradiation, chemotherapy or antibody use, as an extraorellular matrix repair and remodeling. The polypeptides are also useful for medulating proteolysis, apoptosis, angiogenesis, infection, cell adhesion, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, Crohn's disease, inflammatory bowel disease, food poisoning, melanoma, cell fusion, inflammation, immunology, trauma and epithelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide, which are useful for treating aggrecanase-associated condition such as osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the cDNA and protein sequences of a novel human aggrecanase polypeptide. The protein of the invention may be used to inhibit the proteolytic activity of aggrecanase, or to inhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU97641 standard; Protein; 242 AA.
  Claim 1; Page 73-74; 92pp; English,
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N-PSDB; ABK52579.
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                                                                                                                                                                                                                                                                                                                            203 AA;
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the aggrecanase-mediated cleavage of aggrecan in cartilage. The protein of the invention is useful for developing inhibitors of aggrecanase protein. The cDNA sequence encoding the aggrecanase protein of the invention is useful for designing probes for obtaining DNA containing aggrecanase for obtaining DNA sequences encoding other aggrecanase molecules. The cDNA sequence is also useful for detecting mRNA encoding aggrecanase in a given cell compulation, and thus for detecting or disgnosting genetic disorders involving the aggrecanase, or disorders involving cellular, organ or cinvolving the aggrecanase is irregularly transcribed or expressed. The DNA sequences may also be useful for preparing vectors for gene therapy applications. An inhibitor of the protein is useful cartilage, by blocking the enzyme's proteolytic activity. An cartilage, by blocking the enzyme's proteolytic activity. An aggrecanase protein is useful care useful for treating various aggrecanase-associated conditions charevel and method for inhibition of its activity are useful for treating various aggrecanase-associated conditions including osteoarthritis and other inflammatory diseases. The containing of the formal aggrecanase protein of the
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disorder or chronic obstructive pulmonary disease
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Best Local Similarity 100.0%;
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25-JUL-2001; 2001US-307393P.
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(ZYMO ) ZYMOGENETICS INC.

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polynucleotide encoding it. The protein of the invention is useful for treating cardiovascular disorders including diseases of the heart and vascular system, such as congestive heart failure, myocardial infarction, isohaemic heart diseases (e.g., stable angina, unstable angina), arrivation, cancernal and ventricular arrhythmia, hypertension), and periphran vascular kinds of eccondary arterial hypertension), and periphran vascular diseases (e.g., chronic periphran arterial occlusive disease, acute arterial thrombosis and embolism, inflammatory vascular disorders, etc), liver disorders and embolism, inflammatory vascular disorders, etc), liver disorders and embolism, inflammatory vascular disorders, etc), liver disorders and embolism, inflammatory vascular disorders, etc), must useful in disgnostic assays for detecting diseases and abnormalities of mutations in the nucleic acid sequences which encode the presence of mutations in the nucleic acid sequences which encode the protein. The sequences are also useful for modulating ADAM-TS-like protein activity in addisease condition. This sequence represents the human ADAM-TS-like
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                                                                                                                                                                                                                                                23; Length 933;
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                                                                                                                                                                                                                                            100.0%; Score 57; DB 2: 100.0%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                  78 AAGGILHLELLV 89
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                                                                                                                                                                                                                      933 AA;
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The present sequence represents a human zdint5 polypeptide. The zdint5 to polypeptide is an anti-angiogenic intestinal polypeptide. Zdint5 is used for modulating extracellular matrix interactions. Zdint5 is useful as a tool for identifying new family members of polypeptides. Zdint5 polymucleotides are useful as probes or primers of polypeptides. Zdint5 polymucleotides are used for tumour suppression of zdint5 gene. Zdint5 polypeptides are confunction with other molecules in colon, small intestine, fetal lung, cestis and B-cells. Zdint5 polypeptides are also useful for promoting wound healing, in the treatment of disorders associated with recovery after gastrointestinal irradiation, chemotherapy or antibody use, after gastrointestinal irradiation, chemotherapy or antibody use, and extracellular matrix repair and remodeling. The polypeptides are also useful for modulating proteolysis, apoptosis, angiogenesis, infection, cell adhesion, cell fusion and signalling. The polypeptides are also useful for treating tumour formation, Crohn's disease, inflammatory bowel disease, food poisoning, melanoma, cell fusion, degenerative diseases, disorders related to immunity, inflammation, immunology, trauma and epithelial
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                                                                                                                                                                       New anti-angiogenic intestinal polypeptides, zdint5 polypeptides, which are members of disintegrin protesses, for modulating extracellular matrix interaction, tumour suppression and wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 57; DB 22; Length 1120; 100.0%; Pred. No. 0.12; 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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                                                                                                                                                                                                                                                                                                                               English
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12-APR-2001; 2001US-0833328.
                                                                                                                                                                                                                                                                                                                               Claim 2; Page 84-88; 92pp;
Holloway JL, Sheppard PO;
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 AAGGILHLELLV 116
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                                                                        WPI; 2001-522477/57
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                                                                                                              N-PSDB; AAH74765.
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AAE24449
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AAE24450
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                                                                                                                                                                                               The invention relates to an isolated or substantially pure Von Willebrand factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for purifying vW which involves providing vWF-cp as a ligand, contacting a colution comprising vWF with the polypeptide ligand under conditions where vWF is bound to the ligand and recovering from the ligand purified vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-vWF cp prolypeptide antibodies from the animal. vWF-cp is useful for vMF cp propagation of prophylaxis and therapy of thromboeis and thromboembolic disease such as thrombotic thrombocytic purpura (TTP), Henoch-Schonlein purpura, preeclampsia, neonatal thrombocytopaenia or hamonlytic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osteoarthritis; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection; cachexia; allergy; cancer; leukaemia; lymphoma; osteoporosis; etherosclerosis; congestive heart failure; myocardial infarction; stroke; neurodegenerative disease; autoimmune disorder; Huntington's; troke; abarkinson's; migraine; pain; depession; multiple sclerosis; burn; infertility; diabetic shock; gene therapy; ADAMTS-M; A Disintegrin And Metalloprotease; thrombospondin domain.
                                                                                                        Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura -
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/label= Mature_ADAMTS-M_protein
/note= "The mature form of the ADAMTS-M protein is
processed by furin cleavage of the prodomain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 57; DB 23; Length 1353; 100.0%; Pred. No. 0.15; 0; Mismatches 0; Indels 0
                  Ξü
                Furlan M, Turecek P, Schwarz
, Kerschbaumer R, Tagliavacca
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/label=_Furin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB04153 standard; protein; 1416 AA.
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                                                                                                                                                                          Claim 1; Page 64-68; 93pp; English.
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                Laemmle B, Gerritsen HE, Fi
Scheiflinger F, Antoine G,
Zimmermann K, Voelkel D;
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                             WPI; 2002-479950/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1353 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment.
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Peptide
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The present sequence represents a ADAMTS protein, designated ADAMTS-M, that exhibits the characteristics of the ADAM (A Disintegrin And Metalloprotease) family of metalloproteases, and contains a thrombospondin domain (TS). The protein is encoded by the CDNA given in the specification describes a newly isolated polynucleotide, comprising a nucleotide sequence encoding an ADAMTS-M polynucleotide as prodomain in the specification, or a metalloproteinase, disintegrin domain, prodomain or its thrombospondin submocif. The polynucleotide, polypeptide and agent are useful for mendecturing a medicament for treating a subject in need of altering activity or expression of ADAMTS-M. The polynucleotide ADAMTS-M polypeptide and agent are useful for manufacturing a medicament for treating arthritis not recurrent and adent and alterate original cordination, asthma. Alzheimer's disease, organ transplant coxicity and rejection, cachexia, allergy, cancer (e.g. solid tumour cancer including colon, breast, lung, prostate, brain or haematopoietic malignancies including conserve heart failure, myocardial infarction, stroke, head trauma, spinal cord injury, neurodegenerative disease, autoimmune disorders, thuntington's disease, Parkinson's disease, autoimmune disorders, multiple sclerosis, abnormal wound healing, burns, infertility or diabetic shock. The polynucleotide and polypeptide are also useful for in gene therapy for treating the disease cited above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful in gene therapy, particularly for treating or preventing e.g. arthritis, Crohn's disease, Alzheimer's disease and organ transplant toxicity and rejection, comprises ADAMTS polynucleotide and encoded polypeptide -
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                                                                                                                                                                          410..473
/label= Thrombospondin_submotif
419..424
                                                                                                                                                                                                                                                                                 /label= Heparin-binding_domain
1099..1156
/label= Thrombospondin_submotif
'label Metalloprotease domain
                              247..272
/label= Zinc-binding_motif
                                                                                                  324..394
/label= Disintegrin_domain
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Matches 12; Conservative
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AAE24453;
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                                                             Human, Von Willebrand factor-cleaving protease, vWF-cp; therapy; enzyme; transgenic animal; immunisation; thromboembolic disease; preeclampsia; thrombocytic thrombocytic purpura; TTP; Henoch-Schonlein purpura; thrombosis; neonatal thrombocytopeenia; haemolytic-uraemic syndrome; transgenic; anticoagulant; chromosome 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and thromboembolic disease such as thrombotic thrombocytic purpura
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Scheiflinger F, Antoine G, Kerschbaumer R, Tagliavacca
Zimmermann K, Voelkel D;
                                               Human Von Willebrand factor-cleaving protease (vWF-cp)
                                                                                                                                                                                                                                                                /note=
554..687
/note= "Spacer"
688..743
'~rte= "Thromspondin type I motif"
                                                                                                                                                              /note= "Mature human vWF-cp protein"
69..75
/note= "Furin cleavage site"
                                                                                                                                                                                                                                     187.439
/note= "Thromspondin type I motif"
441.553
/note= "Cysteine rich region"
                                                                                                                                                                                                                                                                                                                                                               /note= "Thromspondin type I motif"
1075..1131
                                                                                                                                                                                                                                                                                                                                               /note= "Thromspondin type I motif"
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                                                                                                                                                                                                                              'note= "Distintegrin like motif"
                                                                                                                                                                                                                                                                                                                                "Thromspondin type I
                                                                                                                                                                                      224..228
/note= "Catalytical side"
                                                                                                                                             label= Signal_peptide
AAE24450 standard; Protein; 1427 AA.
                                                                                                                            .ocation/Qualifiers
                                                                                                                                                                                                              /note= "Met turn"
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12-APR-2001; 2001US-0833328
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                               (first entry)
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                                                                                                                                                                                                                       301..377
                                                                                                                                                        .1427
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                                                                                                                                                                       Cleavage-site
                                                                                                                Homo sapiens
                               04-OCT-2002
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                                                                                                                                       Peptide
                                                                                                                                                        Protein
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purifying vWF which involves providing vWF-cp is useful for solutifying vWF which involves providing vWF-cp as a ligand, contacting a solutifying vWF which involves providing vWF-cp as a ligand, contacting a solution comprising vWF wWF the bound to the ligand and recovering from the ligand purified where vWF is bound to the ligand and recovering from the ligand purified vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies which involves immunisaing an animal with vWF-cp and isolating the anti-vWF cp polypeptide antibodies from the animal. vWF-cp is useful for producing a preparation of prophylaxis and therapy of thrombosis and thench-Schonlein purpura, predict thrombocitic produced and the produced vWF. The invention is useful for has another produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp protein. vWF-cp gene is located on chromosome 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
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12-APR-2001; 2001US-0833328
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Best Local Similarity 100.
Matches 12; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy rechniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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whre, wwp.cp is useful for producing anti-wWF cp polypeptide antibodies which involves immunising an animal with vWF-cp and isolating the anti-wWF cp polypeptide antibodies from the animal. vWF-cp is useful for producing a preparation of prophylaxis and therapy of thrombosis and thromboenbolic disease such as thrombocitic thrombocytic purpura (TTP). Henoch-Schonlein purpura, preclampsia, neonatal thrombocycopaenia or haemolytic-uraemic syndrome. vWF-cp can also be used for processing plasmatic or recombinantly produced vWF. The invention is useful for construction expression systems and generating transgenic animals which express the polypeptide in vivo. The present sequence is human vWF-cp N-terminal peptide.
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food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #11301.
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23-AUG-2000; 2000US-0649167.
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Matches 9; Conservative
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ABG11310
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Whuman; open reading frame; ORFX; detection; cytostatic; hepatotropic; wulnerary; antipaciatic; antiparkinsonian; nootropic; neuroprotective; wulnerary; antipaciatic; antiarthritic; immunosupressant; cardiant; kw anticonvulsant; osteopathic; castintic; antidiabetic; antidiabetic; kw hypotensive; dermatological; immunosuppressive; antidiabetic; whypotensive; dermatological; immunosuppressive; antidiametory; kw antiviral; antibacerial; antifungal; antirheumatic; antidhyroid; wn entrodegenerative disorder; probliferative disorder; hypotherative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; kw severe combined immunodeficiency; milection; wlere combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; w bone damage; cartilage damage; antiinflammatory disease; coagulation; w thrombosis; contraceptive.
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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99US-0127636.
99US-0127728.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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N-PSDB; AAC77119.
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Best Local Similarity
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which represent the human ORFX open reading frames 1 to 3161. The ORFX acquences have activities such as: cytostatic; hepatotropic; vulnerary; antiposoriatic; antipostatic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; antidabetic; hypotenarve; dermarcological; immunosuppressure; antidabetic; hypotenarve; dermarcological; immunosuppressure; antithyoid; and antiansemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoparthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anemia, burns, wounds, bone and cartilage damage, concentral hemoglobinuria, antiinflammatory disease, to enhance
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food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation; to inhibit thrombosis; and as a contraceptive
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23-AUG-2000; 2000US-0649167.
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Matches 8, Conservative
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving contributions in a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cinaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to produce other types of dasorders or other traits of assess biodiversity and caid sequences. AsG00010-AsG30177 represent novel human dispensite amino acid sequences of the invention.

Concern the sequence data for this patent did not appear in the printed specification, but was obtained in alectronic format directly from WIPO cat fire. The wipo int/pub/published_pot_sequences.
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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37393; MUD:94008990; PMID:8404852 26 <gau></gau>	ò 8 6	19 18 790 GSAIATLQKELSATSSAQKITKSVKAPTVKPSETRVRAEPTPLPOFPFADTPDTYKSEAG 849
Rimpords, S.; Politou, A.S.; Pastore, A.  submitted to the Brookhaven Protein Data Bank, February 1996 A;Reference number: A66736; PDB:1TIT A;Contentes: annotation; conformation by (1)H-NMR, residues 5253-5341 R;Pfuhl, M.; Pastore, A. submitted to the Brookhaven Protein Data Bank, August 1996	S a S	VEVKKEVGVSITGTTVREERFEVLHGREAKVTETARVPAPVEIPVTPPTLVSGLKNVTVI 9
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fibronectin type III repeat homology; immunoglobulin homology; prd ve splicing; calmodulin binding; cardiac muscle; duplication; glycd	8 8	1030 PGEPAAPYFITKPVVQKLVEGGSVVFGCQVGGNFRFHVTMNASGVFLITGINING 1003
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7602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18 195,25627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248 5190/Binding site: phosphate (Ser) (covalent) #status experimental	S 8 6	FVQEPEVGETAPGFVYSEYEKEYEKEQALIRKKMAKDTVVVRTYVEDQEFHISSFEERLI
ch 1 Similarity 0.4%; Pred. No. 49; 101; Conservative 16; Mismatches 23; Indels 24887; Gaps 28;	S A S	31 1210 KEIEYRIIKTTLEELLEEDGEEKMAVDISESEAVESGFDLRIKNYRILEGMGVTFHCKMS 1269
11	3 8	1270 GYPLPKIAWYKDGKRIKHGERYQMDFLQDGRASLRIPVVLPEDEGIYTAFASNIKGNAIC 1329
ELLVGGEEEVPAKKTKTIVSTAQISESRQTRIEKKIEAHFDARSIATVEMVIDGAAGQOL 249	ò	31
PHKTPPRIPPKBKSRSPTPPSIAAKAQLARQQSPSPIRHSPSPVRHVRAPTPSPVRSVSP 309	<b>a</b> 8	1330 SGKLYVEPAAPLGAPTYIPTLEPVSRIRSLSPRSVSRSPIRMSFARMSFARMSFARMSFA 1369
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VAAVDMARVREPVISAVEQTAQRTTTTAVHIQPAQEQVRKEAEKTAVTKVVVAADKAKEQ 489	8 8	် မ
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ELKSRTKEIITTKQEQMHVTHEQIRKETEKTFVPKVVISAAKAKEQETRISEEITKKQKQ 549	ò	37 36 37 36 37 36 37
VTQEAIMKETRKTVVPKVIVATPKVKEQDLVSRGREGITTKREQVQITQEKMRKEAEKTA 609	8 8	36
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LSTIAVATAKAKEQETILRTRETMATRQEQIQVTHGKVDVGKKAEAVATVVAAVDQARVR 669	ò	37 38

ò	95 65	
g	2890 HQLIIMNTSTEDSAEYTFVCGNDQVSATLTVTPIMITSMLKDINAEEKDTITFEVTVNYE 2949	
à	85 65	
q	2950 GISYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGDAADYTFVAGKATSTATLYVEA 3009	<u>ق</u>
ò	85 65	
qq	3010 RHIEFRKHIKDIKVLEKKRAMFECEVSEPDITVQWMKDDQELQITDRIKIQKEKYVHRLL 3069	60
ò	85	
q	3070 IPSTRMSDAGKYTVVAGGNVSTAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDV 3129	0
ò	85 65	
g	3130 DAHWYKDGIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYTFVAGRNRSSVTLYVNA 3189	6
ò	85 65	
q	3190 PEPPQVLQELQPVTVQSGKPARFCAMISGRPQPKISWYKEEQLLSTGFKCKFLHDGQEYT 3249	6
ò	85 65	
g	3250 LLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEVPEVVSPDQEMPVYPPAIITPLQDTV 3309	6
ò	85 65	
qq	3310 TSEGQPARFQCRVSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLEIAEAYPEDEGTYT 3369	6.
ò	85 65	
đ	3370 FVANNAVGQVSSTANLSLEAPESILHERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLS 3429	6
ò	85 85	
g	3430 KINETLELLSESPVYPTKFDSEKEGTGPIFIKEVSNADISMGDVATLSVTVIGIPKPKIQ 3489	39
ò	85	
g	3490 WFFNGVLLTPSADYKFVFDGDDHSLIILFTKLEDEGEYTCMASNDYGKTICSAYLKINSK 3549	
ò	85 65	
Q	3550 GEGHKDTETESAVAKSLEKLGGPCPPHFLKELKPIRCAQGLPAIFEYTVVGBPAPTVTWF 3609	60
ò	85 65	
d	3610 KENKQLCTSVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENMLGESTCAAELLVLLED 3669	69
ò	85	
g	3670 TDMTDTPCKAKSTPEAPEDFPQTPLKGPAVEALDSEQEIATFVKDTILKAALITEENOOL 3729	53
ò	85 28	
රු	3730 SYEHIAKANELSSQLPLGAQELQSILEQDKLTPESTREFLCINGSIHFQPLKEPSPNLQL 3789	68
ò	59	
qq	3790 QIVQSQKTFSKEGILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPLKTLLAËPËGN 3849	40
ò	59	
qq	3850 YPQSSIEPPMHSYLTSVAEEVLSLKEKTVSDTNREGRVTLQKQEAQSALILSQSLAEGHV 3909	60
ò	59 99	
qq	3910 ESLQSPDVMISQVNYEPLVPSEHSCTEGGKILIESANPLENACODSAVRIEEGKSLRFPL 3969	69

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QQ	4030	LNLKIQICRALQAAVASEQPGLFSEWLRNIEKVEVEAVNITQEPRHIMCMYLVTSAKSVT	4089
ò	99		65
g	4090	EEVTIIIEDVDPQMANLKMELRDALCAIIYEEIDILTAEGPRIQQGAKTSLQEEMDSFSG	4149
ò	99		65
g	4150	SQKVEPITEPEVESKYLISTEEVSYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKP	4209
ò	99	9	65
g	4210	SEEKEESSSESGTEEVATVKIQEAEGGLIKEDGPMIHTPLVDTVSEEGDIVHLTTSITNA	4269
ò	99		. 59
g	4270	KEVNWYFENKLVPSDEKFKCLQDQNTYTLVIDKVNTEDHQGEYVCEALNDSGKTATSAKL	4329
ò	99	INGW	69
g	4330	TVVKRAAPVIKRKIEPLEVALGHLAKFTCEIQSAPNVRFQWFKAGREIYESDKCSIRSSK	4389
ò	70		69
QQ	4390	YISSLEILRTQVVDCGEYTCKASNEYGSVSCTATLTVTVPGGEKKVRKLLPERKPEPKEE	4449
ò	70		. 69
g	4450	VVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPRPVEEVEVPTVTKRERKI PEPTK	4509
ò	70		69
g	4510	VPEIKPAIPLPAPEPKPKPEAEVKTIKPPPVEPEPTPIAAPVTVPVVGKKAEAKAPKEEA	4569
ò	70		69
g	4570	AKPKGPIKGVPKKTPSP1EAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKD1IL	4629
ò	70		69
g	4630	TESEFVGSSA1 FECLVSPSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAG	4689
ò	70		69
엄	4690	EYTCVLRLGNKEKTSTAKLVVEELPVRFVKTLEEEVTVVKGQPLYLSCELNKERDVVWRK	4749
ò	70		69
g	4750	DGKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYTVTVENANNLECSSCVKVVEVIRD	4809
ò	70		69
8	4810	WLVKPIRDQHVKPKGTA1FACDIAKDTPNIKWFKGYDE1PAEPNDKTEILRDGNHLYLKI	4869
ò	70		69
g	4870	KNAMPEDIAEYAVEIEGKRYPAKLTLGEREVELLKPIEDVTIYEKESASFDAEISEADIP	4929
ઠે	70		69
g	4930	GQWKLKGELLRPSPTCEIKAEGGKRFLTLHKVKLDQAGEVLYQALNAITTAILTVKEIEL	4989
ò	70		69
g	4990	) DFAVPLKDVTVPERRQARFECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILVINDS	5049
ò	70		69

요	5050	QFDDEGVYTAEVEGKKTSARLFVTGIRLKFMSPLEDQTVKEGETAIFVCELSHENMAVVM :	6010
ò	70		69
Q	5110	FKNDAKLHTSRTVLISSEGKTHKLEMKEVTLDDISQIKAQVKELSSTAQLKVLEADPYFT !	5169
ò	70		69
අු	5170	VKLHDKTAVEKDEITLKCEVSKDVPVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLK	5229
ઠે	70		69
qq	5230	DKGEYVCDCGTDKTKANVTVEARLIEVEKPLYGVEVFVGETAHFEIELSEPDVHGOWKLK	5289
ò	70		69
g	5290	GQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIFITPL	5349
ò	70		69
g	5350	SDVKVFEKDEAKFECEVSREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDE	5409
ò	70		69
qq	5410	AKYMFEAEDKHTSGKLI1EGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQ	5469
ઠે	70		69
엄	5470	RLHTTRSVSMQDEGKTHSITFKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGKLQD	5529
ò	70		69
g	5530	YTGVEKDEVILQCEISKADAPVKWFKDGKEIKPSKNAVIKTDGKKRMLILKKALKSDIGQ	5589
ò	70		69
g	5590	YTCDCGTDKTSGKLDIEDREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEAL	5649
ò	70		69
qq	5650	LQTPDCEIKEEGKIHSLVLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVT	5709
ò	70		69
g	5710	VTAGETATFDCELSYEDIPVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVQ	5769
ò	70		69
ପୁ	5770	LTAKDFKTHANLFVKEPPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILK	5829
ò	70		69
g	5830	SKKYEIVADGRVRKLVIHDCTPEDIKTYTCDAKDFKTSCNLNVVPPHVEFLRPLTDLQVR	5883
ò	70		69
g	5890	EKEMARFECELSRENAKVKWFKDGAEIKKGKKYDIISKGAVRILVINKCLLDDEAEYSCE	5949
ò	70		69
g	5950	VRTARTSGMLTVLEEEAVFTKNLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIETG	6009
ò	70		69
qq	6010	RYEILTEGRKRILVIQNAHLEDAGNYNCRLPSSRTDGKVKVHELAAEFISKPQNLEILEG	6909
ò	70		69
QQ	6070	EKAEFVCSISKESFPVQWKRDDKTLESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVG	6129
ò	70		69
g	6130	AARAAAHLTVI EKLR I VVPLKDTR VKEQQEVV FNCEVNT EGAKAKW FRNEEA I FDSSKY I	6189

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5		. :
d G	6190 ILQKDLVYTLRIRDAHLDDQANYNVSLTNHRGENVKSAANLIVEEEDLRIVEPLKDIETM	6249
ò		69
qq	6250 EKKSVTFWCKVNRLNVTLKWTKNGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDEGEYIVT	6309
ò	70	69
QQ	6310 AGQDKSVAELLIIEAPTEFVEHLEDQTVTEFDDAVFSCQLSREKANVKWYRNGREIKEGK	6369
ò	70	69
QQ	6370 KYKFEKDGSIHRLIIKDCRLDDEČEYACGVEDRKSRARLFVEEIPVEIIRPPQDILEAPG	6429
ò	70	69
qq	6430 ADVVFLAELNKDKVEVQWLRNNMVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIAK	6489
ò	70	69
QQ.	6490 DKEARAKLELAAAPKIKTADQDLVVDVGKPLTMVVPYDAYPKAEAEWFKENEPLSTKTID	6549
ò	70	69
q	6550 TTAEQTSFRILEAKKGDKGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNLEVTETFDGEV	6099
ò	70	69
q	6610 SLAWEEPLTDGGSKIIGYVVERRDIKRKTWVLATDRAESCEFTVTGLQKGGVEYLFRVSA	6999
ò	70	69
qq	6670 RNRVGTGEPVETDNPVEARSKYDVPGPPLNVTITDVNRFGVSLTWEPPEYDGGAEITNYV	6729
ò	70	69
qq	6730 IELRDKTSIRWDTAMTVRAEDLSATVTDVVEGQEYSFRVRAQNRIGVGKPSAATPFVKVA	6789
ò	70TANLTSS	76
Q	6790 DPIERPSPPVNLTSSDQTQSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLV	6849
ò	77	. 91
q <sub>0</sub>	6850 PELTYKVTGLEKGNKYLYRVSAENKAGVSDPSEILGPLTADDAFVEPTMDLSAFKDGLEV	6069
ò	77	76
QQ	6910 IVPNPITILVPSTGYPRPTATWCFGDKVLETGDRVKMKTLSAYAELVISPSERSDKGIYT	6969
ò	77	92
g	6970 LKLENRVKTISGEIDVNVIARPSAPKELKFGDITKDSVHLTWEPPDDDGGSPLTGYVVEK	. 7029
ò	77	81
q	7030 REVSRKTWTKVMDFVTDLEFTVPDLVQGKEYLFKVCARNKCGPGEPAYVDEPVNMSTPAT	, 7089
ò	82	81
셤	7090 VPDPPENVKWRDRTANSIFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKM	1 7149
ò	82	81
đ	7150 EVTGLEEGKWYAYRVKTLNRQGASKPSRPTEEIQAVDTQEAPEIFLDVKLLAGLTVKAGT	7209
ò	82	81
g	7210 KIELPATVTGKPEPKITWTKADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYIIEAV	7269

Д	7390 TRLEPSDITKDAVTLTW	TKDAVTLTWCEPDDDGGSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKG 7	7449
ě	CCC		81
ò	82		10
엄	7450 LTNKKKYRFRVLAENLAGPGKPSKSTEPI	LIKDPIDPPWPPGKPTVKDVGKTSVRLNWTK	7509
ò	82		81
QC	7510 PEHDGGAKIESYVIEML	PEHDGGAKIESYVIEMLKTGTDEWVRVAEGVPTTQHLLPGLMEGQEYSFRVRAVNKAGES 7	7569
ò	82		81
qq	7570 EPSEPSDPVLCREKLYP	EPSEPSDPVLCREKLYPPSPPRWLEVINITKNTADLKWTVPEKDGGSPITNYIVEKRDVR 7	7629
ò	82		81
QQ	7630 RKGWQTVDTTVKDTKCT	RKGWQTVDTTVKDTKCTVTPLTEGSLYVFRVAAENAIGQSDYTEIEDSVLAKDTFTTPGP `	7689
ò	82		81
q	7690 PYALAVVDVTKRHVDLK	PYALAVVDVTKRHVDLKWEPPKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNFRVT ;	7749
ò	82		81
q	7750 DVIEGTEVQFQVRAENE	DVIEGTEVQFQVRAENEAGVGHPSEPTEILSIEDPTSPPSPPLDLHVTDAGRKHIAIAWK '	7809
ò	82		81
පු	7810 PPEKNGGSPIIGYHVEM	PPEKNGGSP11GYHVEMCPVGTEKWMRVNSRP1KDLKFKVEEGVVPDKEYVLRVRAVNA1	7869
ò	82		81
g	7870 GVSEPSEISENVVAKDP	SENVVAKDPDCKPT1DLETHD11V1EGEKLS1PVPFRAVPVPTVSWHKDGKE	7929
ò	82		81
q	7930 VKASDRLTMKNDHISAH	SAHLEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDI	7989
ò	82	á	81
ą	7990 KASDITKSSCKLTWEPP	KASDITKSSCKLTWEPPEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWTVKDLIPN	8049
ò	82		81
q	8050 GEYFFRVKAVNKVGGGE	GEYFFRVKAVNKVGGGEYIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYD	8109
ò	82		81
g	8110 GGSKIMGYIIEKIAKGE	GGSKIMGYIIEKIAKGEERWKRCNEHLVPILTYTAKGLEEGKEYOFRVRAENAAGISEPS	8169
ò	82		81
d	8170 RATPPTKAVDPIDAPKV	RATPPTKAVDPIDAPKVILRTSLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEEIK	8229
ò	82		81
Q	8230 KRAAPLVRRRKGEVQEEE	PFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVEND	8289
ò	82		81
đ	8290 HGIAKAPCTVSVLDTPGP	PPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKP	8349
ò	82		81

בַ	9350	DSEWIVVTSTI.RHCKYSVTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAP	8409
ב נ	6		81
۾ .	8410	DKPI VEDVTSNSMLVKWNEPKDNGSPI LGYWLEKREVNSTHWSRVNKSLLNALKANVDGL	8469
≽	82		. 81
۵	8470	LEGLTYVFRVCAENAAGPGKFSPPSDPKTAHDP1SPPGPP1PRVTDTSSTT1ELEWEPPA	8529
≿:	82		81
ą	8530	FNGGGEIVGYFVDKQLVGTNKWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGP	8589
≿	82	***	81
ą	8590	PGETOPVTVAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELD	8649
≿	82		81
ą	8650	KDRVVI DNVGTKSELI I KDALRKDHGRYVI TATNSCGSKFAAARVEVFDVPGPVLDLKPV	8709
⋩	82		81
ą	8710	· VTNRKMCLLNWSDPEDDGGSEITGFIIERKDAKWHTWRQPIETERSKCDITGLLEGQEYK	8769
≿	82		81 ·
ą	8770	FRVIAKNKFGCGPPVEIGPILAVDPLGPPTSPERLTYTERQRSTITLDWKEPRSNGGSPI	8829
≿	82		81
ą	8830	OGYIIEKRRHDKPDFERVNKRLCPTTSFLVENLDEHOMYEFRVKAVNEIGESEPSLPLNV	8889
à	82		81
ą	8890	I VIQDDEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDAL	8949
à	82		81
ဍ	8950	) QITKEEVSRSEAKTELSIPKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPPRNLAV	6006
⋧	82		81
ą	9010	) TDIKAESCYLTWDAPLDNGGSEITHYVIDKRDASRKKAEWEEVTNTAVEKRYGIWKLIPN	6906
ጵ	82		81
ą	9070	) GQYEFRVRAVNKYGISDECKSDKVVIQDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNG	9129
ል	82		81
g	9130	) GSPITGYWLEKREEGSPYWSRVSRAPITKVGLKGVEFNVPRLLEGVKYQFRAMAINAAGI	9189
à	82	MD	83
ą	9190	) GPPSEPSDPEVAGDPIFPPGPPSCPEVKDKTKSSISLGWKPPAKDGGSPIKGYIVEMQEE	9249
à	94		83
g	9250	) GTTDWKRVNEPDKLITTCECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIQE	9309
ò	84		83
g	9310	) EPEVFIDIGAQDCLVCKAGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQ	9369
ò	84		83
QQ	9370	O LETAENSSVIIIPECKRSHTGKYSITAKNKAGQKTANCRVKVMDVPGPPKDLKVSDITRG	9429
ò	84		83

硆	9430	SCRLSWKMPDDDGGDR1KGYV1EKRT1DGKAWTKVNPDCGSTTFVVPDLLSEQOYFFRVR	9489
ò	84		83
ם	9490	AENRFGIGPPVETIQRTTARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHY	9549
ò	84		83
d	9550	IVECLAMDPTGTKKEAWRQCNKRDVEELQFTVEDLVEGGEYEFRVKAVNAAGVSKPSATV	6096
ò	84		83
g	9610	GPCDCQRPDMPPSIDLKEFMEVEEGTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLY	6996
δ	84		83
g	9670	DTHVNKLVVDDTCTLVIPQSRRSDTGLYTITAVNNLGTASKEMRLNVLGRPGPPVGP1KF	9729
ò	84		83
đ.	9730	ESVSADQMTLSWFPPKDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTIPKLLEGHE	9789
ò	84	NITOS	88
q	9790	YVFRIMAQNKYGIGEPLDSEPETARNLFSVPGAPDKPTVSSVTRNŚMŤVŇWEEPEYDGGS	9849
ò	8		88
đ	9850	PVTGYWLEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPA	6066
ò	83		88
q	9910	SLPSDPATARDPIAPPGPPFPKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEE	6966
ò	89		88
Ор	9970	WEKGKDKEVRGTKLVVTGLKEGAFYKFRVSAVNIAGIGEPGEVTDVIEMKDRLVSPDLQL	10029
ò	8		88
qq	10030	DASVRDRIVVHAGGVIRIIAYVSGKPPPTVTWNNNBRTLPQEATIETTAISSSMVIKNCO	10089
ò	8	QG2d	92
qq	10090	RSHQGVYSLLAKNEAGERKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGS	10149
ò	93		95
qq	10150	PITNYVIEKRESDRRAWTPVTYTVTRONATVQGLIQGKAYFFRIAAENSIGMGPFVETSE	10209
ò	93		95
qq	10210	ALVIREPITVPERPEDLEVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIGTEKFHKV	10269
ò	93		95
Q	10270	TNDNLLSRKYTVKGLKEGDTYEYRVSAVNI VGQGKPSFCTKPITCKDELAPPTLHLDFRD	10329
ò	93		95
g	10330	KLTIRVGEAFALTGRYSGKPKPFKVSWFKDEADVLEDDRTHIKTTPATLALEKIKAKRSDS	10389
ò	93		92
q	10390	GKYCVVVENSTGSRKGFCQVNVVDHPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKITN	10449
ò	93		95
d d	10450	YIIEKKEVGKDVWMPVTSASAKTTCKVSKLLEGKDYIFRIHAENLYGISDPLVSDSMKAK	10509
ò	93		92
đ	10510	DRFRVPDAPDQPIVTEVTKDSALVTWNKPHDGGKPITNYILEKRETMSKRWARVTKDPIH	10569

			à	102
ò	93	92	q	11650 WERVHKGSI
ОР	10570 PY	PYTKFRVPDLLEGCQYEFRVSAENEIGIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTC 10629	ò	102
ò	93	92	අ	11710 LSGVLTVK
g	10630 NS	NSVDLTWQPPRHDGGSKILGYIVEYQKVGDEEWRRANHTPESCPETKYKVTGLRDGQTYK 10689	ò	1,02
ò	93	97	đ	11770 KRSDGGKY
Ω	10690 FR	FRVLAVNAAGESDPAHVPEPVLVKDRLEPPELILDANMAREQHIKVGDTLRLSAIIKGVP 10749	ò	102
ò	86		셤	11830 EIQNYILE
g	10750 FP	FPKVTWKKEDRDAPTKARIDVTPVGSKLEIRNAAHEDGGIYSLTVENPAGSKTVSVKVLV 10809	ò	102
ò	86		qq	11890 VIAKTKYD
g	10810 LD	LDKPGPPRDLEVSEIRKDSCYLTWKEPLDDGGSVITNYVVERRDVASAQWSPLSATSKKK 10869	ò	102
ò	86		g	11950 KSAIPERR
යි	10870 SH	SHFAKHLNEGNQYLFRVAAENQYGRGPFVETPKPIKALDPLHPPGPPKDLHHVDVDKTEV 10929	ò	102
ò	86	26	සු	12010 DTTKHSIT
d	10930 SL	SLVMNKPDRDGGSPITGYLVEYQEEGTQDWIKFKTVTNLECVVTGLQQGKTYRFRVKAEN 10989	ò	102
ò	- 86	97	셤	12070 LDENQEYE
අ	VI 06601	IVGLGLPDTTIPIECOEKLVPPSVELDVKLIEGLVVKAGTTVRFPAIIRGVPVPTAKWTT 11049	ò	102
ò	86		g	12130 FAIVRGRP
q	11050 DG	DGSEIKTDEHYTVETDNFSSVLTIKNCLRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGP 11109	ò	102
ò	86		q	12190 KAVFVNVR
q	TI OLLLI	PTGPINILDVTPEHMTISWQPPKDDGGSPVINYIVEKQDTRKDTWGVVSSGSSKTKLKIP 11169	ò	102
ò	86	26	. A	12250 TVTPEVKK
q	11170 HL	HLQKGCEYVFRVRAENKIGVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAATVSWTL 11229	ò	102
ò	86	26	සු	12310 ATEMTKNS
q	11230 PK	PKSDGGSPITGYYMERREVTGKWVRVNKTPIADLKFRVTGLYEGNTYEFRVFAENLAGLS 11289	ò	102
ò	86	101 101	. අ	12370 KKYKFRVA
g	11290 KP	KPSPSSDPIKACRPIKPPGPPINPKLKDKSRETÄÖLÜWHTKPLSDGGSPILGYVVECQKPG 11349	ò	102
ò	102	101	g	12430 HPTCKWKK
g	11350 TA	TAQWNRINKDELIRQCAFRVPGLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILHPP 11409	ò	102
ò	102	101	g	12490 VVMDAPGP
g	11410 EV	EVELDVTCRDVITVRVGQTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVEL 11469	ò	102
ò	102	101	g	12550 TKTSCRVG
g	11470 Q1	QIKEAVRADHGKYIISAKNSSGHAQGSAIVNVLDRPGPCQNLKVTNVTKENCTISWENPL 11529	ò	102
ò	102	101	qa	12610 CIFVAWDR
đ	11530 DN	DNGGSEITNFIVEYRKPNQKGWSIVASDVTKRLIKANLLANNEYYFRVCAENKVGVGPTI 11589		102
ò	102	101	q	12670 YALNKAGS
g	11590 ET	11590 ETKTPILAINPIDRPGEPENLHIADKGKTFVYLKWRRPDYDGGSPNLSYHVERRLKGSDD 11649	ò	102

ò	102		101
a	11650	WERVHKGSIKETHYMVDRCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQKPVLDLK	11709
ò	102		101
q	11710	LSGVLTVKAGDTIRLEAGVRGKPFPEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKA	11769
ò	102		101
qq	11770	KRSDGGKYVVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGC	11829
ò	102		101
đ	11830	EIQNYILEKCETKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESKP	11889.
ò	102		101
q	11890	VIAKTKYDKPGRPDPPEVTKVSKEEMTVVWNPPEYDGGKSITGYFLEKKEKHSTRWVPVN	11949
ò	102		101
q	11950	KSAI PERRMKVQNLLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPI EPPGPPTNFRVV	12009
ò	102		101
đ	12010	DTTKHSITLGWGKPVYDGGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTS	12069
ò	102		101
q	12070	LDENQEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRL	12129
ò	102		101
d d	12130	FAIVRGRPAPKVTWRKVGIDNVVRKGQVDLVDTWAFLVIPNSTRDDSGKYSLTLVNPAGE	12189
ò	102		101
đ	12190	KAVFVNVRVLDTPGPVSDLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWS	12249
ò	102		101
g	12250	TVTPEVKKTSFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLE	12309
ò	102		101
q	12310	ATEMTKNSATLAWLPPLRDGGAKIDGYIISYREEEQPADRWTEYSVVKDLSLVVTGLKEG	12369
ò	102		101
q	12370	KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKILMPEQITIKAGKKLRĪĒAHVYGKP	12429
ò	102		101
đ	12430	HPTCKWKKGEDEVVTSSHLAVHKADSSSILIIKDVTRKDSGYYSLTAENSGTDTOKIKV	12489
ò	102		101
q	12490	VVMDAPGPPQPPFDISDIDADACSLSWHIPLEDGGSNITNYIVEKCDVSRGDWYTALASV	12549
ò	102		101
g	12550	TKTSCRVGKLI PGQEYI FRVRAENRFGI SEPLTSPKMVAQFPFGVPSEPKMARVTKVNKD	12609
ò	102		101
q	12610	CIFVAWDRPDSDGGSP11GYLIERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFRI	12669
∂	102		101
q	12670	YALNKAGSSPPSKPTEYVTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFV	12729
ć	•		101

۵	12730	BACKL PGDKWVRCNTAPHQI PQEEYTATGLEEKAQYQFRA JARTAVNI SPPSEPSDPVTI	12789
≿	102		101
۾	12790	LAENVPPRIDLSVAMKSLLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAM	12849
≿	102		101
ရွ	12850	QRNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAM	12909
≿	102		101
ą	12910	LSWEPPLEDGGSEITNYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYQFRICAEN	12969
⋩	102	•	101
ą	12970	KYGVGDPVFTEPAIAKNPYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEK	13029
≿	102		101
ð	13030	RETQAVNWTKVNRKPI I ERTLKATGLQEGTEYEFRVTAINKAGPGKPSDASKAAYARDPQ	13089
≿	102		101
ą	13090	YPPAPPAFPKVYDTTRSSVSLSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPQNLQK	13149
⋩	102		101
g	13150	TRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPDKHYPKDILIPPEGEHDADLRKTLILR	13209
≿	102		1.01
ક	13210	AGVTMRLYVPVKGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYIL	13269
à	102		101
ရ	13270	TLENSCGKKEYTIVVKVLDTPGPPINVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKR	13329
à	102		101
g	13330	DAERKSWSTVTTECSKTSFRVPNLEEGKSYFFRVFAENEYGIGDPGETRDAVKASQTPGP	13389
à	102		101
g	13390	VVDLKVRSVSKSSCSIGWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLT	13449
à	102		101
g	13450	) EGKEYTFRVSAENENGEGTPSEITVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPI	13509
à	102		101
요	13510	) KGKPAPSVSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGKYTITLKNVAGTKEG	13569
ò	102		101
임	13570	) TISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTC	13629
ò	102		101
셤	13630	) ASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPPNIVD	13689
à	102	2	. 101
QQ	13690	) VRHDSVSLTWTDPKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEY	13749
ò	102		. 101
8	13750	O EFRVMAINLAGVGKPSLPSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLT	13809
ò	102	2	. 101

14949	0 KITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEP	14890	ద
107	8	10	ò
14889	0 IAYEFRVIAENWAGKSKPSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGF	14830	임
107	80	108	ò
14829	0 VTAVTKDSMTISWHEPLSDGGSPILGYHVERKERNGILWQTVSKALVPGNIFKSSGLTDG	14770	පු
107	8	108	ò
14769	O VELATTVIRTTYKATRLTTGLEYQFRVKAQNRYGVGFGITSAWIVANYPFKVPGPPGTPQ	14710	g
101	8	108	ò
14709	O VGDVITIQVHDIPGPPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTW	14650	Q
107	8	108	ò
14649	0 IPVLGRPKPTVTWKKGDQILKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGE	1459(	qq
107	8	108	ò
14589	0 LTEGEEYTFQVMAVNSAGRSAPRESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE	14530	qq
107	8	108	ò
14529	O PPDSLNIMDITKSTVSLAMPKPKHDGGSKITGYVIEAQRKGSDQWTHITTVKGLECVVRN	14470	qq
101		108	ò
14469	) REATRKSYSTATTKCHKCTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASFAPS	14410	g
107		108	ò
14409	) MITENPAGKKSGFVNVRVLDTARPSPQLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEK	14350	g
101		108	ò
14349	) VVRAGLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFV	14290	g
107		108	ò
14289	:    ALRITOFVVPDLQTKEKYNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTL	14230	qq
101	-LYITRE	102	ò
14229	) KDAAYPPGPPSNPHVTDTTKKSASLAWGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGT	14170	QQ
101		102	ò
14169	) HVERREKKSLRWVRAIKTPVSDLRCKVTGLQEGSTYEFRVSAENRAGIGPPSEASDSVLM	14110	qq
101		102	ò
14109	SAVNHYGKGEPVQSEPVKMYDRFGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSEITGY	14050	qq
101		102	ò
14049	EKATLTWTPPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRV	13990	g
101		102	ò
13989	QITSTPTSSMLTIKYATRKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSA	13930	g
101		102	ò
13929	IICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDIT	13870	qq
101		102	ò
13869	GYIVEKRDLPSKSWMKANHVNVPECAFTVTDLVEGGKYEFRIRAKNTAGAISAPSESTET	13810	a

			ò	108
ò	108	107	<u>а</u>	16030 ES
요	14950	SDAITCRDDVEAPKIKVDVKFKDTVILKAGEAFRLEADVSGRPPPTMEWSKDGKELEGTA 15009	ۇ 	
ò	108	107	ි අ <sub>ධ</sub>	16
qq	15010	KLEIKIADFSTNLVNKDSTRRDSGAYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTE 15069	ò	108
ò	108	107		16
đ	15070	VTSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYI 15129	· 6	108
ò	108	107	. A	16
qq	15130	FRVMAVNKYGVGEPLESEPVLAVMPYGPPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEI 15189	3 8	108
ò	108	107	· 6	16
අ	15190	INYIVERRDKAGQRWIKCNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPF 15249	- è	108
ò	108	107	<u> </u>	16
qq	15250	YKACDTVFKPGPPGNPRVLDTSRSSISIAWNKPIYDGGSEITGYMVEIALPEEDEWQIVT 15309	ò	108
ò	108	107	· 40	16390 CT
g	15310	PPAGLKATSYTITGLTENQEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADL 15369	6	110
ò	108	107	: ad	16450
අ	15370	RKVVTIRACCTLRLFVPIKGRPDPEVKWARDHGESLDKASIESASSYTLLIVGNVNRFDS 15429		112
ò	108	107	. dd 	16
g	15430	GKYILTVENSSGSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTMDPPLLDGGSKIKNY 15489	ò	112
ò	108	107	: qa	16
QQ	15490	IVEKRESTRKAYSTVATNCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKAS 15549	ò	112
ò	108	107	- 40 	16
qq	15550	ERPLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEA 15609	· ò	112
ò	108	107	් අධ	16690 QA
g	15610	) TITGLIQGEEYSFRVSAQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLK 15669	8	112
ò	108	107	. A	16
දුර	15670	) VDVPFIGRPTPAVTWHKDNVPLKQTTRVNAESTENNSLLTIKDACREDVGHVVVKLTNSA 15729	ò	112
ò	108	107	q <sub>Q</sub>	16810 VV
Q	15730	) GEAIETLNVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGGSSINNYIVEKRDTSTT 15789	ò	
ò	108	107	ag —	16870 TT
8	15790	15790 TWQIVSATVARTTIKACRLKTGCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGT 15849	ò	
ò	108		qa	16930 GT
đ	15850	) PVVTLSSRDSMEVQWNEPISDGGSRVIGYHLERKERNSILWVKLNKTPIPQTKFKTTGLE 15909	- ò	112
ò	108		ପ୍	16990 LE
qq	15910	EGVEYEFRVSAENIVGIGKPSKVSECYVARDPCDPPGRPEAIIVTRNSVTLQWKKPTYDG	λο	. 112 -
ò	108		qa	17050 DG
q	15970	15970 GSKITGYIVEKKELPEGRHMKASFTNIIDTHFEVTGLVEDHRYEFRVIARNAAGVFSEPS 16029	ۀ 	. 112 -

ò	108		107
g	16030	ESTGAITARDEVDPPRISMDPKYKDTIVVHAGESFKVDADIYGKPIPT10WIKGDQELSN	16089
ò	108		101
g	16090	TARLEIKSTDFATSLSVKDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVI	16149
ò	108		107
q	16150	SGVTAEKCTLAWKPPLQDGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNE	16209
ò	108		107
Q	16210	YTFRIMAVNKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGS	16269
ò	108		107
g	16270	EILGYVLEKRDKEGIRWTRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPS	16329
ò	108		101
QQ	16330	AYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPIYDGGCEIQGYIVEKCDVNVGEWTM	16389
ò	108	70	109
q	16390	CTPPTGINKTNIEVEKLLEKHEYNFRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLÖL	16449
ò	110	BL	111
QQ	16450		16509
ò	112		111
g	16510	DSGKYTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIK	16569
ò	112		111
q	16570	NYIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIK	16629
ò	112		111
q	16630	VAEVPQPPGKITVDDVTRNSVSLSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSL	16689
ò	112		111
q	16690	QAVITNLTQGEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDVKPAFSSYSVQVGQD	16749
ò	112		111
qq	16750	LKMEVPISGRPKPTITWTKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN	16809
ò	112		111
q	16810	VVGQKTASIEIVTLDKPDPPKGPVKFDDVSAESITLSWNPPLYTGGCQITNYIVQKRDTT	16869
ò	112		111
qq	16870	TTVWDVVSATVARTTLKVTKLKTGTEYQFRI FAENRYGQSFALESDPIVAQYPYKEPGPP	16929
ò	112		111
q	16930	GTPFATAISKDSMVIQWHEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTOFKAQN	16989
· &	112		111
qq	16990	LEEGIEYEFRVYAENIVGVGKASKNSECYVARDPCDPPGTPEPIMVKRNEITLQWTKPVY	17049
ò	112		111
Ω	17050	DGGSMITGYIVEKRDLPDGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISK	17109
•			111

ą	17110	PSDSTGPITAKDEVELPRISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEI 17169	
		PDGNR 116	
S 6	211		
3 2	2111	NVBCVT	
5 8	17230	SEKCSLTWSPPL	
ò	127	126	
g	17290	NEYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDG 17349	
ò	127	126	
D D	17350	GSEIIGYIVEKRDRSGIRWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSP 17409	•
ò	127	130	
g	17410		
ò	131	130	
g	17470	QIVTPQTGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDL 17529	
ò	131	133	
qq	17530	DSELRKGIVVRAGGSARIHIPFKGRPMPEITWSREEGEFTDKVQIEKGVNYTQLSIDNCD 17589	
ò	134		
Q	17590	RNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAK 17649	
ò	134	133	
q	17650	VKNYVIDKRESTRKAYANVSSKCSKTSFKVENLTEGAIYYFRVMAENEFGVGVPVETVDA 17709	
ò	134	133	
Д	17710	VKAAEPPSPPGKVTLTDVSQTSASLMWEKPEHDGGSRVLGYVVEMQPKGTEKWSIVAESK 17769	
ò	134	133	
QQ	17770	VCNAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAG 17829	
ò	134	133	
Q	17830	EDLKIEIPVIGRPRPNISWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDFGKYTVTA 17889	
ò	134	133	
QQ	17890	TNSAGTATENLSVIVLEKPGPPVGPVRFDEVSADFVVISWEPPAYTGGCQISNYIVEKRD 17949	
ò	134	133	
qq	17950	TTTTTWHMVSATVARTTIKITKLKTGTEYQFRIFAENRYGKSAPLDSKAVIVQYPFKEPG 18009	
ò	134	133	
g	18010	PPGTPFVTSISKDQMLVQWHEPVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIQDTKFKT 18069	
ò	134	133	
qq	18670	) TGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKP 18129	
ò	134		
QQ	18130	) AYDGGSKITGYIVEKKDLPDGRWMKASFTNVLETEFTVSGLVEDQRYEFRVIARNAAGNF 18189	
ò	134	133	

8	18190	SEPSDSSGAITARDEIDAPNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGK 182	249
à	134	133	m
Db	18250	ELEETAARMEIKSTIQKTTLVVKDCIRTDGGQYILKLSNVGGTKSIPITVKVLDRPGSPE 183	309
ò	134	133	<u>m</u>
. a	0	GPLKVTGVTAEKCYLAMNPPLQDGGANISHYIIEKRETSRLSWTQVSTEVQALNYKVTKL 183	1369
ò	134	133	£.
g	18370	LPGNEYIFRVMAVNKYGIGEPLESGPVTACNPYKPPGPPSTPEVSAITKDSMVVTWARPV 184	3429
ò	134	133	£3
අ	18430	DDGGTEIEGYILEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENNAGVGE 184	18489
ò	134	133	33
q	18490	PSEPSVFYRACDALYPPGPPSNPKVTDTSRSSVSLAWSKPIYDGGAPVKGYVVEVKEAAA 185	3549
ò	134	133	33
g	18550	DEWITCTPPTGLQGKQFTVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPE 186	18609
ò	134	133	33
g	18610	IELDADLRKVVVLRASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEVTSSFTMLVID 186	18669
ò	134	133	33
g	18670	NVTRFDSGRYNLTLENNSGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDG 187	8729
ò	134	133	33
q	18730	GAKITNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAET 187	8789
ò	134	133	33
q	18790	TEPVKVSEPPLPPGRVTLVDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEKWSTCT 188	8849
ò	134	133	33
g	18850	QVKTLEATISGLTAGEEYVFRVAAVNEKGRSDPRQLGVPVIARDIEIKPSVELPFHTFNV	18909
ò	134	133	33
g	18910	KAREQLKIDVPPKGRPQATVNWRKDGQTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYE	18969
ò	134	133	33
qq	18970	LCVSNSAGSITVPITIIVLDRPGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIVEK	19029
ò	134	13	133
g	19030	KETTSTTWHIVSQAVARTSIKIVRLTTGSEYQFRVCAENRYGKSSYSESSAVVAEYPFSP	19089
ò	134	13	.33
QQ	19090	PGPPGTPKVVHATKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQV 1	9149
à	134	13	133
qq	19150	KVSGLDEGLMYEYRVYAENIAGIGKCSKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWS 1	19209
ò	134	13	133
g	19210	KPHYDGGAKITGYIVERRELPDGRWLKCNYTNIQETYFEVTELTEDQRYEFRVFARNAAD 1	19269
ò	134	13	133
qq	19270	SVSEPSESTGPIIVKDDVEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKD	19329

				ò	134
ò	134		133	- 4	מאחמאי סויסכ
g	19330 GIEIEERARTEIISTDI	GIEIEERARTEIISTDNHTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPP	19389	3	
à			133	ò	134
<b>3</b>			7 7	q	20470 GPPGGP
g		AGPLEINGLTAEKCSLSWGRPQEDGGADIDYYHRKKRETSHLAWTICEGELUMISCKVIK	19449	ò	138
ò	134		133	đ	20530 TTKIIK
QQ	19450 LLKGNEYIFRVTGVNK	LLKGNEY1 FRVTGVNKYGVGEPLESVA1KALDPFTVPSPPTSLE1TSVTKESMTLCWSRP	19509	ò	138
ò	134		133	d d	20590 SRPIAD
8	19510 ESDGGSEISGYIIERR	ESDGGSE1SGY11ERREKNSLRWYRYNKKPVYDLRVKSTGLREGCEYEYRVYAENAAGLS	19569	ò	
ò	134		133	q	20650 GOGPFS
q	19570 LPSETSPLIRAEDPVF	LPSETSPLIRAEDPVFLPSPPSKPKIVDSGKTTITIAWVKPLFDGGAPITGYTVEYKKSD	19629	ì à	
ò	134		133	ે દે	200000000000000000000000000000000000000
qq	19630 DTDWKTSIQSLRGTEY	DTDWKTS1QSLRGTEYT1SGLTTGAEYVFRVKSVNKVGASDPSDSSDPQ1AKEREEEPLF	19689	3 8	
ò	134		133	\$ 4	2000
QQ	19690 DIDSEMRKTLIVKAGA	DIDSEMRKTLIVKAGASFTMTVPFRGRPVPNVLWSKPDTDLRTRAYVDTTDSRTSLTIEN	19749	a d	
ò	134		133	ठें ह	
Q	19750 ANRNDSGKYTLTIQNV	ANRNDSGKYTLTIQNVLSAASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVPENDGG	19809	au d	20830 SLLTA
ò			133	ò	
g A		APVKNYH1 EKREASKKAWVSVTNNCNRLSYKVTNLQEGA1 YYPRVSGENEFGVGI PAETK	19869	g G	20890 DPPLI
è			133	ò	
;		PERMITTER PERMITTER STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET	19929	යු	20950 IGEPCE
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ò			133	qq	21010 QTWSH
g		AKSTHHVVSGLRENSEYFFRVFAENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTV	19989	à	138
ò			133	qq	21070 DIPGA(
g	19990 YVRAGSNLKVDIPISG	YVRAGSNLKVDI PI SGKPLPKVTLSRDGVPLKATMRFNTEI TAENLTINLKESVTADAGR	20049	ò	138
ò	134		133	අ <u>ධ</u>	21130 KKEHG
g	20050 YEITAANSSGTTKAFI	YEITAANSSGTTKAFINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSQVTNYI	20109	ò	138
ò	134		133	qq	21190 GEITC
ద	20110 LLKRETSTAVWTEVSA	LLKRETSTAVWTEVSATVARTWMKVMKLTTGEEYQFRIKAENRFGISDHIDSACVTVKLP	20169	ò	138
ò	134		133	qq	21250 IIVAK
g	20170 YTTPGPPSTPWVTNVT	YTTPGPPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWQKANKLVIRT	20229	ò	138
ò	134		133	d d	21310 NTSPI
g	20230 THFKVTTISAGLIYEF	THFKVTTISAGLIYEFRVYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSL	20289	ò	
8	134		133	, da	21370 TRETI
q	20290 SWQQPAFDGGSKITGY	SWQQPAFDGGSKITGYIVERRDLPDGRWTKASFTNVTETQFTISGLTQNSQYEFRVFARN	20349	ò	138
ò	134			qa	21430 RIIAR
<u>6</u>	20350 AVGSISNPSEVVGPIT	AVGSISNPSEVVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEW	20409	ò	138

ò	134		133
g	20410	YKDDKELQTNALVCVENTTDLASILIKDADRLNSGCYELKLRNAMASASATIRVQILDKP	20469
ò	134	CLIT	137
g	20470	GPPGGP1EFKTVTAEK1TLLWRPPADDGGAKITHYIVEKRETSRVVWSMVSEHLEEC11T	20529
ò	138		137
q	20530	TTKIIKGNEYIFRVRAVNKYGIGEPLESDSVVAKNAFVTPGPPGIPEVTKITKNSMTVVM	20589
ò	138		137
Q	20590	SRPIADGGSDISGYFLEKRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAA	20649
ò	138		137
ద	20650	GQGPFSEPYKAADPIDPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIR	20709
ò	138		137
qq	20710	QGEEEEWTTVSTKGEVRTTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDIL	20769
ò	138		137
q	20770	EAPEIDLDVALRTSVIAKAGEDVQVLI PFKGRPPPTVTWRKDEKNLGSDARYSI ENTDSS	20829
ò	138		137
QQ	20830	SLLTI PQVTRNDTGKY ILTI ENGVGEPKSSTVSVKVLDTPAACQKLQVKHVSRGTVTLLM	20889
ò	138		137
Q	20890	DPPLIDGGSP11NYV1EKRDATKRTWSVVSHKCSSTSFKL1DLSEKTPFFFRVLAENEIG	20949
ò	138		137
g	20950	1GEPCETTEPVKAAEVPAPIRDLSMKDSTKTSVILSWTKPDFDGGSVITEYVVERKGKGE	21009
ò	138		137
đ	21010	QTWSHAGISKTCEIEVSQLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELIITPEVDLS	21069
ò	138		137
셤	21070	DIPGAQVTVRIGHNVHLELPYKGKPKPSISWLKDGLPLKESEFVRFSKTENKITLSIKNA	21129
ò	138		137
පු	21130	KKEHGGKYTVILDNAVCRIAVPITVITLGPPSKPKGPIRFDEIKADSVILSWDVPEDNGG	21189
ò	138		137
쉽	21190	GEITCYSIEKRETSQTNWKMVCSSVARTTFKVPNLVKDAEYOFRVRAENRYGVSOPLVSS	21249
ò	138		137
Q	21250	IIVAKHOFRIPGPPGKPVIYNVTSDGMSLTWDAPVYDGGSEVTGFHVEKKERNSILWOKV	21309
ò	1,38		. 137
q	21310	NTSPISGREYRATGLVEGLDYQFRVYAENSAGLSSPSDPSKFTLAVSPVDPPGTPDYIDV	, 21369
ò	138		. 137
qq	21370	TRETITLKWNPPLRDGGSKIVGYSIEKRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEF	21429
ò	138		137
Ор	21430	RIIARNAVGTISPPSQSSGIIMTRDENVPPIVEFGPEYFDGLIIKSGESLRIKALVOGRP	21489
è			137

Op	21490 VPRVT	<pre>VPRVTWFKDGVEIEKRMNMEITNVLGSTSLFVRDATRDHRGVYTVEAKNASGSAKAEIKV 21</pre>	21549
ò	138	13	137
q	21550 KVQDTI	KVQDTPGKVVGPIRFTNITGEKMTLWWDAPLNDGCAPITHYIIEKRETSRLAWALIEDKC 21	21609
ò	138	13	137
q	21610 EAQSY	EAQSYTAIKLINGNEYQFRVSAVNKFGVGRPLDSDPVVAQIQYTVPDAPGIPEPSNITGN 2)	21669
ò	138	17	137
g	21670 SITLT	SITLTWARPESDGGSEIQQYILERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEFH 2:	21729
ò	138	71	137
g	21730 VMAEN	VMAENAAGVGPASGISRLIKCREPVNPPGPPTVVKVTDTSKTTVSLEWSKPVFDGGMEII 2:	21789
ò	138	T	137
qq	21790 GYIIB	GYIIEMCKTDLGDWHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGÄGKGDSCEVTGTI 2:	21849
ò	138	1.	137
q	21850 KAVDR	KAVDRLTAPELDIDANFKQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHT 2:	21909
ò	138	7.	137
q	21910 TDSFS	TDSFSTLTVENCNRNDAGKYTLTVENNSGSKSITFTVKVLDTPGPPGPITFKDVTRGSAT 2	21969 ·
ò	138		137
qq	21970 LMWDA	LMWDAPLLDGGARIHHYVVEKREAŚRRSWQVISEKCTRQIFKVNDLAEGVPYYFRVSAVN 2:	22029
ò	138		137
g	22030 EYGVG	EYGVGEPYEMPEPIVATEQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQ 2	22089
ò	138	1	137
g	22090 KGSDL	KGSDLWVEAGHTKQLTFTVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVIIKEPQIEPT 2	22149
ò	138	1	137
q	22150 ADLTG	ADLTGITNQLITCKAGSPFTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLT 2	22209
ò	138	1	137
q	22210 VKDSM	VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGPVTGPIEVSSVSAESCVLSWGEPK 2	22269
ઠે	138	1	137
đ	22270 DGGGT	DGGGTEITNYIVEKRESGTTAWQLVNSSVKRTQIKVTHLTKYMEYSFRVSSENRFGVSKP 2	22329
ઠે	138	1	137
đ	22330 LESAF	LESAPIIAEHPFVPPSAPTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTIL 2	22389
õ	138	1	137
Q	22390 WVKEN	WVKENKVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPE 2	22449
ò	138	1	137
g	22150 VTDV1	VTDVTRSTVSLIWSAPAYDGGSKVVGYIIERKPVSEVGDGRWLKCNYTIVSDNFFTVTAL 2	22509
ò	138	1	137
g	22510 SEGD7	SEGDTYEFRVLAKNAAGVISKGSESTGPVTCRDEYAPPKAELDARLHGDLVTIRAGSDLV 2	22569
ò	138		137

g	22570 L	LDAAVGGKPEPKIIWTKGDKELDLCEKVSLQYTGKRATAVIKFCDRSDSGKYTLTVKNAS 22	6797
ò	138 -	13	37
셤	22630 G	GTKAVSVMVKVLDSPGPCGKLTVSRVTQEKCTLAWSLPQEDGGAEITHYIVERRETSRLN 22	2689
ò	138 -	13	37
g	22690 W	WVIVEGECPTLSYVVTRLIKNNEYIFRVRAVNKYGPGVPVESEPIVARNSFTIPSPPGIP 22	22749
ò	138 -	13	137
엄	22750 B	EEVGTGKEHIIIQWTKPESDGGNEISNYLVDKREKESLRWTRVNKDYVVYDTRLKVTSLM 22	22809
ò	138 -	13	137
qq	22810 E	EGCDYQFRVTAVNAAGNSEPSERSNFISCREPSYTPGPPSAPRVVDTTKHSISLAWTKPM 2%	22869
ò	138 .	27	137
g	22870 }	YDGGTDIVGYVLEMQEKDTDQWYRVHTNATIRNTEFTVPDLKMGQKYSFRVAAVNVKGMS 22	22929
ò	138 -	27	137
g	22930 E	EYSESIAEIEPVERIEIPDLELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQGID 2	22989
ò	138	17	137
임	22990 I	LASRAIIDTTESYSLLIVDKVNRYDAGKYTIEAENQSGKKSATVLVKVYDTPGPCPSVKV 2:	23049
ò	138	7	137
Q	23050 1	KEVSRDSVTITWEIPTIDGGAPINNYIVEKREAAMRAFKTVTTKCSKTLYRISGLVEGTM 2:	23109
ò	138	7	137
qq	23110	HYFRVLPENIYGIGEPCETSDAVLVSEVPLVPAKLEVVDVTKSTVTLAWEKPLYDGGSRL 2:	23169
ઠે	138	T	137
g	23170	TGYVLEACKAGTERWMKVVTLKPTVLEHTVTSLNEGEQYLFRIRAQNEKGVSEPRETVTA 2:	23229
ò	138	1.	137
g	23230	VTVQDLRVLPTIDLSTMPQKTIHVPAGRPVELVIPIAGRPPPAASWFFAGSKLRESERVT 2:	23289
ò	138	1	141
q	23290	VETHTKVAKLTIRETTIRDTGEYTLELKNVTGTTSETIKVIILDKPGPPTGPIKIDEIDA 2	23349
ò	142		141
g	23350 '	TSITISWEPPELDGGAPLSGYVVEQRDAHRPGWLPVSESVTRSTFKFTRLTEGNEYVFRV 2	23409
ò	142	1	141
g	23410	AATNRFGIGSYLQSEVIECRSSIRIPGPPETLQIFDVSRDGMTLTWYPPEDDGGSQVTGY 2	23469
ò	142	1	141
g	23470	IVERKEVRADRWVRVNKVPVTMTRYRSTGLTEGLEYEHRVTAINARGSGKPSRPSKPIVA 2	23529
ò	142	1	141
q	23530	MDPIAPPGKPQNPRVTDTTRTSVSLAWSVPEDEGGSKVTGYLIEMQKVDQHEWTKCNTTP 2	23589
ò	142	1	141
අ	23590	TKIREYTLTHLPQGAEYRFRVLACNAGGPGEPAEVPGTVKVTEMLEYPDYELDERYQEGI 2	23649
ò	142	1	141
g	23650	FVRQGGVIRLTIPIKGKPPPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYD 2	23709

ò	142	141	
q	23710	LVLENKCGKKAVYIKVRVIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADILGYILE 23769	
ò	142	141	
QQ	23770	RREVPKAAAWYTIDSRVRGTSLVVKGLKENVEYHFRVSAENQFGISKPLKSEEPVTPKTPL 23829	
ò	142	141	
g	23830	NPPEPPSNPPEVLDVTKSSVSLSWSRPKDDGGSRVTGYYIERKETSTDKVVRHNKTQITT 23889	
ò	142	141	
Q	23890	TMYTVTGLVPDAEYQFRIIAQNDVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKDS 23949	
ò	142	141	
g	23950	VTLQWEKPECDGGKEILGYWVEYRQSGDSAWKKSNKERIKDKQFTIGGLLEATEYEFRVF 24009	
ò	142	141	
임	24010	AENETGLSRPRRTAMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKW 24069	
ò	142	141	
g	24070	YRFGKELIQSRKYKMSSDGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATP 24129	
ò	142	141	
qq	24130	QFHPGYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHL 24189	
ò	142	141	
QQ	24190	VMKNVQRKTHAGKYKVQLSNVFGTVDAILDVEIQDKPDKPTGPIVIEALLKNSAVISWKP 24249	
ò	142	141	
qq	24250	PADDGGSWITNYVVEKCEAKEGAEWQLVSSAISVTTCRIVNLTENAGYYFRVSAQNTFGI 24309	
ò	142	141	
Q	24310	SDPLEVSSVVIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDGGAKIRNYYLEKREK 24369	
ò	142	141	
QQ	24370	) KONKWISVTTEEIRETVFSVKNLIEGLEYEFRVKCENLGGESEWSEISEPITPKSDVPIQ 24429	
ò	142	141	
QQ	24430	) APHFKEELRNLNVRYQSNATLVCKVTGHPKPIVKMYRQGKEIIADGLKYRIQEFKGGYHQ 24489	
ò	142	141	
g	24490	) LIIASVTDDDATVYQVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAVHALRGEVVS 24549	
ò	142	141	
q	24550	) IKIPPSGKPDPVITWQKGQDLIDNNGHYQVIVTRSFTSLVFPNGVERKDAGFYVVCAKNR 24609	
ò	142	141	
qq	24610	) FGIDQKTVELDVADVPDPPRGVKVSDASRDSVNLTWTEPASDGGSKITNYIVEKCATTAE 24669	
ò	142	141	
g	24670	) RWLRVGQARETRYTVINLFGKTSYQFRVIAENKFGLSKPSEPSEPTITKEDKTRAMNYDE 24729	
ò	142	2	
පු	24730	) EVDETREVSMTKASHSSTKELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKG 24789	

3 3	19 3178 PIPEGMAEAETIRITEILADAKTDDINGLAASQPTAASLAYVIFTSGSTGRPKGVMVEHR	GIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLLESTAL	Db 3358 NAYGPTENTVMSILPPALLKQCLDNSPALVKTLSVLYIGGDRLDASDAAKARGLVQTQAF 3357  Qy 19	. 19 3418	QY         19           Db         3478           IEPAEVEYALLSHDLVTDAAVVTHSQENQDLEMVGFVAARVADVREDESSNQVQEWQTHF         3537           OV         19	3538 DSIAYADITTIDQQSLGRDFMSWTSMYDGSLIKKSQMQEWLDDTMRSLLDSQPPCHVLEV	Db         3598         GTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGLEDRIRVEVGTATDIDRL 3657           Qy         19	37		Db 3958 RERLQTLLPAYMIPAQINVELDNLDFLTDHQGRPEEALTNHPLHRAQSRRVERQI 3957  Qy 19	19	19
F;12715-13159/Domain: acctate-CoA ligase homology <al10> F;13623-13690/Domain: acyl carrier protein homology <ac10> F;14213-14676/Domain: acyl carrier protein homology <ac11> F;14638-14765/Domain: acyl carrier protein homology <ac11> F;14638-14765/Domain: acyl carrier protein homology <ac11> F;1600.2558,4045,5537,7034,8094,9589,11086,12158,13654,14729/Binding site: phosphopanted Query Match 34.2%; Score 264; DB 2; Length 15281; Best Local Similarity 0.8%; Pred. No. 17; Batches 102; Conservative 24; Mismatches 21; Indels 12475; Gaps 32;</ac11></ac11></ac11></ac10></al10>	Qy 1 AAGGIL	AMDTGRLSALSPDLIVINSVAQYFPSREYLAEVVEALVRIPGVRRIFFGDMRTYATHKDF	Qy         7	2278 KVNNELSSYRYGAVLHIRNHNQNQSRSIHKINAESWIDFASSQMDRQGLARLLKENKDAE	DD 2338 SIAVFNIPYSKTIVERHIAKSLADDHDGDDTHSSIDGVAMISAAREKASQCFSLDVHDLV 2397  QY 12	Qy 12 11  Db 2458 LQRVESRRIEAQVREQLQVLLPAYMIPARIVVLQNMPLNTSGKVDRKELTLRAKVTAART 2517	PSSELVAPRDSIEAIICKEFKDVLGVEVGITDNFFNVGGHSLLATKLAARLSRQLNAQIA VKDIFDRPVIADLAATIQQDTTEHNPILPTSYTGPVEQSFAQGRLWFLDQLNVGATWYLM	Qy         12         11           Db         2638         PFAVRLRGPLVVSALAAALLALEERHETLRTTFIEQEGIGWQVIHPPAPKELRVIDVSGE         2697           Qy         12         11	Db 2698 EESTIQKILEKEQTTPFNLASEPGFRLALLKTGEDEHILSTVMHHAISDGWSVDIFQOEI 2757  Qy 1211  Db 2758 GQFYSAILRGHDPLAQIAPLSIQYRDFATWQRQIFQVAEHRRQLAYWTKQLADNKPAELL 2817	Qy         12         11           Db         2818         TDFKRPPMLSGRAGEIPVVVDGLIYEKLQDFCRIRQVTAFTVLLAAFRAAHYRMTGTEDA         2877           Qy         12         11	Db 2878 TIGTPIANRNRPELEGLIGFFVNTQCMRITVDVEDSFETLVHOVRETTLAAHANODVPFE 2937 Oy 12 11	Db 2938 QIVSNILPGSSDTSRNPLVQLMFALHSQQNLGKVRLEGIEBEIISIAETTRFDIEFHLYQ 2997  Qy 12 11  Db 2998 EAERLNGSIVYAADLFVPETIQSVITIFQGILQKGLGEPDMPVASMALDGGLESLRSTGL 3057

4138	ALTAALLALEKKHELLKITITTEQNGVGMQKVNFVVIETLKITULSNGUGUTLFTLKKEQT
19	18
4198	APFHLETEPGWRVALLRLGPGDYILSVVWHHIISDGWSVDVLFQELGQFYSTAVKGHDPL 4257
19	18
4258	SQTTPLPIHYRDFALWQKKPTQESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGQAG 4317
19	. 18
4318	EMSVTIEGALYKNLEEFCRVHRVTSFVVLLAALRAAHYRLTGSEDATIGTPIANRNRPEL 4377
19	
4378	4378 EQIIGFFVNTQCIRITVNEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDAS 4437
19	18
4438	4438 RNPLVQLMFAVHSQKNLGELKLENAHSEVVPTEITTRFDLEFHLFQQDDKLEGSILYSTD 4497
19	
4498	4498 LFEAVSVQSLLSVFQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSV 4557
19	18
4558	4558 VDVFHEQVSINPDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCE 4617
19	18
4618	4618 TIIAFLGILKANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVP 4677
19	18
4678	4678 IRDTFTTLTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMVQHRNIVRLVKNSNVV 4737
19	. 23
4738	4738 AKQPAAARIAHISNLAFDASSWEIYAPLLNGGAIVCADYFTTIDPQALQETFQEHEIRGA 4797
24	
4798	4798 MLPPSLLKQCLVQAPDMISRLDILFAAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILS 4857
24	23
4858	TIYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDGLARGYMDPKL 4917
24	
4918	4918 DADRFIQLTVNGSEQVRAYRTGDRVRYRPKDFQIEFFGRMDQQIKIRGHRIEPAEVEQAF 4977
24	23
4978	4978 LNDGFVEDVAIVIRTPENQEPEMVAFVTAKGDNSAREEEATTQIEGWEAHFEGGAYANIE 5037
24	EDT 26
5038	   EIESEALGYDFMGWTSMYDGTEIDKDEMREWLNDTMRSLLDGKPAGRVLEVGTGTGMIMF 5097
27	BRYV 30
5098	: 5098 NLGRSQGLERYIGLEPAPSAAEFVNNAAKSFPGLAGRAEVHVGTAADVGTLQGLTSDMAV 5157
31	30
5158	I INSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAMNRDFAAARAAYSLADNASKD 5217
31	0.000

ą	5218 RVRQKMMELBEKEEELLVDPAFFTALASQLQDRIQHVEILPKRMKATNELSSYRYAAVLH 52	2711
ò	31 30	_
ор	5278 ISDEPLPIYKIDPEAWINFEGSRLTREALAQVLKENENAESVAISNIPYSKTVVERHIVR 533	137
ò	31 30	_
q	5338 SLDQEDANAPEESMDGSDWISAVRTRAQQCHTLSASDLFDIAEDAGFRVEVSWARQHSOH 53	197
ò	31 33 31 33 33 33	_
QQ	5398 GALDAVFHHLKPATEDSRVLIKFPTDHQGRPLKSLTNQPLLPAQSRRAELLIREGLQTLL	5457
ò		_
qq	5458 PPYMIPSQITLIDRMPLNANGKVDRRELARRAKITQKSKPVEDIVPPRNSVEATVCKGFT	5517
ò	34 33	_
g	5518 DVLGVEVGITDNFFNLGGHSLMATKLAARLGRQLNTRISVRDVFDQPVVADLAAVIORNS	5577
ò	34 34 34 34 34 38	<b></b>
ą	5578 APHEPIKPADYTGPVPQSFAQGRLWFLDQLNVGATWYLMPLGIRLHGSLRVDALATAISA	5637
ò	39	œ
qq	5638 LEQRHEPLRTTFHEEDGVGVQVVQDHRPKDLRIIDLSTQPKDAYLAVLKHEQTTLFDLAT	5697
ò	39	<b>6</b> 0
q	5698 EPGWRVALIRLGEEEHILSIVWHHIISDGWSVEVLFDEMHRFYSSALRQQDPMEOILPLP	5757
ò	39	ω.
g	5758 IQYRDFAAWQKTEEQVAEHQRQLDYWTEHLADSTPAELLTDLPRPSILSGRANELPLTIE	5817
ò	39 38	m
ф	5818 GRLHDKLRAFCRVHQATPFVILLAALRAAHYRLTGAEDATLGTPIANRNRPELENMIGFF	5877
ò	39 38	<b>6</b> 0
q	5878 VNTQCMRIAIEENDNFESLVRRVRSTATSAFANQDVPFESIVSSLLPGSRDASRNPLVQV	5937
ò	39 38	œ
qq	5938 ILAVHSQQDLGKLTLEGLRDEAVDSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLRTI	5997
ò	39 38	80
qq	5998 ESVVSVFLETLRRALDQPLTPLAVLPLTDGVGEIASKGLLDVPRTDYPRDANIVEVFQQH	6057
ò	39	80
qq	6058 VRATPDAIAVKDATSILTYAQLDQQSDRLAIWLSRRHMMPETLVGVLAPRSCETIIAMFG	6117
ò	39	38
q	6118 IMKANLAYLPLDINSPAARLRSILSAVDGNKLVLLGSGVTAPEQENPEVEAVGIQEILAG	6177
ò	39	38
Q	6178 IGLDKTQGSNARPSATSLAYVIFTSGSTGKPKGVMVEHRSVTRLAKPSNVISKLPQGARV	6237
ò	39 38	ω,
g	6238 AHLANIAFDASIWEIATTLINGATLVCLDYHTVLDCRTLKEVFERESITVVTLMPALLKQ	6297
à	, 39	<b>6</b> 0

Ω	6298	CVAEIPETLAHLDLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTVISTIYEVDADE	6357	
>	99		38	
ء	6358 1	MFVNGVPIGKTVSNSGAYVMDRNQQLVPSGVVGELVVTGDGLARGYTDPSLNKNRF1Y1T	6417	
>	9.6		38	
Ω	6418	VNGESIRAYRTGDRVRYRPHDLQIEFFGRMDQQVKIRGHRIEPGEVESALLSHNSVQDAA	6477	
>	39		38	
Д	6478	VVI CAPADQDSGAEMVAFVAARNTEDEDTQEEEAVDQVQGWETHFETAAYSEVKDIRQSE	6537	
>	39	2	38	
Q	6538	VGNDFMGWTSMYDGSEIDKTDMHEWLNDTWRMILDAREPGHVLEIGTGTGMVMFNLAKCP	6597	
<u>≻</u>	39		38	
Ω	6598	GLQGYVGFEPSKSAAQFVNDAAQSFPALKDGRSIVHVGTATDINKAGPIQPRLVVINSVA	6657	
	39		38	
۵	6658	QYFPTPEYLFRVVEALVQIPSVERIVFGDMRTNAINRDFVASRALHTLGEKANKRLVRQM	6717	
ج _	39	BLLRDPS	45	
۵	6718		6777	
<u>~</u>	46		45	
ð	6778	<b>EQSTIHQVSPNAWIDFAADGLDRQTLINLLKEHKDAGTVAIGNIPYSKTIVERFVNKSLS</b>	6837	
≿	46.		45	
۵	6838	EDDMEEGQNSLDGSAWVAAVRMAAQSCPSLDAMDVKEIAQEAGYQVEVSWARQWSQNGAL	6897	
≿	46	OV971		
a	6898	DAIFHHFEPPKEGARTLIEFPTDYEGRNVNTLTNRPLNSIQSRRLGTQIREKLQTLLPPY	6957	
⋧	20		49	
ð	6958	MI PSRIMVLDQMPVNNNGKI DRKELVRRAI VAPKPRSAATRVAPRNEI EAI LRDEFEDVL	, 7017	
ጵ	20		49	
႙	7018	GTEVSVLDNFFDLGGHSLMATKLAARVSRRLDAHISIKDVFDOPVLADLAASIQRESAPH	7077	
à	50		49	
අ	7078	EPIPORPYTGPAEOSFAQGRLWFLDQLNLGATWYLMPLAIRIRGQLRVAALSAALFALER	1 7137	
તે	20		. 49	
g	7138	RHETLRTTFEESDGVGVQIVGEARNSDLRVHDVSTGDDGEYLEVLRREQTVPFDLSSEPG	3 7197	
à	20	FRUHLUK	. 56	
8	7198	  WRVCLVKTGEEDHVLSIVMHHIIYDGWSVDILRGELGQFYSAALRGQDPLLHANPLPIQY	1257	
ò	5.7		- 56	
a	7258	RDFAAWQREAKQVEEHQRQLGYWSKQLVDSTPAELLTDLPRPSILSGRAGSVDVTIEGSV	7317	
ò	57		- 61	
8	7318	YGALQSFCRTRSVTTFVVLLTVFRIAHFRLTAVDDATIGTPIANRNRPELETLVGCFVNT	r 7377	
ò	62		- 61	
g	7378	QCMRISIADDDNFEGLVRQVRNVATAAYANQDVPFERIVSALVPGSRNTSRNPLVQLMFA	A 7437	

ò	62	61
g	7438	VQSVEDYDQVRLEGLESVAMPGEASTRFDMEFHLVPGDQKLTGSVLYSSDLFEQGTIQNF 7497
ò	62	61
පු	7498	VDIFQECLRSVLDQPLTPISVLPFSNAISNLESLDLLEMPTSDYPRDRTVVDLFREQAAI 7557
ò	62	
g	7558	CPDSIAVKDSSSQLTYAQLDEQSDRVAAWLHERHMPAESLVGVLSPRSCETIIAYFGIMK 7617
ò	62	61
g	7618	ANLAYLPLDVYAPDARLAAILDTVEGERLLLLGAGVPQPGIQIPRLSTAYIAEALSHATT 7677
ò	62	65 6PBG 65
q	7678	VDVTSIPQPSATSLAYVIFTSGSTGKPKGVMIEHRGIVRLVRDTNVNVFPESGSALPVSH 7737
ò	99	59
q	7738	FSNLAWDAATWEIYTAVLNGGTVVCIDRDTMLDIAALNSTFRKENVRAAFFTPAFLKQCL 7797
ò	99	APNITANL
qq	7798	AETPELVANLEILHTAGDRLDPGDANLAGKTAKGGIFNVLGHTENTAYSTFYPVVGEETF 7857
ò	74	73
QQ	7858	VNGVPVGRGISNSHAYIIDRHQKLVPAGVMGELILTGDGVARGYTDSALNKDRFVYIDIN 7917
ò	74	73
q	7918	GKSTWSYRTGDKARYRPRDGQLEFFGRMDQMVKIRGVRIEPGEVELTLLDHKSVLAATVV 7977
ò	74	73
οp	7978	VRRPPNGDPEMIAFITIDAEDDVQTHKAIYKHLQGILPAYMIPSHLVILDQMPVTDNGKV 8037
ઠે	74	73
g	8038	DRXDLALRAQTVQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEVGITDGFFDLGGHSLLA 8097
ò	74	73
පු	8098	TKLAARLSRQLNTRVSVKDVFDQPILADLADIIRRGSHRHDPIPATPYTGPVEQSFAQGR 8157
ò	74	73
a	8158	LWFLEQLNLGASWYLMPFAIRMRGPLQTKALAVALNALVHRHEALRTTFEDHDGVGVQVI 8217
ઠે	74	73
qq	8218	QPKSSQDLRIIDLSDAVDDTAYLAALKREQTTAFDLTSEPGWRVSLLRLGDDDYILSIVM 8277
ò	74	73
g	8278	HHIISDGWTVDVLRQELGQFYSAAIRGQEPLSQAKSLPIQYRDFAVWQRQENQIKEQAKQ 8337
ò	74	73
g	8338	LKYWSQQLADSTPCEFLTDLPRPSILSGEADAVPMVIDGTVYQLLTDFCRTHQVTSFSVL 8397
ò	74	23
g	8398	LAAFRTAHYRLIGTLDATVGTPIANRNRPELEGLIGFFVNTQCMRMAISETETFESLVQO
ò	74	23
QQ	8458	VRLTTTEAFANQDVPFEQIVSTLLPGSRDTSRNPLVQVMFALQSQQDLGRIQLEGMTDEA 8517

⋩	74	73
ą	8518	LETPLSTRLDLEVHLFQEVGKLSGSLLYSTDLFEVETIRGIVDVFLEILRRGLEQPKQRL 8577
à	74	. 73
ą	8578	MAMPITDGITKLRDQGLLTVAKPAYPRESSVIDLFRQQVAAAPDAIAVWDSSSTLTYADL 8637
à	74	73
ą	8638	DGQSNKLAHWLCQRNMAPETLVAVFAPRSCLTIVAFLGVLKANLAYLPLDVNAPAARIEA 8697
à	74	73
ą	8698	ILSAVPGHKLVLVQAHGPELGLTMADTELVQIDEALASSSSGDHEQIHASGPTATSLAYV 8757
ጵ	74	
ę,	8758	MFTSGSTGKPKGVMIDHRSIIRLVKNSDVVATLPTPVRMANVSNLAFDISVQEIYTALLN 8817
à	74	73
g	8818	GGTLVCLDYLTLLDSKILYNVFVEAQVNAAMFTPVLLKQCLGNMPAIISRLSVLFNVGDR 8877
à	74	73
g	8878	LDAHDAVAASGLIQDAVYNAYGPTENGMQSTMYKVDVNEPFVNGVPIGRSITNSGAYVMD 8937
ઠે	74	73
g	8938	GNQQLVSPGVMGEIVVTGDGLARGYTDSALDEDRFVHVTIDGEENIKAYRTGDRVRYRPK 8997
· &	74	73
q	8668	DFEIEFFGRMDQQVKIRGHRIEPAEVEHALLGHDLVHDAAVVLRKPANQEPEMIAFITSQ 9057
ò	74	73
셤	9028	EDETIEQHESNKQVQGWGEHFDVSRYADIKDLDTSTFGHDFLGWTSMYDGVDIPVNEMKE 9117
ò	74	15.11.1
g G	9118	:         WLDETTASLLDNRPPGHILEIGAGTGMILSNLGKVDGLQKYVGLDPAPSAAIFVNEAVKS 9177
ò	79	18
q	9178	LPSLAGKARVLVGTALDIGSLDKNEIQPELVVINSVAQYFPTSEYLIKVVKAVVEVPSVK 9237
ò	79	18
g	9238	RVFFGDIRSQALNRDFLAARAVRALGDNASKEQIREKIAELEESEEELLVDPAFFVSLRS 9297
ò	79	18
පු	9298	QLPNIKHVEVLPKLMKATNELSSYRYAAVLHISHNEEEQLLIQDIDPTAWVDFAATQKDS 9357
ઠે	79	SVC 81
පු	9358	QGLRNLLQQGRDDVMIAVGNIPYSKTIVERHIMNSLDQDHVNSLDGTSWISDARSAAAIC 9417
ò	82	81
g	9418	TSFDAPALTQLAKEEGFRVELSWARQRSQNGALDAVFHRLATDANCERSRVLVHFPTDHO 9477
ò	82	81
qq	9478	GRQLRTLTNRPLQRAQSRRIESQVFEALQTALPAYMIPSRIIVLPQMPTNANGKVDRKQL 9537
ò	82	81
Q	9538	arraqvvakkkavsarvaprndteivlceeyadilgtevgitdnffdmgghslmatklaa 9597
ò	82	81

g	9598	RLSRRLDTRVTVKEVFDKPVLADLAASIEQGSTPHLPIASSVYSGPVEQSYAQGRLWFLD 965
ò	82	81
qq	9658	QFNLNATWYHMSLAMRLLGPLNMDALDVALRALEQRHETLRTTFEAQKDIGVQVVHEAGM 971
ò	82	θ1
qq	9718	KRLKVLDLSDKNEKEHMAVLENEQMRPFTLASEPGWKGHLARLGPTEYILSLVMHHMFSD 977
ò	82	GWS
g	9778	  GWSVDILRQELGQFYSAALRGRDPLSQVKPLPIQYRDFAAWQKEAAQVAEHERQLAYWEN 9837
ò	85	88
QQ	9838	QLADSTPGELLTDFPRPQFLSGKAGVIPVTIEGPVYEKLLKFSKERQVTLFSVLLTAFRA 989
ò	85	84
q	9898	THFRLTGAEDATIGTPIANRNRPELEHIIGFFVNTQCMRLLLDTGSTFESLVQHVRSVAT 995
ò	85	84
q	9958	DAYSNQDIPFERIVSALLPGSRDASRSPLIQLMFALHSQPDLGNITLEGLEHERLPTSVA 10017
ò	85	98
gg	10018	TRFDMEFHLFQEPNKLSGSILFADELFQPETINSVVTVFQEILRRGLDQPQVSISTMPLT 1007
ò	8	88
С	10078	DGLIDLEKLGLLEIESSNFPRDYSVVDVFRQQVAANPNAPAVVDSETSMSYTSLDQKSEQ 1013
ò	89	06
q	10138	IAAWLHAQGLRPESLICVWAPRSFETIVSLFGILKAGYAYLPLDVNSPAARIQPILSEVE 101
ò	91	06
q	10198	GKRLVLLGSGIDMPQSDRMDVETARIQDILTNTKVERSDPMSRPSATSLAYVIFTSGSTG 102
ò	91	06
g	10258	RPKGVMIEHRNILRLVKQSNVTSQLPQDLRMAHISNLAFDASIWEIFTAILNGGALICID 1031
ò	91	06
q	10318	YFTLLDSQALRTTFEKARVNATLFAPALLKECLNHAPTLFEDLKVLYIGGQBLDATDAAK 103
ò	91	06
qq	10378	IQALVKGTVYNAYGPTENTVMSTIYRLTDGESYANGVPIGNAVSSSGAYIMDQKQRLVPP 104
ò	91	06
qq	10438	GVMGELVVSGDGLARGYTNSTLNADRFVDIVINDQKARAYRTGDRTRYRPKDGSIEFFGR 10.
ò	91	06
đ	10498	MDQQVKIRGHRVEPAEVEQAMLGNKAIHDAAVVVQAVDGQETEMIGFVSMASDRFSEGEE 105
ò	91	03 10DT 93
qq	10558	EITNQVQEWEDHFESTAYAGIEAIDQATLGRDFTSWTSMYNGNLIDKAEMEEWLDDTMQS
ò	94	66
පු	10618	ILLDKEDARPCAEIGTGTGMVLFNLPKNDGLESYVGIEPSRSAALFVDKAAQDFPGLOGKT 10
ò	94	66 63

۾	10678	QILVGTAEDIKLVKDFHPDVVVINSVAQYFPSRSYLVQIASELIHMTSVKTIFFGDMRSW	10737
≿	94	DP	95
۵	10738	ATNRDFLVSRALYTLGDKATKDQIRQEVARLEENEDELLVDPAFFTSLTSQWPGKVKHVE	10797
≥.	96		95
۵	10798	ILPKRMRTSNELSSYRYAAVLHICRDGEGRNRYGRRVHSVEENAWIDFASSGMDRHALVQ	10857
≿	96		95
ą	10858	MLDERRDAKTVAIGNI PHSNTINERHFTTSLDTEGEGIAQDSLDGSAWQSATKAMAARCP	10917
≿	96		95
۵	10918	CLSVTELVEIGQAAGFRVEVSWARQRSQHGALDVVFHHLEDDRVGRVLINFPTDFERLPP	10977
≿	96		95
ø.	10978	STGLTSRPLQRIQNRRFESQIREQLQTLLPPYMVPSRIVVLERMPLNANSKVDRKELARK	11037
≿	96		97
ð	11038	ARTLQTIKPSATRVAPRNDIEAVLCDEFQAVLGVTVGVMDNFFELGGHSLMATKLAARLS	11097
à	96		101
ð	11098	RRLDTRVSVKDIFNQPILQDLADVVQTGSAPHEAIPSTPYSGPVEQSFSQGRLWFLDQLN	11157
≿	102		101
ą	11158	LNASWYHMPLASRLRGPLRIEALQSALATIEARHESLRTTFEEQDGVPVQIVRAARNKQL	11217
≿	102		101
ą	11218	RIIDVSGTEDAYLAALKQEQDAAFDLTAEPGWRVALLRLGPDDHVLSIVWHHIISDGWSV	11277
à	102	Ι.Ι.	103
ရ	11278	DILROELGOLYSNASSQPAPLPIQYRDFAIWQKQDSQIAEHQKQLNYWKRQLVNSKPAEL	11337
à	104		103
g	11338	LADFTRPKALSGDADVIPIEIDDQVYQNLRSFCRARHVTSFVALLAAFRAAHYRLTGAED	11397
તે	104		103
8	11398	ATIGSPIANRNRPELEGLIGCFVNTQCLRIPVKSEDTFDTLVKQARETATEAQDNQDVPF	11457
તે	104		111
g	11458	ERIVSSMVASSRDTSRNPLVQVMFAVHSQHDLGNIRLEGVEGKPVSMAASTRFDAEMHLF	11517
ò	112		111
요	11518	EDOGMLGGNVVFSKDLFESETIRSVVAVFQETLRRGLANPHANLATLPLTDGLPSLRSLC	11577
ò	112	- Carlo	113
g	11578	   LQVNQPDYPRDASVIDVFREQVASIPKSIAVIDASSQLTYTELDERSSQLATWLRRQVTV	11637
ò	114	GNRQV	118
ਰ.	11638	PEELVGVLAPRSCETIIAFLGIIKANLAYLPLDVNAPAGRIETILSSLPGNRLILLGSDT	11697
ò	119	E	119
g	11698	9 QAVKLHANSVRFTRISDALVESGSPPTEELSTRPTAQSLAYVMFTSGSTGVPKGVMVEHR	11757
ò	120		122
g	11758	:     GITRLVKNSNVVAKQPAAAAIAHLSNIAFDASSWEIYAPLLNGGTVVCIDYYTTIDIKAL	11817

ò	123		122
g	11818	eavekqhhirgamlppallkoclvsaptmissleilfaagdrissqdailarravgsgvy	11877
ά	123		122
q	11878	NAYGPTENTVLSTIHNIGENEAFSNGVPIGNAVSNSGAFVMDQNQQLVSAGVIGELVVTG	11937
ò	123		122
qq	11938	DGLARGYTDSKLRVDRF1Y1TLDGNRVRAYRTGDRVRHRPKDGQ1EFFGRMDQQ1K1RGH	11997
ò	123		122
g	11998	RIEPAEVEQALARDPAISDSAVITQLTDEEEPELVAFFSLKGNANGTNGVNGVSDQEKID	12057
ò	123		122
QQ	12058	GDEQHALLMENKIRHNLQALLPTYMI PSRI IHVDOLPVNANGKI DRNELAVRAQATPRTS	12117
ò	123		122
g	12118	SVSTYVAPRNDIETIICKEFADILSVRVGITDNFFDLGGHSLIATKLAARLSRRLDTRVS	12177
ò	123		122
QQ	12178	VRDVFDTPVVGQLAAS1QQGSTPHEA1PALSHSGPVQQSFAQGRLWFLDRFNLNAAWYIM	12237
ò	123		122
g	12238	PFGVRLRGPLRVDALQTALRALEERHELLRTTFEEQDGVGMQIVHSPRMRDICVVDISGA	12297
ò	123		122
g	12298	NEDLAKLKEEQQAPFNLSTEVAWRVALFKAGENHHILSIVWHHIISDGWSVDIFQQELAO	12357
ò	123		122
g	12358	FYSVAVRGHDPLSQVKPLPIHYRDFAVWQRQDKQVAVHESQLQYWIEQLADSTPAEILSD	12417
ò	123		122
g	12418	FNRPEVLSGEAGTVPIVIEDEVYEKLSLFCRNHQVTSFVVLLAAFRVAHYRLTGAEDATI	12477
ઠે	123		122
g	12478	GTPIANRNRPELEDLIGFFVNTQCMRIALEHDNFLSVVRRVRSTAASAFENQDVPFERL	12537
ò	123	2	122
QQ	12538	VSALLPGSRDASRNPLVQLMFVVHSQRNLGKLQLEGLEGEPTPYTATTRFDVEFHLFEQD	12597
ò	123		122
q	12598	KGLAGNVVFAADLFEAATIRSVVEVFHEILRRGLDQPDIAISTMPLVDGLAALNSRNLPA	12657
ò	123		122
q	12658	VEDIEPDFATEASVVDVFQTQVVANPDALAVTDTSTKLTYAELDQQSDHVAAWLSKQKLP	12717
ò	123		122
g	12718	AESIVVVLAPRSSETIVACIGILKANLAYLPMDSNVPEARRQAILSEIPGEKFVLLGAGV	12777
ò	123		122
q	12778	PIPDNKTADVRMVFISDIVASKTDKSYSPGTRPSASSLAYVIFTSGSTGRPKGVMVEHRG	12837
ò	123		122
g	12838	VISLVKQNASRI PQSLRMAHVSNLAFDASVWEI FTTLLNGGTLFCI SYFTVLDSKALSAA	12897

121 122	
	Db 13978 GTPIANRNRPELENLIGCFVNTQCMRITIGDDETFESLVQQVRSTTATAFENQDVPFEK1 14037
UD 12898 FSDHKINIIELFFFALLKULLAUAFSVLSSEESLIIGGUKEUGAUAINVNLLVAKAIMAI 12937	Qy 137 144
Oy 123 122	Db 14038 VSTLSAGSRDTSRNPLVOLLFAVHSOOGLGRIQLDGVVDEPVLSTVSTRFDLEFHAFQEA 14097
Db 12958 GPTENSVMSTIYTIEHETFANGVPIGTSLGPKSKAYIMDQDQQLVPAGVMGELVVAGDGL 13017	145
Qy 123 122	-
Db 13018 ARGYIDPSLNTGRFIHITIDGKQVQAYRTGDRVRYRPRDYQIEFFGRLDQQIKIRGHRIE 13077	2 P. C. C. C. C. C. C. C. C. C. C. C. C. C.
Oy 123 122	-
Db 13078 PAEVEQALLSDSSINDAVVVSAQNKEGLEMVGYITTQAAQSVDKEEASNKVQEWEAHFDS 13137	27 CALL
Oy 123 122	TWVAVLA PRSCETI I A FLAILKANLA YMPLDVNT PSARMEAII SSVPGRRLILVGSGVRH
Db 13138 TAYANIGGIDRDALGQDFLSWTSMYDGSLIPREEMQEWLNDTWRSLLDNQPPGKVLEIGT 13197	145
Qy 123 122	-
Db 13198 GTGMVLFNLGKVEGLQSYAGLEPSRSVTAWVNKAIETFPSLAGSARVHVGTAEDISSIDG 13257	145
Qy 123 122	14
Db 13258 LRSDLVVINSVAQYFPSREYLAELTANLIRLPGVKRIFFGDMRTYATNKDFLVARAVHTL 13317	145
Qy 123 122	14
Db 13318 GSNASKAMVRQQVAKLEDDEEELLVDPAFFTSLSDQFPDEIKHVEILPKRMAATNELSSY 13377	145
Qy 123122	14458
Db 13378 RYAAVIHVGGHQMPNGEDEDKQWAVKDINPKAWVDFAGTRMDRQALLQLLQDLQDRQRGDDVV 13437	145
Qy 123 122	1
Db 13438 AVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAWISRTQSRAKECPALSVADLIEIGKG 13497	145
Qy 123 122	7
Db 13498 IGFEVEASWARQHSQRGGLDAVFHRFEPPRHSGHYMFRFPTEHKGRSSSSLTNRPLHLLQ 13557	1.5
Qy 123 122	,
Db 13558 SRRLEAKVRERLQSLLPPYMIPSRITLLDQMPLTSNGKVDRKKLARQARVIPRSAASTLD 13617	145GVT 147
Qy 123 126	:   :  TISVXV2:ITTEREDICTERETER 00511
Qy 127 126	RESULT 3
Db 13678 FDQPVLADLAASILQGSSRHRSIPSLPYEGPVEQSFAQGRLWFLDQFNIDALWYLIPFAL 13737	130132 probable peptide synthetase - Aureobasidium pullulans C.soacias: aureobasidium mullulans
Oy 127 126	C; Date: 02.5ep-2000 #sequence_revision 02.5ep-2000 #text_change 17-Nov-2000
Db 13738 RMRGPLQVDALAAALVALEERHESLRTTFEERDGVGIQVVQPLRTTKDIRIIDVSGMRDD 13797	R; Petry R.B.; Thornewell, S.J.; Tobin, M.B.; Skatrud, P.L.
Oy 127 ACSPTW	A) Description: Discovery of an MDR-like gene adjacent to a peptide synthetase in Aure
Db 13798 DAYLEPLQKEQQTPFDLASEPGWRVALLKLGKDDHILSIVMHHIISDGWSTEVLQRELGQ 13857	A; Accession: T30192 A; Accession: T30192 A; Crans indiano: translared from GB/EMBL/DDBJ
Qy 133 132	Molecule type: DNA
Db 11858 FYLAAKSGKAPLSQVAPLPIQYRDFAVWQRQEEQVAESQRQLDYWKKQLADSSPAELLAD 11917	A; Crossacros EmBL: U85909; NID: 94099310; PID: 94099313; PIDN: AAD00581.1
0γ 133	A; Introne: 2078/3; 4142/3; 6075/3; 7963/3; 7985/2 C:Superfamily: acvl carrier protein homology
Db 13918 YTRPNVLSGEAGSVSFVINDSVYKSLVSFCRSRQVTTFTTLLAAFRAAHYRMTGSDDATI 13977	<acp1< td=""></acp1<>
Oy 133SCLISCLI	cyı

F; 5615 F; 7503 F; 9683	15-5685/Domain: )3-7573/Domain: )3-9752/Domain:	omain: acyl carrier protein homology <acp3> omain: acyl carrier protein homology <acp4> omain: acyl carrier protein homology <acp5></acp5></acp4></acp3>
Mat	Query Match Best Local ( Matches 94	h Similarity 1.1%; Pred. No. 55; 94; Conservative 27; Mismatches 27; Indels 8749; Gaps 30;
ò	1 AAG	8
qq	111 575 AAG	 AAGLDSLRAIQVASQLRRQGCADLGALELLSVSNVLALDELVRAKADESNINDNDSEKWK 634
ò	4	
g	635 QTV	OTVHELRSSVERDFESKAFVSGIEDVLPCTPLQDAMLVETAKRPQAYCNELRLTVSPKIP 694
ò	4	C
S S	695 VER	VERVRQALFALAQRHTALRSGFMPSGVSHCAYTQVIWKTLVTSQFAHVKSFTTGWSVTNR 754
ò	8	13
g	755 ETL	:    ETLLRPLHFQYKCSGAEAEILVAIHHALYDQMSVEVILEDLETLLQNERTPERPSFGAVN 814
ò	14	13
g	815 KFF	KFFNLRRSEDQTSHLDFWGEYLSDVTPGRLPNLSPKMMPPQPLQSIQHTIEMDMETLRQA 874
ò	14	VGP 16
g	875 AHS	AHSYSCSAHVFFQAAYAILLGFYMGTEDTVFGTVFSGRTLPIVEIESMVGPLLSTLPTRI 934
ò	17	pyPQAHQEp 25
g	935 NTL	   II
ò	26	25
g	995 RAQ	RAQTILINLVEAHDYLEFNLTLELEPTQQGVKTKATYQSSLLPLQHVKTLLQQLDALVKIV 1054
ò	26	25
g	1055 VAR	VARPETHMNEISDQLPISVLSVANSEPQSFVYKAGLGSLVENHALNNSGGLALVFAHDIR 1114
ò	26	
g	1115 EGT	EGTSRMESLTYGELNTRANQLANYLISQGAKRDELICVCMEKSVSLYLSILAAVKAGCGY 1174
ò	26	
g G	1175 LPL	LPLVPETPAARIRQILAEADVKFCLTDSSMAPVIADVSRCHIMNVDTTDCSAQSCTGPQL 1234
ò	26	36 36
g	1235 DFK	DFKPTDIAYAVFTSGTTGKPKGVLVTQENILSNLEVLSKIYPVPEGSRLLQACNQAFDVS 1294
ò	37	36
g	1295 VFE	EIFFTWYTGMCLCSASKDVMFRDFEKAINELEITHLSLTPTVAALTDPAHIPRVKFLV 1354
ò	37	
a	1355 TAC	TAGEAVTHHVHGAWAGKGLYQGYGPSETTNICTVNSAVESDHVINNIGPAFENTSAFVLT 1414
ઠે	37	. 36
셤	1415 QGE	QGDDFQLVPLGGLGELCFGGQQVFRGYQNMPELTESKIINHPNYGRIYRSGDLGRLLPDG 1474
ò	37	36
đ	1475 TII	TILIQGRTDDQRKIRGQRIELGEISGCLLQFPSVQNCAIEVIKTADKERLMAFWIPSGYS 1534
ò	37	36

q	1535 KDSYSILQPDKNLEEIIKSIYAHLADNLPAYMVPDALVPVSAIPQTSQGKIDKRRLASDG	JG 1594
ò	37	36
q	1595 SALTVEDLNAYSRGADDDETSELSATEQQLASALADTLQMSQTSIGRSTSFFALGLDSVS	VS 1654
ò	37	36
qq	1655 AIRLATNLRKEYGYSIDVSQILKRPTIARLAPLLGGESSKQTNEPVTADCEAAVGSY	LHD 1714
ò	37	36
р	1715 ESVVSQLHEHGQTVSQVLPCTPLQEAMLSARDTSGSSAYRNKTLFSLHGSVDKLKACWEV	EV 1774
ò	37	36
qq	1775 MLQRHDILRTIFLSTEDSRFPFVQAVLSOWTLPWQECDDIPDQLSTLLDSAKAGGDSIVD	VD 1834
ò	37	36
q	1835 HSPPWKIQVYRSESTVYLLLDWHHALYDANAMSNLLYEVEQLYKDQSLSAPVSFKPFLNF	NF 1894
ò	37	36
අු	1895 MISTSVEEADALFRDQLREFVPKPFKRTDVKSGFGTITGRLNYSPKMVETFLSKHSTTML	ML 1954
ò	37	36
QQ	1955 SLTQAMWMKTLAASQSYSDVCCGNVVSGRSVPVDGIESLVAPCFNTIPVRVDLSKHRSNL	NL 2014
ò	37	36
g	2015 GLVKALQRVNIDSLPYQLTPLRRIQAQAGTNGKRLFDSLVLLQQDTTDLDSAIWRLEGE	ES 2074
ò	37GAELLRD	43
q	2075 GVMDMDETLSILNPLPTLLEGPELLHELISGPETSGTALEYLDADGKTITLSYLDLHRRS	RS 2134
ò	,	43
g	2135 EHLAWRLIEVSRHISRKDLGIVPIYIPQCISLYISQLAILKSGAAFCPLNLDVPGERLKF	KF 2194
ò		43
qq	2195 ILKDTSASILLTTAAMRPKLPELEGITVIVVDDELSEFKSDREPAGEKITSPDTSSLAYI	YI 2254
ò		43
QQ	2255 MYTSGSTGLPKAVCLSHRAVTQSLLAHDRPIPSFSRFLQFASPTFDVSVF <b>GI</b> FFPWYRGA	GA 2314
ò		43
đ	2315 TLVSVERNRLLGDLPGTITSLNIDAAELTPSVAASLVRHRENVPTLRALLTIGEMLNTQV	'QV 2374
ò	44	43
q	2375 IQQFGGSIGKSGILYGMYGPTEAAIHCTLQPGFGVDLPAGTIGIPLDTVSCFIVKPTEST	ST 2434
ò	/ 44PSLGAOFR	51
б	2435 KHASQLEILPIGEIGELVIGGHQLADGYLNREEQTRAAFVTHPKFGGLYRTGDKARLHRN	IRN 2494
ò	, 52	51
q	2495 GTLECYGRISSGQVKLRGQRVELGEIEHAASKAGGCHAVIASVISGLLVLFCIGDPHRVS	NS 2554
ò		51
අ	O 2555 SKDIKSACQKWLPAYMIPSDIVLLDDFPYLPSGKVDKKRLETDYNSNTAQHVSGSSDLS	SE 2614
ò	۴ 52	51

ą	2615	NAREITRIIESVLGVSIDHSTDLSAAGLDSLRAIQVASQLRRQGCADLGALELLSVSNVL	2674
à	52	HV.	53
ą	2675	ALDELVRAKADESNINDNDSEKWKQTVHELRSSVERDFESKAFVSGIEDVLPCTPLQDAM	2734
à	54		53
g	2735	LVETAKRPQAYCNELRLTVSPKI PVERVRQALFALAQRHTALRSGFMPSGVSHCAYTQVI	2794
ò	54		53
8	2795	WKTLVTSQFAHVKSFTTGWSVTNRETLLRPLHFQYKCSGAEAEILVAIHHALYDQWSVEV	2854
ò	54	•	53
g	2855	ILEDLETLLQNERTPERPSFGAVNKFFNLRRSEDQTSHLDFWGEYLSDVTPGRLPNLSPK	2914
ò	54		53
q	2915	MMPPQPLQSIQHTIEMDMETLRQAAHSYSCSAHVFFQAAYAILLGFYMGTEDTVFGTVFS	2974
ò	54		. 23
g	2975	GRTLP1VEIESMVGPLLSTLPTRINTLESRKFSDVLSRLQEDNRKIMRHSMTSLADIKKA	3034
ò	8.		53.
a	3035	CGFNPGEAVFDSIFVWQETARPDARAQTLLNLVEAHDYLEFNLTLELEPTQQGVKTKATY	3094
ò	54		59
엄	3095		3154
ò	9		59
යු	3155	GSLVENHALNNSGGLALVFAHDIREGTSRMESLTYGELNTRANQLANYLISQGAKRDELI	3214
ò	9		62
q	3215	CVCMEKSVSLYLSILAAVKAGCGYLPLVPETPAARIRQILAEADVKFCLTDSSMAPVIAD	3274
ò	63		62
Q	3275	VSRCHIMNVDTTDCSAQSCTGPQLDFKPTDIAYAVFTSGTTGKPKGVLVTQENILSNLEV	3334
ò	63		99
qq	3335	: LSKIYPVPEGSRLLQACNQAFDVSVFEIFFTWYTGMCLCSASKDVMFRDFEKAINELEIT	3394
à	67		73
gg	3395	HLSLTPTVAALTDPAHIPRVKFLVTAGEAVTHHVHGAWAGKGLYQGYGFSETTNICTVNS	3454
ò	74		73
QQ	3455	AVESDHVINNIGPAFENTSAFVLTQGDDFQLVPLGGLGELCFGGQQVFRGYQNMPELTES	3514
ò	74		73
g	3515	KIINHPNYGRIYRSGDLGRLLPDGTILIQGRTDDQRKIRGQRIELGEISGCLLQFPSVQN	3574
ò	74		73
g	3575	. CAIEVIKTADKERLMAFWIPSGYSKDSYSILQPDKNLEEIIKSIYAHLADNLPAYMVPDA	3634
ò	74		73
g	3635	. LVPVSAI PQTSQGKI DKRRLASDGSALTVEDLNAYSRGADDDETSELSATEQQLASALAD	3694
ò	74		73
8	3692	; TLQMSQTSIGRSTSFFALGLDSVSAIRLATNLRKEYGYSIDVSQILKRPTIARLAPLLGG	3754

ò	74	66
q	3755	ESSKQTNEPVTADCEAAVGSYLHDESVVSQLHEHGQTVSQVLPCTPLQEAMLSARDTSGS 3814
ò	74	73
q	3815	SAYRNKTLFSLHGSVDKLKACWEVMLQRHDILRTIFLSTEDSRFPFVQAVLSQWTLPWQE 3874
ò	74	73
q	3875	CDDIPDQLSTLLDSAKAGGDSIVDHSPPWKIQVYRSESTVYLLLDMHHALYDANAMSNLL 3934
ò	74	73
g	3935	YEVEQLYKDQSLSAPVSFKPFLNFMISTSVEEADALFRDQLREFVPKPFKRTDVKSGFGT 3994
ò	74	73
g	3995	ITGRLNYSPKMVETFLSKHSTTMLSLTQAMWMKTLAASQSYSDVCCGNVVSGRSVPVDGI 4054
ò	74	73
q	4055	ESLVAPCFNTIPVRVDLSKHRSNLGLVKALQRVNIDSLPYQLTPLRRIQAQAGTNGKRLF 4114
ò	74	73
qq	4115	DSLVLLQQDTTDLDSAIWRLEGESGVMDMRPKLPELEGITVIVVDDELSEFKSDREPAGE 4174
ò	74	76
g	4175	
ò	77	9.2
q	4235	SVFEIFFPWYRGATLVSVERNRLLGDLPGTITSLNIDAABLTPSVAASLVRHRENVPTLR 4294
ò	77	16
g	4295	ALLTIGEMLNTQVIQQFGGSIGKSGILYGMYGPTEAAIHCTLQPGFGVDLPAGTIGIPLD 4354
ò	77	9494
g	4355	TVSCFIVKPTESTKHASQLEILPIGEIGELVIGGHQLADGYLNREEQTRAAFVTHPKFGG 4414
ò	77	94
qq	4415	LYRTGDKARLHRNGTLECYGRISSGQVKLRGQRVELGEIEHAASKAGGCHAVIASVISGL 4474
ò	77	92
g	4475	LVLFCIGDPHRVSSKDIKSACQKWLPAYMIPSDIVLLDDFPYLPSGKVDKKRLETDYNSN 4534
ò	77	94
QQ	4535	TAQHVSGSSDLSENAREITRIIESVLGVSIDHSTDLSAAGLDSLRAIQVASQLRRQGCAD 4594
ò	77	80
QQ	4595	  LGALELLSVSNVLALDELVRAKADESNINDNDSEKWKQTVHELRSSVERDFESKAFVSGI 4654
ò	81	08
đ	4655	EDVLPCTPLQDAMLVETAKRPQAYCNELRLTVSPKIPVERVRQALFALAQRHÇALRSGFM 4714
ò	81	08
d d	4715	PSGVSHCAYTQVIWKTLVTSQFAHVKSFTTGWSVTNRETLLRPLHFQYKCSGAEAEILVA 4774
ò	81	08
qq	4775	IHHALYDQWSVEVILEDLETLLQNERTPERPSFGAVNKFFNLRRSEDQTSHLDFWGEYLS 4834

	g	5915	PFKRTDVKSGFGTITGRLNYSPKMVETFLSKHSTTMLSLTQAMWMKTLAASQSYSDVCCG 5	5974
	δ	98	5	76
	q	5975	NVVSGRSVPVDGI ESLVAPCFNTI PVRVDLSKHRSNLGLVKALQRVNI DSLPYQLTPLRR (	6034
	ò	98		97
	q	6035	IQAQAGTNGKRLFDSLVLLQQDTTDLDSAIWRLEGESGVMDMYTSGSTGLPKAVCLSHRA (	6094
	ò	98		16
	. q	6095	VTQSLLAHDRFIPSFSRFLQFASPTFDVSVFEIFFPWYRGATLVSVERNRLLGDLPGTIT (	6154
	ò	98	5	16
	q	6155	SLNIDAAELTPSVAASLVRHRENVPTLRALLTIGEMLNTQVIQQFGGSIGKSGILYGMYG (	6214
	ò	86		16
	ΩD	6215	PTEAAIHCTLÖPGFGVDLPAGTIGIPLDTVSCFIVKPTESTKHASQLEILPIGEIGELVI (	6274
	ò	98		97
	QQ	6275	GGHQLADGYLNREEQTRAAFVTHPKFGGLYRTGDKARLHRNGTLECYGRISSGQVKLRGQ (	6334
	ò	98		98
	qq	6335	RVELGEIEHAASKAGGCHAVIASVISGLLVLFCIGDPHRVSSKDIKSACQKWLPAYMIPS (	6394
	ò	66	DLVLYITRF	107
	đ	6395	:     DIVLLDDFPYLPSGKVDKKRLETDYNSNTAQHVSGSSDLSENAREITRIIESVLGVSIDH	6454
	ò	108		101
	g	6455	STDLSAAGLDSLRAIQVASQLRRQGCADLGALELLSVSNVLALDELVRAKADESNINDND (	6514
	ò	108		101
	qq	6515	SEKWKQTVHELRSSVERDFESKAFVSGIEDVLPCTPLQDAMLVETAKRPQAYCNELRLTV (	6574
	ò	108		101
	g	6575	SPKI PVERVRQALFALAQRHTALRSGFMPSGVSHCAYTQVIWKTLVTSQFAHVKSFTTGW	6634
	ò	108	DLB	110
	g	6635	SVTNRETLLRPLHFQYKCSGAEABILVAIHHALYDQWSVEVILEDLETLL@WERTPERPS	699
-	ò	111		110
	<del>Q</del>	6695	FGAVNKFFNLRRSEDQTSHLDFWGEYLSDVTPGRLPNLSPKMMPPQPLQSIQHTIEMDME	6754
	ò	111		110
	g	6755	TLRQAAHSYSCSAHVFFQAAYAILLGFYMGTEDTVFGTVFSGRTLPIVEIESMVGPLLST	681
	ò	111		110
	Q	6815	LPTRINTLESRKFSDVLSRLQEDNRKIMRHSMTSLADIKKACGFNPGEAVFDSIFVWQET	. 687
	ò	111		110
	QQ	6875	ARPDARAQTLLNLVEAHDYLEFNLTLELEPTQQGVKTKATYQSSLLPLQHVKTLLQQLDA	693
	ઠે	111		110
	q	6935	LVKIVVARPETHMNEISDQLPISVLSVANSEPQSFVYKAGLGSLVENHALNNSGGLALVF	669
_				

111

ò

Ω	6995	AHDIREGTSRMESLTYGELNTRANQLANYLISQGAKRDELICVCMEKSVSLYLSILAAVK	7054
>	111		110
Д	7055	AGCGYLPLVPETPAARIRQILAEADVKFCLTDSSMAPVIADVSRCHIMNVDTTDCSAQSC	7114
>	111		110
Q	7115	TGPQLDFKPTDIAYAVFTSGTTGKPKGVLVTQENILSNLEVLSKIYPVPEGSRLLQACNQ	7174
>	111		110
A	7175	AFDVSVFE1FFTWYTGMCLCSASKDVMFRDFEKAINELEITHLSLTPTVAALTDPAH1PR	7234
>	111	•	110
Q	7235	VKFLVTAGEAVTHHVHGAWAGKGLYQGYGPSETTNICTVNSAVESDHVINNIGPAFENTS	7294
<u>&gt;</u>	111		110
۵	7295	AFVLTQGDDFQLVPLGGLGELCFGGQQVFRGYQNMPELTESKIINHPNYGRIYRSGDLGR	7354
≽	111	_LPDGNRQVRG	120
ڡۣ	7355	  LPDGTILIQGRTDDQRKIRGQRIELGEISGCLLQFPSVQNCAIEVIKTADKERLMAFWI	7414
≽	121		120
۵	7415	PSGYSKDSYSILQPDKNLEEIIKSIYAHLADNLPAYMVPDALVPVSAIPQTSQGKIDKRR	7474
≥	121		120
ā	7475	LASDGSALTVEDLNAYSRGADDDETSELSATEQQLASALADTLQMSQTSIGRSTSFFALG	7534
≥-	121	VVTQ	126
ā	7535	   LDSVSAIRLATNLRKEYGYSIDVSQILKRPTIARLAPLLGGESSKQTNEPVTADCEAAVG	7594
<u>≻</u>	127		126
۾	7595	SYLHDESVVSQLHEHGQTVSQVLPCTPLQEAMLSARDTSGSSAYRNKTLFSLHGSVDKLK	7654
≿	127	AC.	128
ရွ	7655	   ACWEVMLORHDILRTIFLSTEDSRFPFVQAVLSQWTLPWQECDDIPDQLSTLLDSAKAGG	7714
≿	129		132
Q	7715		7774
≿	133		132
മ	7775	PFLNFMISTSVEEADALFRDQLRËFVPKPFKRTDVKSGFGTITGRLNYSPKMVETFLSKH	7834
≿	133		132
ą	7835	STTMLSLTQAMWMKTLAASQSYSDVCCGNVVSGRSVPVDGIESLVAPCFNTIPVRVDLSK	7894
⋩	133		132
ð	7895	HRSNLGLVKALQRVNIDSLPYQLTPLRRIQAQAGTNGKRLFDSLVLLQQDTTDLDSAIWR	7954
⋩	133	10S	135
ရွ	7955	LEGESGVMDFPCIVELAPTNESYTLSLHFNRSYLDDEVVSNLHQACLSAFASCIRYPSSD	8014
⋧	136		135
ð	8015	. VSDF1DFDADLVAGVLKPDTKHMQPVEAAKTNRSEKSGSSGDESWSPLELQIRAAYSAVS	8074
⋩	136		135
ą	8075	; SAPEDRIRRDTTIYKLGLDSISAIQLANRLRKDGLLVQASDVMESPSCSELASAVQSRSQ	8134

ò	136	ITEDIGED
g	8135	: ::     TPVLDERGFDFEGFDKHYRGAALQSHRIATEKVASVRPCTPLQSGMLSEYTHSDGHQYFN 8194
ò	144	143
q	8195	HTFYAIEADIDSSKLQSAWSKVLEQHELLRTGFVGTDDHEHPFVMLTYTEFDVIDLEIQA 8254
ò	144	143
qq	8255	SSREGSVYEYSEQKASESVKNNLHLPPWRWSLLGVEGRQCLQFSAHHAIFDAESLRLIMT 8314
ò	144	143
g	8315	DLQSALSNGYVPTRLTIDGALGHILSNSQADVESQRTFWSQKLSGAPVTRFPNMTPVRIS 8374
ò	144	143
g	8375	DTEAANVELVLNYKRSKLEARCQELGVSMQSVGQAAWARLLSAYTGESQVTFGVVLSGRT 8434
ò	144	143
qq	8435	SPATADAAFPCITTLPVSTNTAVDDSQFLKDLMSYNATIOKHQFTPLTNIRNYAESTSEA 8494
ò	144	143
q	8495	LFDSLFVYQRPMNDVVDSSSWKIIREKASVELAVSVEMEALSEDGLGLRLTIDPAQVPHE 8554
ò	144	143
Q	8555	QGKIMLQQMEVMIAGLLKFEDAINTSVMSIIPPKDPIIATDFKYLHEMTEASVKSYSDRI 8614
ò	144	143
qq	8615	AMEFVDALEDGQISSRHWTYROLDEEANKIAHLLIDRGVKPGDIIATSFDKCPEASFAFY 8674
ò	144	143
qq	8675	GILKAGCAFCAIDPTAPAARKAFILEDSNARVLLTSDSIRSELRELTQCDIIDLINFENK 8734
ò	144	143
q	8735	NELSTSSVPVSGLAPSSVSYVLYTSGTTGTPKGCEITHDNAVQLVMSFKRLFKGRWTDES 8794
ò	144	143
qq	8795	RWLOFASYHFDVSVLEQFWTWIVGMRLVCAPRDLILEDIAGFLDTMQITHLDLTPSLGRL 8854
ò	144	143
qq	8855	LDPALVPSLHKGVF1TGGESLKQDQINTWGDVGCLFNFYGPTECTIGVTVFPCVPKEGKP 8914
ò	144	143
g	8915	SNIGWQFDNVGCYVLAPGTQTPVLRGAIGELCISGKLVGKGYLNRPELTADCFPYLDAFG 8974
ò	144	143
qq	8975	ERVYRTGDLVRLFHDGSIDFLGRKDNQVKLRGQRLEIDEIEAVIKRCQDIQDTVCIVAKH 9034
ò	144	143
g	9035	PKQDKDQLIAFIGINESRKQGKPELCPAESTRHLIQTARAACEERLPGYMVPTHFLPIQR 9094
ò	144	143
QQ	9095	IPLSVNNKVEEKLLRQLYADLPTTVIQTYATQADSQQSLSDGEQKVAQALAELLKIDDND 9154
ò	144	143
qq	9155	LTPSSNIFSLGLSSISAIQFSKKLKASGFTTVQVATVLKNPTISRLTKALATSTGRSGGE 9214

	Oy 17DVFQAH	23	DD 386 MVMALQHVLVPRTLHVDEPSRHVDWTDGAVALVTENQPWPDMGRPRRAGVSSFGISGTNA 445	23	Db 446 HVILESAPPTQAVDDVPPAEAPVVASELVPLVISARTLPALVEYEDRLRAYLAAYFGVUV 5U5	U1	Ογ 23 22	Db 566 FARIHQQVWGLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVVGHSVGELAA 625	OY 23 31  Db 626 GYVSGLWSLEDACTLVSARARLMQALPPGGVWAVPVSEDEARAVLGEGVEIAAVNGPSS 685	Ογ 32 31	9	Oy 32	0 ° °	w	32	Db 866 GLAEASGVLFTSQVSRSGDLWLQDQTVLPATAFAEMALAAADETGCGLVEELTVEALLLL 925	φγ 32	Db 926 PDDGAVQYWVSEPDDAGRRQLSIHARYSDDELWTRLATATLATTTGRVSGWQAGEAWP 985	Ογ 32	Db 986 PAGAVPVEARVPSLRGVWRRGSEVFAEVALDDTHDATRFLLHPGLMTAARMAVGEETPAA 1045		DETLSVEAVDSTGLPVLTARSLALDAVPVNEPATSATD		Db 1106 LLTLTWAGIATRQQQTGLTVGAFEDLAABGDAPVPDVVVFTALPGNDPLAQTKLLTAQV 1165	UY 39 TOTAL TO THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRANSMERS OF THE TRAN		1	γο 3938	Db 1286 LVAERGVRHLLLLSRGTPDRALLSELAELGAAVDTAACDVSDRAELARVLARVSPEHPLT 1345		
	9215 IADAKQVISACRQRHMGTVTRVLRCKADDIEAIAPCTPLQQGIISRSLASESSLYFNSFK 9274 Qy 144	9275 FNAQGVDLQKLEGAFNQALERTQILRTFFIETDDGYVQAVRKTGHLPWWTLEVYDLASVD 9334 Qy	143	9335 GVFAKRKÇKWRSYNTSHLTVPFEIVIVRSGSETFVSVDLHHALYDGNSFDILMNNVSKLY 9594 Oy	SQEADFGKPFVDCLAFGPLRNUQGAKQFWLDHLPDVKSASMPPLIDNPASHDVLCTASL 9454	144LGVI 148	9455 DILNQADELRRSLGVTV 9471	4 T10	T30225 polyketide synthase - Streptomyces hygroscopicus C;Specias: Streptomyces hygroscopicus C;Specias: Streptomyces hygroscopicus C:Date: 22-Oct-1999 #sequence revision 22-Oct-1999 #text_change 17-Nov-2000	A.; Haydock, S.F.; Khaw, L.E.; Staun	tter for rapamycin in Streptomyces hyg 5756	<del></del>			r protei		1-2042/Domain: 1-0xoacyl-[acyl-carrier-protein] synthase I homology <oas2> 1-2404/Domain: lacyl-carrier-protein] S-malonyltransferase homology <amti></amti></oas2>	-3243/Domain: acyl carrier protein homology <acp2>-3681/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <oas3></oas3></acp2>	-4052/Domain: [acyl-carrier-protein] S-malonyltransferase homology <amt2> -5231/Domain: acyl carrier protein homology <acp3></acp3></amt2>	-5667/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS4> -6847/Domain: acyl carrier protein homology <acp4></acp4>	-7285/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS5>-8482/Domain: acyl carrier protein homology <acd5< td=""><td>-8921/Domain: 3-oxoacy1-(acy1-carrier-protein) synthage 1 nomblogy voncy 2925/Domain: (acy1-carrier-protein) 3-malonyltransferase homology <amt3></amt3></td><td>9-10140/Domain: acyl carrier process sources</td><td>Pred. No. 92; 17; Mismatches 25;</td><td>4,-</td><td>86 AAGKSYCVQGGFLDSAGGFDASFFGISPREALAMDPQQRLVLEASWEAFERAGIEPGSLR 145</td><td>9</td><td>146 GSDIGVFMGAYPGGYGVGADLGGFGATAGAVSVLSGRVSYFFGLEGPAVTVDTACSSSLV 205</td><td>4</td><td>206 ALHQAAYALRQGECSLALVGGVTVMATPQSFVEFSRQRGLASDGRCKAFADSADGTGWAE 265</td><td>4GILHLELLVAVVAV</td></acd5<>	-8921/Domain: 3-oxoacy1-(acy1-carrier-protein) synthage 1 nomblogy voncy 2925/Domain: (acy1-carrier-protein) 3-malonyltransferase homology <amt3></amt3>	9-10140/Domain: acyl carrier process sources	Pred. No. 92; 17; Mismatches 25;	4,-	86 AAGKSYCVQGGFLDSAGGFDASFFGISPREALAMDPQQRLVLEASWEAFERAGIEPGSLR 145	9	146 GSDIGVFMGAYPGGYGVGADLGGFGATAGAVSVLSGRVSYFFGLEGPAVTVDTACSSSLV 205	4	206 ALHQAAYALRQGECSLALVGGVTVMATPQSFVEFSRQRGLASDGRCKAFADSADGTGWAE 265	4GILHLELLVAVVAV

Q	1346 AVIHTAGVVDDGVVESLSAQRLETVFRPKADGAWHLHELTRDADLAAFVMYSSAAGVWAG	1405
ò	39	38
a a	1406 AGQGNYAAANAFLDALAEERRAEGLPALAVAWGLWEDASGLTAQLTDTDRDRIRRGGLRA	1465
ò	39	38
g	1466 ISAEHGMRLFDNASRHSEPVLVAAPMEPVRDAEVPALLRSLHRPNVRRAALAGGAQWLAA	1525
ò		38
g	) 1526 LAPEERAKALLKVVRDTAATVLGHADARTIPVTGAFRDLGIDSLTAVELRNGLAKVTGLR	1585
ò	. 39	. 38
g	1586 LPATLVFDYPTPAVLAARLGELFTGENPVLVRTASVVGQDEPLAIVGMACRLPGGVSSPE	1645
ò		. 38
QQ	) 1646 DLWRLVESGTDAISGFPADRGWDAESLFDPDPDAVGKSYCVEGGFLDSAASFDAGFFGIS	1705
ò		38
q	1106 PREALAMDPQQRLIMEVSWEAFERAGIEPGSVRGSDTGVFMGAYAGGYGAGLGGFAAT	1765
ò	39	. 38
c C	1766 ASATSVLSGRVSYFFGLEGPAITVDTACSSSLVALYQAGYALRQGECSLALVGGVTVMAT	1825
ò		. 38
q	1826 PQSFVEFSRKSGLDSDGRCKAFADSADGTGWAEGVGVLLVERLSDAQAKGHQVLAVVRSS	1885
ò		. 38
QQ	) 1886 AVNQDGASNGLSAPNGPSQQGVIRQALANAGLTTAEVDVVEAHGTGTTLGDPIEAQAVIA	1945
ò	. 39	. 38
q	1946 TYGODRERPLLLGSLKSNIGHAQAASGVSGVIKMVMALQHNTVPRTLHVDEPSRHVDWAA	, 2005
ò	. 39	. 38
g	2006 GAVELVRENOPWPGTDRPRRAGVSSFGVSGTNAHVILESAPPAQPAEEAQPVETPVVASD	2065
ò		.38
g	2066 VLPLVISAKTQPALTEHEDRLRAYLAASPGVDTRAVASTLAVTRSVFEHRAVLLGDDTVT	2125
ò	39	. 38
g	2126 GTAVSDPRVVFVFPGGGWQWLGMGSALRDSSIVFAERWAECAPALREFVDWDLFTVLDDP	2185
ò		. 38
q	2186 AVVDRVDVVQPASWRMMVSLAAVWQAAGVRPDAVIGHSQGEIAAACVAGAVSMRDAARIV	7 2245
ò	39	. 38
qq	2246 TLRSEAIARGLAGRGAMASVALPAQDVELVDGAWIAAHNGPASTVIAGTPEAVDHVLTAH	1 2305
ò	39	. 43
đ	O 2306 EARGVRVRRITVDYASHTPHVELIRDELLDITSDSSSQAPVVPWLSTVDGSWVDSPLDVE	3 2365
ò		- 43
g	2366 YWYRNLREPVGFHPAVGQLQAEGDTVFVEVSASPVLLQAMDDDVVTVATLRRDDGDATRM	1 2425
ò	- bard	- 47
g	2426 LTALAQAYVHGVTVDWPAILGTATTRVLDLPTYAFQHQRYWLRSVDRAAADGHPLLGTVV	7 2485

ò	4.8	14
qq	2486	DLPASDGVVLTGRVSLATHTWLADHAVRGSVLLPGTAFVDLVVRAADEVESDVVDELVIE 2545
ò	4 8	47
QQ	2546	TPLLLPQTGGVQLSVSVGGADESGHRAVMVFSQADNTDTWTRHVTATVSTSDSTVSLPEF 2605
ò	48	AO 49
q	2606	aswppaqarpvsvadfydrlaaagteygpafqglqaawrdgdtvyaevvlaeeqaqeaar 2665
ò	20	FRVH 53
QQ	2666	 FAVHPALLDAAMHASVLHTPDTDQQSVRMPFSWNHVQIRATDTAMLRVAATPTTDGWSVR 2725
ò	54	53
q	2726	VADDIGRPVATIGSLVTRPVTADTLGSAADDLLTLVWTEIPTPQQSSLSVGRYEDLADGD 2785
ò	54	53
QQ	2786	VPVPDVAVYTARPEADGSPDPLVQTRTLTAQVLQTAQAWLGGERFTDSTLVVRTGTGLAA 2845
ò	54	53
qq	2846	AAVSGLMRSAQSEHPGRFVLVESDDDSLTLHQLAATVGLDEPRLRVNDGRFEVPRLARVN 2905
ò	54	53
qq	2906	AAEPESETVWDPHGTVLITGGSGVLAGALARHLVTERGVRHLLLLSRTTADEGLLNELGE 2965
ò	54	53
qq	2966	LGARVETADCDVSDRAGLARVLAGVSPEHPLTAVIQTAGALDDGVLETLTAQRLDTVLRP 3025
ò	54	53
q	3026	KADGAWHLHELTRNTGLAAFVMYSSAAGVMGNPGQGNLAAATAFLDALADQRRAEGLPAL 3085
ò	54	53
qq	3086	ALAWGSSEETSDLIGLRTISAERGMRLFDSASHRGEPLLMAASLDPARAAEVPALLRSLR 3145
ò	54	53
q	3146	RPVARRAASADGGVQWLAALAPAEREKALLKVVCDSAAVVLGHADARTIPVTGAFKDLGV 3205
ò	54	83
d	3206	DSLTAVELRNSLVKATGLRLPATMVFDYPTALAARLDELFTGENPAPVREPVPAVAQD 3265
ò	54	53
QQ	3266	EPLAIVGMACRLPGGVSSPEDLWRLVESGTDAVSGFPTDRGWDVEGLFDPDPDAAGKSYR 3325
ò	54	53
qq	3326	AEGGFLDTAAGFDAGFFGISPREALAMDPQQRLLLEVSWEAFERAGIEPGSVRGSDTGVF 3385
ò	54	53
đ	3386	IGAFPVGYGAGAAREGYGATAAPNVLSGRLSYFFGLEGPAITMDTACSSSLVALHLAAQA 3445
ò	54	53
qq	3446	LRNGECSMALAGGVTVMATPEVFTEFARQRGLASDGRCKAFADSADGAGFSEGAGLLLVE 3505
ò	54	53
Q	3506	RLSDARRNGHQVLAVVRGSAVNQDGASNGFTAPNGPAQQRVIRQALANAGLTTAEVDVVE 3565

ò	54	TNKWI	59
g	3566	AHGTGTTLGDP1EAQAV1ATYGQDREQPLLLGTLKSNVGHTQAAAGVSGV1KMVMALQHS	3625
ò	9		. 69
8	3626	TVPRTLHVNEPSRHVDWSAGAVELVTENQSWPVTGRPRRAGVSAFGVSGTNAHVVLESAP	3685
ò	9		64
qq	3686	PAOSVNNAQPVATPVVVASELVPLVISAKTLPALTËHËDRLRAYLAASPGADMRAVGSTLA	3745
ò	65		64
Q	3746	LTRSVFEHRAVLLGHDTVTVTGTGTAVSNPRVVFVFPGQGWQWLGMGSALRGSSVVFAER	3805
ò	9		64
g	3806	MAECAAALSEFVDWDLFAVLDDPAVVDRVDVVQPASWAVMVSLAAVWQADGVRPDAVIGH	3865
ò	65		64
g	3866	SOGEIAAACVAGAVSLRDAARSVTLRSQAIARGLAGRGAMASVALPAHEIELVDGAWIAA	3925
ò	65	STANTINGAP	75
g	3926	HNGPASTVVAGAPEAVDRVLAVHEARGVRVRRIAVDYASHTPHVELIRDELLÖİTAGIGS	3985
ò	97	TS	77
Q	3986	QAPUVPWLSTVDGTWVEGPLDVEYWYRNLREPVGFDSAVGQLRAEGDTVFVEVSASPVLL	4045
ò	78		77
g	4046	QAMDDDVVTVATLRRDDGDATRMLTALAQAFVEGVTVDWPAILGTATTRVPDLPTYAFQH	4105
ò	78		77
g	4106	QRFWAEGADRSVAGGHPLLGVAVELPESDGVLLTGRVSLATHAWLADHAVRGSVLLPGTG	4165
ò	78		77
g	4166	FVELVVRAADEVGCDVVDELVIETPLLLPSSASVHLSVSVGEADESGRRGVTVFSRADGA	4225
ò	7.8		77
Q	4226	DAWTRHVSATIGVSGAALSLPELAAWPPAQAOPVGLGDFYDRLTGAGYEYGPAFQGLQAA	4285
ò	78		77
g	4286	WRDGDTVFAEVALAEEQAEEAARFAVHPALLDAALDAGILNTLDNAEQGVRLPFSWNGVQ	4345
ò	78		77
g	4346	VRATGSATLRVADNPTSDGWSVRVADDSGRPVATVDSLVTRPVTADTLGSAADDLLTVVW	4405
ò	78		77
g	4406	TEIPTPQQTGLSVGRFEDLADGDVPVPEVVVCTALPDSSENPLAPLDPPDPLVQTRTLTT	4465
ò	78		77
qq	4466	; QVLQAVQAWLAGERFTDSTLVVRTGTGLATAGVSGLMRSAQSEHPGRFVLVECDDNLTLQ	4525
ò	78		. 81
Q	4526	; QLAATVGLDEPRLRVCDGRFEVPRLARANTPESSPLTIPGDRAWLLEQSHSGTLRDLALV	4585
ò	82		. 81
g	4586	; PAETAERPLOSGEVRVDVRAAGLNFRDVLIALGTYPGEAVIGAEAAGVVLEVGPEVQDLA	1 4645
ò	82	GWSQT	. 98 .

g	 4646 PGDRVFGLVGGGFGAVAIADRRMLGVIPDGWSFT	TAASVPVVFATAYYGLVDLAGLSAGE 4705
ò	Qy 87	98
QQ	Db 4706 SVLIHAAAGGVGMAATQIARHLGARIYATASTGKQHVLREAGLEDARIGDSRTTGFREMV	IVLREAGLEDARIGDSRTTGFREMV 4765
ò	Oy 87	98
g	Db 4766 LDTTDSRGVDVVLNSLSGDFVDASLDLLPRGGRFVEMGKTDIRDPHQVTADRPGTSYQA	EMGKTDIRDPHQVTADRPGTSYQAF 4825
ò	Oy 87	98
q	Db 4826 DLMDAGPDRLREIIADLLALFAQGVLLPLPVRAWDIRQAREAFSWMSRARHIGKIVLTVP	IRQAREAFSWMSRARHIGKIVLTVP 4885
ò	ογ 87	98 86
QQ	Db 4886 QQLDANGTVLVTGGSGVLAGIAARHLVAEQGVRHLLLLSRSTPDDALINELGELGARVDT	JLLSRSTPDDALINELGELGARVDT 4945
ò	Oy 87	06
đ	Db 4946 AICDVSDRAGLARILAGVSPEHPLTAVIHTAGALDDGVVESLTAQQLETVLRPKADGAWH	OGVVESLTAQQLETVLRPKADGAWH 5005
ò	ςγ 91	06
g	Db 5006 LHELTRDADLAAFVMYSSAAGVLGSGGQGNYAAANAFLDAL	AFLDALAEORRGEGLPALAVAWGLW 5065
ò	òy 91	06
q	Db 5066 EDASGLTAEMTDTDRDRIRRGGLRAISAGHGMGLLDAAASRHGEPVLLAAAMEPVREAEV	JAASRHGEPVLLAAAMEPVREAEVP 5125
ò	ογ 91	06
qq	Db 5126 ALLRLLHRPVARRAASTGGSSVQWLARLAPVEREKALLKLVCDGAATVLGHADASTIPAT	ALLKLVCDGAATVLGHADASTIPAT 5185
ò	Qy 91	06
g	Db 5186 AAFKDLGIDSLTAVELRNSLTKATGLRLPATLVFDY	YPTPTALAARLGEWFVGETPVPVRT 5245
ò	Оу 91	06
QQ	Db 5246 SVSVVAQDEPLAIVGMACRLPGGVSSPEDLWRLLESGTDAVSGFPTDRGWDVENLFGPAA	SGTDAVSGFPTDRGWDVENLFGPAA 5305
ò	Qy 91	06
d d	5306 GDSYRLQGGFLDAAAGFDASFFGI	SPREALAMDPQQRLVLEVSWEAFERAGIEPGSVRGT 5365
ò	Qy 91	06
d	Db 5366 DTGVFMGAYPGGYGIGADLGGFGATASAVSVLSGRVSYFFGLEGPAI	VSYFFGLEGPAITVDEACSSSLVAL 5425
ò	Qy 91	06
qq	Db 5426 HQAGYALRQGECSLALVGGVTVMATPQTFVEFARQGGLAGDGRSKAFADSADGAGFSEGV	GGLAGDGRSKAFADSADGAGFSEGV 5485
ò	Qy 91	06
Q	Db 5486 GVLLVERLSDAQAKGHQVLAMLRSSAVNQDGASNGLTAPNGPSQQRVIQAALSNAGLAAH	LTAPNGPSQQRVIQAALSNAGLAAH 5545
ò	Qy 91	06
qq	Db 5546 EVDVVEAHGTGTTLGDPIEAQALLATYGQDREQPLLLGSVKSNLGHTQAAAGVSGVIKMV	LLGSVKSNLGHTQAAAGVSGVIKMV 5605
ò	Qy 91	06
q	Db S606 MALGRGFVPRTLHVDEPSRHVDWSAGAVALVTENQPWPDMGRARRAGVSSFGI	PWPDMGRARRAGVSSFGISGTNAHV 5665
ò	Oy 91	06
a	Db 5666 ILESAPPTQPADNAVIERAPEWLPMVISARTQSALTEHEGRLRAYLAASPGVDMRAVAST	TEHEGRLRAYLAASPGVDMRAVAST 5725
è		06

ð	5726	LAITRSVFEHRAVLLGDDTVTGTAATDPRVVFVFPGQGSQRAGMGEELAAAFPVFARIHQ	5785
≿	91		06
ą	5786	QVWDLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVVGHSVGELAAGYVSGL	5845
≿	91		06
ð	5846	WSLEDACTLVSARARLMQALPAGGVMVAVPVSEDEARAVLGEGVEIAAVNGPSSVVLSGD	5905
≿	91		06
ą	5906	EAAVLQAAEGLGKWTRLATSHAFHSARMEPMLEEFRAVAEGLTYRTPQVSMAAGDQLTTT	5965
≿	91	•	06
ð	5966	EYWVRQVRDTVRFGEQVASYEDAVFVELGADRSLARLVDGVAMLHGDHEAQAAVSALAHL	6025
≿	91		06
ď	6026	YVNGVTVDWPALLGDAPATRVLDLPTYAFQHQRYWLEGTDRMAAGGHPLLGEAVAVPGSD	6085
≿	91		06
ą	9809	GVLLTGRVSLATHPWLADHAVRGSVLLPGTGFVELVVRAADEVGCDVIDELVIETPLLLP	6145
≿.	91		06
ą	6146	QTGGVQLSVAVAESDDSGRRAVTVFSRADNVDTWTRHATVTVSNSDTTLSLPDLSAWPPA	6205
≿	91		06
ð	6206	QAQPVNVADFYDQLTVVAYEYGPAFQGLQAAWRDGDTVHAEVALAEEQAQDAARNAVHPA	6265
≿	91		06
ą	6266	LLDAALHAGILNT PDTEQGVRLPFSWNQVQVHAVGSAMLRVAVTQAADGWSVRVADDTGR	6325
⋩	91		06
ą	6326	PVATIGSLVTRPVTADTLGSTTDDLLALTWTEIPAPQETSLTIGRFEDLADADVPVPEVV	6385
⋩	91		06
ą	6386	VFTARPDSSENPLAQTRTLTAQVLQKIQAMLAEERFTDSTLIVRIGTGLAAAAVSGLMRS	6445
⋩	91	DDT	93
ð.	6446	GOSEHPGRFVLVESDDDTLAPDQLAATVELDEPRLRISDGRFEVPRLTRTHAAEPESEKV	6505
<b>`</b> ≿	94		93
ဌ	6506	WDPDGTVLITGGSGVLAGIAARHLVAERGVRHLLLLSRSAPDGALISELGELGAQVATAV	6565
≿	94		93
٠ ۾	9959	. CDVSDRPGLVRVLADVSPEHPLTAVIHTAGVVDDGVVESLTAQRLDTVLRPKADGAWHLH	6625
ጵ	94		93
ą	6626	: ELTRDADLAAFVMYSSAAGVFGSAGGGNYAVANAFLDALAEQRRAEGLPALALAWGLWEG	6685
ጵ	94	- d G	95
ą	9899	; TSGLTANLTDTDHDRIRRSGMRAISAEHGMRLFDGASRRRDPVLVAAAMEPVREAEVPAM	6745
à	96	GHADLGHADL	100
g	6746	. LRSLHRPVARRAASGGAVRCLAALAPEERAKALVKVVCDSAATVLGHADVDSIPVTAAFR	6805
ጵ	101		100
g	6806	: DLGVDSLTAVELRNSLTKATGLRLPATLVFDYPTPGALAARLEELFTGENPVQVRTPVSA	6865

ò	101	007
g	6866	VGQDEPLAIVGMACRLPGGVSSPEDLWRLVESGTDAISGFPTDRGWDVENLFDSDPDAAG 6925
ò	101	100
q	6926	KSYCVEGGFLATAANFDASFFGISPREALAMDPQQRLVLEVSWEAFERAGIEPGSVRGSD 6985
ò	101	100
qq	9869	TGVFMGAFPGGYGIGADLEGYGATAGLNVLSGRLSYFFGLEGPAVTVDTACSSSLVALHQ 7045
ò	101	101
QQ	7046	AGYALRQGECSLALIGGVTVMATPHTFVEFSRQRGLASDGRCKAFADSADGTGWSEGVGV 7105
ò	102	LVITRE
qq	7106	:   LLVERLSDAQAKGHQVLAVVRSSAVNQDGASNGLSAPNGPSQQRVIRQALANAGLTTAEV 7165
ò	108	107
qq	7166	DVVEAHGTGTTLGDPIEAQAVIATYGQDRDQPVLLGSVKSNVGHTQAAAGVSGVIKMVMA 7225
ò	108	107
Dp	7226	LQHGLVPRTLHVDEPSRHVDWTDGAVELVTENQSWPEAGRPRRAGVSSFGVSGTNAHVIL 7285
ò	108	107
QQ	7286	ESAPPTQAVDDVRPADAPVVASVMASELVPLVISAKTQSALAEYEGRLRAYLAASPGVDM 7345
ò	108	107
Q	7346	RAVASTLAMTRSVFEHRAVIVGDDTVSGTAATDPRVVFVFPGQGSQRAGMGAELAAAFPV 7405
ò	108	110
q	7406	FARIHQQVWDLLDVPDLEVNETGYAQPALFALQVALFGLLESWGVRPDAVIGHSVGBLAA 7465
ò	111	115
q	7466	AYVSGLWSLEDACTLVSARARLMQALPAGGVMVAVPVSEDEARAVLGEGVEIAAVNGPSS 7525
ò	116	115
q	7526	VVLSGDEAAVLQAAEGLGKWTRLATSHAFHSARMEPMLEEFRAVAQGLTYHAPGVVMAAG 7585
ò	116	119
g	7586	  DRVMTAEXWVRQVRDTVRFGEQVASYEDAVFVELGADRSLARLVDGVAMLHGDHETQAAI 7645
ò	120	122
q	7646	GALAHLYVNGVTVDWTALLGDVPVTRVLDLPTYAFQQQRYWAEVGRSADVSGAGLDAVGH 770\$
ò	123	122
q	7706	PLLGAVVALPGSDGVLLTGRVSLATHAWLADHAVRGSVLLPGTGFVELVVRAADEVGCDV 7765
ò	123	122
g	7766	VDELIVEAPLLLPQTGGVQVSVSVGEADESGHRVVTIFSRADNADTWVRHVSAVISTSDS 7825
ò	. 123	122
පු	7826	TVSLSEFASWPPAQAQPVDVTGFYDPLMAEGYEYGPAFQGLQAAWRYGDTVFAEVALAEE 7885
ò	123	122
q <sub>0</sub>	7886	OVREAARYPSVHPALLDAALHACTLECADAEVGVGLPFSWDGVRVHAGGSAMLRVAVTQA 7945

ò	123 -	122
qq	7946 A	ADGWSVRVADEIGRPVANVGSLVTRPVTADALGSAADDLLALTWAEIPAPEGTGLTVGRF 8005
ò	123 -	122
q	8006	EELVSDGDVPVPEVAVFTALPDNDDDPLEQTRKLTGQVLQAVQEWLGGERFSDSTLVVRT 8065
ò	123 -	122
g	9908	GTGLAAAGVSGLMRSAQSEHPGRFVLVESDDDALALDQLAAAVGLDEPRLRISDGRFEAP 8125
ò	123 -	122
g	8126 R	RLTRTHAABPESEKVWDPDGTVLTTGGSGVLAGIAVRHLVTERGVRHLLLLSRSAPDEAL 9185
ò	123 -	-0LG
පු	8186 I	INOLGELGARVETAACDVSDRAALAQVLAGVSPEHPLTAVIHTAGVLDDGVVESLTAQRL 8245
ò	126 -	125
සු	8246 D	DAVLRPKADGAWNLHELTRDADLAAFVMYSSAAĞVLGSGGQGNYAAANAFLDALAEQRHA 8305
ò	126 -	125
QQ	8306 E	EGLPALAVAWGLWEDASGLTAQLTDTDRDRIRRGGLRAISAEHGMGLFDSASRHSEPVLV 8365
ò	126 -	125
q	8366 4	AAPMEPVRDAEVPALLRSLHRPVARRAAAAGGARWLAALAPAEREKALLKLVSDGAATVL 8425
ò	126 -	125
q	8426	GHADTSTIPATTAFKDLGIDSLTAVELRNSLAKATELRLPATLVFDYPTPTALAARLDEL 8485
ò	126 -	. 125
g	8486	FTGENPAPVRGPVSAVAQDEPLAIVGMACRLPGGVSSPEDLWRLVESGTDAISGFPTDRG 8545
ò	126 .	125
g	8546 V	WDVENLYDPDPDAPGKSYSVQGGFLDAAAGFDASFFGISPREALAMDPQQRLMLEVSWEA 8605
ò	126 .	125
g	9098	FERAGIEPGSVRGSDTGVFIGAYPGGYGIGADLGGFGTTAGAASVLSGRVSYFFGLEGPA 8665
ò	126	131 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
В	8666	FTVDTACSSSLVALHQAGYALRQGECSLALVGGVTVMPTPQTFVEFSRQRGLSADGRCKA 8725
ò	132	131
g	8726	FADAADGTGWAEGVGVLLVERLSDAQANGHQILAVVRSSAVNQDGASNGLSAPNGPSQQR 8785
ò	132	131
qq	8786	VIRAALSNAGLAPHEVDVVEAHGTGTTLGDPIEAQAVIATYGQGRGEPLLLGSLKSNVGH 8845
ò	132	133
qq	9846	I TQAAAGUSGUIKMUMALQHSMVPRTLHVDEPSRHVDWSAGAVELVAENQPWPETGRPRRA 8905
ò	134	133
qq	9068	GVSSFGISGTNAHVILESAPAQSVGDTAGSTPVLVSELVPLVISAKTQPALTEHEDRLRA 8965
ò	134	133
g	. 9968	YLAASPGVDIRAVASTLAVTRSVFEHRAVLLGDETVTGTAVSDPRIVFVFPGQGWQWLGM 9025
ò	134	133

9986 GTDHDRIRRSGLRTITAERGMRLFDIASRQGEPVLVATPMEPVREVEVPALLRLHRPVA 10045 9926 AFVMYSSAAGVLGSAGQGNYAVANAFVDALAEQRRAEGLPALALAWGLWEDASGLTAKLT 9985 9686 DPLAQTRRLTAEVLQAVQVWLAGERFTDSTLVVRTGTGLAAAAVSGLMRSAQSEHPGRFV 9745 9806 GGSGVLAGIAARHLVAERGVRHLLLLSRSAPDEALISELAELGAAVVDTAVCDVSDRAGL 9865 9866 ARVLAGVSPDHPLTAVIHTAGVLDDGVVESLTARRLDTVLRPKADGAWNLHELTRDIDLA 9925 9086 WQAAGVRPDAVIGHSQGEIAAACVAGAVSMRDAARIVTLRSQAIARGLAGRGAMASVALP 9145 9206 RDELLDİTSDSSSQDPLVPWLSTVDGTWVDSPLDGEYWYRNLREPVGFHPAVSQLQAQGD 9265 9266 TVFVEVSASPVLMQAMDDDVVTVATLRRDDGDATRMLTALAQAYVHGVTVDWRAVLGDVP 9325 9326 ATRVLDLPTYAFQHQRYWAEAGRSADVSAAGLDAVGHPLLGAVLAMPGSDGVMLTGRVSL 9385 9386 ATHAWLADHAVRGSVLLPGTGFVELVVRAADEVACDVVDELIVEAPLLLPQTGGVQLSVS 9445 9446 VGEADESCHRAVTVFSRADSADAWVRHVSATVSVSDTTVPTSDLTAWPPAQAKPVDVAGF 9505 9506 YDQLTRAGYEYGPAFQGLQAAWRDGDTVFAEVALAEEQTQDAARFAVHPAVLDAALHAGI 9565 9566 LNTPDADRDTVRLPFSWNHVQVHVTGSATLRVAMTRVADGWGVRVADDIGRPVATIGSLV 9625 9626 TRPVAADALGSAVDDLFALTWTEIPVSQQVGVTVGKFEDLADGEVPMPDVVVFTALPDSG 9685 9746 LVESDDDTLTPDQLAATVGLDEPRLRVIDGRYEAPRLTRTGVAEPEPEGVWDPDGTVLIT 9805 9026 GSALRDSSVVFAERMAECAAALSEFVDWDLFAVLDDPAVVDRVDVVQPASWAVMVSLAAV 9085 9146 AQDVELVDGAWIAAHNGPASTVIAGTPEAVDHVLTALRQRGAGAADHVDYASHTPHVELI 9205 143 ----- 143 140 ------139 140 ----- 139 10046 RRAASTGDSSAQWLVGLAPEERAKALLKVVRDSAATVLGHADARSIPATGAFKDLGV 10102 140 ----TGF----143 ---------ITED-----143 143 143 136 143 143 143 143 136 ង g g g ò g ò g ò g ઠે ద 유 ò 셤 g g ò ઠે ò ò ò õ ò

g	2540	QLDVLPAAERNLLLETFNQTRQDYPTDLCIQHLFEAQVRTQPDAIAVAFQAQRLSYAELN 2599	
ጵ	14		
ą	2600	RQANRLAHHLIGLGIGPDDRVAICVERGVEMMVGLLGVLKAGAAYVPLDPAYPAERLAYM 2659	
⋩	18	17	
ą	2660	IEDSQPAALMTQRHLQEYLPTLTLPLVLLDDDQRKTFTERDDNPVVEALGVRNLAYVIYT 2719	
≿	18	17	
ရ	2720	SGSTGNPKGVMIEHRGLVNYSVDAARLFDLSPTDTVLQQNTLNFDLSVEEIFPALLAGAT 2779	
À	18	17	
q	2780	LTPSREIFGSEGTENHGINPTVLHLTAAHWHTLVAEWHKQPQVAEGRLQHVRLINVTGDA 2839	
ጵ	18	17	
ą	2840	LSAQKLKLWDEVRPAHTRLINTYGPTEATVSCTAAYVSHDAAAGSEGSGNATIGKFWANT 2899	
ጵ	18		
g	2900	RIYLLDÄHÖQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERFLADPFSESPDARMYKTGD 2959	
ጵ	26		
ą	2960	LARYMADGRIEYLGRNDFQVKVRGFRIELGEIEARLGNCTGVKEAVVIAREDNPGDKRLV 3019	
ጵ	31	12	
ą	3020	AYVVAQPQSQLTAADLRAELAPQLAEYMLPSAFVLLDELPITPNRKLDRKALPAPDADAL 3079	
ጵ	33	NTN 35	
ą	3080	ISRGYEAPQGETETQIVAIWQDLLGIEQVGRHDHFFELGGHSLLAVSLIERLRKQG	
à	36	J	
ą	3140	VKTVFTAPTVREMALAISQDKHVLFQVPANRIPAHCTQLTPDMLPLVELSVAQIELITSA 3199	
ጵ	37	36	
අ	3200	) VAGGAANIQDIYPLAPLQDGILFHYLLNRERDAYLMRSMIEFDSRARLDAFLEGLQTVID 3259	
ጵ	37	36	
g	3260	RHDILRSSVHWIGLPQAVQVVHRQAQLPVHTLTLTPEEDALSQLDRLSDPGRLRLDLRQA 3319	
⋧	37	36	
ą	3320	PLLLAYIARDPNSERWLLALIDHHMISDHVTVELILEEIRLLMRGQSADLLPPQPYRDFV 3379	
à	37	36	
ą	3380	) AQTLASPSSAHEAYFTRRLADVDSPTAPFELLEVQGDGNDVEEAKLALNSDLCIRIRTQA 3439	
à	37	39 GAE 39	
g	3440		
તે	40	39	
ရ	34.00	) LTTQGAQELVMATHRDLSELLSHEQASLALAQRCSSVATGVPLFSSLLNYRHQGEDNRLQ 3559	
à	4	39	
g	3560	) WPGMRLLDGTERTNYPLCLSVNDYGSELDLIIHSMQPANPQRLCAMMQCALEQLTDALAH 3619	
ò	40	39	

4759	) GADEREHLLAGLNATEAPFPQDRTIHQLFEERVQAQPDAIAVAFGAQRLSYAELNRQANR	4700	g
68		90	ò
4699	) AQFDLTLDMAEVDEQLVGTLEYATALFDESTMRRYLGYFQRVLEAMVADDQQVLEHVALL	4640	g
68		90	ò
4639	) LDAQAHQDLPFEQVVEVINPLRSLSHSPIFQAMLSWENNEASDLTLGDMTLKSIELAADT	4580	QQ
68	; III	85	ò
4579	) GLLGRLAGQDDVVIGTPVANRTRSEVEGLVGLFVNTLAIRVDLSDKPTAETLLARVKQQT	4520	g
8 4		85	ò
4519	) TLADAPALLMLPTDRARPALQDYAGAALPVVFDKDLTRGLKALSQRRGSTLFMTVMAAWA	4460	qq
84		85	ò
4459	   SDGMSVDVLTRELSALYAAFSQDQDDPLAPLELQYLDYAVWQRRWLSGDVLQQQSNFWQQ	4400	qq
84	CGWS	81	ò
4399	FOLICAMHDLOGLADAEEKLQALASEESLQSPDLQQGPLIRGRLIRMAEDHHVLLLTLHHIV	4340	qq
80		81	ò
4339	) EGASAAYHIPAGLSLHGNLNLKALQRALERIVARHEGLRTTFWQGDDGQPVQRISPADTG	4280	q
80		81	ò
4279	HQLGVELGLAALFAHPEVSALAVAIAQAGRSKFPDIVPVARDQAWPLSFGQQRLWFLAQM	4220	gg
80		81	ò
4219	) APADDAFASREHVEPQGATEIALAQIWQSLLDLERVGRHDQFFELGGHSLLAMRLISQAR	4160	qq
90	TEPEGAPNIT ANLTSGLLSV	61	ò
4159	PGEKRFVAYVVAQPQTQITAAELRAELAPQLAEYMLPSAFVLLDELPLTPNRKFDRKALP	4100	QQ
09		61	ò
4099	RMYKTGDLARYMADGRIEYLGRNDFQVKVRGFRIELGEIEARLGNCKGVKEAVVIAREDN	4040	qq
09	FRVHL	50	ò
4039	) GKPMANTRIYLLDAHQQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERFLADPFSESPDA	3980	QQ
6 4		50	ò
3979	INVTGDALSAQKLKLWDEVRPAHTLLINTYGPTEATVSCTAAYVSYDAAAGSEGSGNATI	3920	g
49		80	ò
3919	) ALLAGATLAPSREIFGSEGTETHGIQPTVLHLTTAHWHTLVAEWHNOPQAAEQRLOHVRL	3860	QQ
6		20	ò
3859	I LAYVIYTSGSTGNPKGVMIEHRGLVNYSVDAARLFDLSQSDTVLQQNTLNFDLSVEEIFP	3800	QQ
49		20	ò
3799	AERLAYMITDSQPAALLTLPGLQDRLPALSMPLVLLDDEQYGGLAECDDNPVVPTLGVRN	3740	g
49	DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	40	ò
3739	I LSYADLINRQANRLAHHLISLGIVPDDRVAICVERGVEMMIGLLGVLKAGAAYVPLDPAYP	3680	g
39		40	ò
3679	TPQMAVTQLDVLPAAERNLLLETFNQTRQDYPTDLCIQHLFEAQVRTQPDAIAVAVQGQR	3620	g

ò	111	110
q	5840	RVAILLDRSVELLASMLATLKCGAAYLALDRLAPEERLRFMLEDSEAIMLLSRSDLTAPD 5899
ò	111	110
q	5900	MTPRLDLDTLELSALNQEPVVPATEVAGETPACIIYTSGSTGVPKGVIVTHNGIVRLVOD 5959
ò	111	110
q	2960	NGYYDFSAEDRVAFSSNPAFDASTPEIWGALLNGCQSVIIEPQVLLEPVAFAALLKRHGV 6019
ò	111	110
qq	6020	TAMISSTALFNLYAGLIPEALAGLRMIMCGGERADPASFRRVREHSAQVRLFNGYGPTEG 6079
ò	111	110
QQ	6080	TTCATSYEIFDVLPDTLSLPIGKPNANVRVYVLDARREPVPMGVVGDIYIGGTGVALGYL 6139
ò	111	120 TILL THE TREE TREE TREE TREE TREE TREE TREE
q	6140	NRPELTAERFSEDPFSQQAGARLYRTGDLARWLPDGNLEYLARNDGQVKVRGFRVELGEI 6199
ò	121	120
qq	6200	ESVLHLYDGVRNSVVVAHEASPGDTRLVAYYTVHAGVAAPDPEDLRAOLSADLAEYMVPS 6259
ò	121	120
q	6260	VFVRLDALPLTLNGKVDQKALPVPDLNAMFERTYVAPEGATEQALAEIFQELLGLERVGR 6319
ò	121	120
Q	6320	HDGFFELGGHSLLAAQLVSRVRQQLNGDMALRQLFNHPTVAELAKVVDGLQTVDSDSIEP 6379
ò	121	120
đ	6380	IERNAPLALSFSQORLWFLDRLDPGASSAYHMPMSLLLRGELDHRALKAALDRLVARHES 6439
ò	121	120
đ	6440	LRTTFELHGEGPVQVIAAADSGFALAEDDLRSGPYEQASLNASRIADSEAAAPFDLRQGP 6499
ò	121	123
셤	6500	1   1   1   1   1   1   1   1   1   1
ò	124	131
අ	6560	DYAAWQRRTFTGERLAEQADLWREHLGGAPTLLSLPTDRPRPVVQSYRGGAVPVTIDA 6617
ò	132	137
đ	6618	ALHQRLERFCQAHNVTLFMGLLSAWSVLMTRLGNERDVVIGVPSANRGRTETENLIGFFV 6677
ò	138	137
g	6678	NALALRVDLTQNPSVAQLLEQVRQTTLAAHEHQDIPFEQVIEALQPPRSMSHSPLCQVAL 6737
ò	138	137
g	6738	SLDNTSIGGELKLPGLSLHPVLQAHETAQFDLMLTLASENGALNGVIEYASDLFDRSTVE 6797
ò	138	137
q	6798	RFAQHFHTLLEAMVEDVAQPVLGLPLLSPAQRLASPALLQPKAVFASGLMVHQRFEQFAA 6857
ò	138	137
q	6858	AHPQNIALVFGRHEVSYQALNRRANRLAHELLAQGVRPDDRVAILAERGTQMICAVLAVL 6917
Š	138	137

ð

ð	6918	KSGAAYVPLDPTYPTERLGYLLTDSAPVALLAQSACLDVLPAHSVPVLTLGADNDSADLA	2269
<b>≿</b>	138		137
g	6978	DESVDRNPEPAALGLSREHLAYVIYTSGSTGLPKGVLVEHGNVARLFDATAGQFNFGHED	7037
≿	138		137
ą	7038	VWTPFHSFAFDFSVWEIWGALCYGGKLVIVPSEVARSPDDFYALVCEQQVTVLNQTPSAF	7097
≿	138		137
g	7098	ROFIQARERSPQEHALREVVFGGEALDFRSLQPWTARTPLSRTRLVNMYGITEITVHATY	7157
≿	138	•	137
ð	7158	YPISQSEIDTAMPSLIGPALDDLCLRILDDYQQPVPVGVNGEIYIGGAGVARHYLNRTEL	7217
≿	138		137
മ	7218	NAERFIADPYALQSGARLYRTGDVAHYRSDGGVVNVGRNDSQIKIRGFRIELGEIEAQLL	7277
<b>≿</b>	138		137
ð	7278	ACPEVREAMVILREDRPGDKRLVAYLIAEDGAAPESALLRSQLASVLAEHMLPSAFVTLE	7337
≿	138		137
ရွ	7338	TWPLTTNGKLDRAALPAPDQFATVSRDYEAPLGAIETTLAAAWQELLGVERVGRQDHFFE	7397
≿	138		137
ą	7398	LGGHSFLVISLIERLRQIGLLLDVSTVFSAPTLQAMAAVLAGGTAAERVAPANLIPVDCT	7457
≿	138		137
ą	7458	ALTPDMLPLVKLTRQELEHIVADVPGGVANVQDIYPLSSLQEGILFHHLLQSEGDAYLMR	7517
⋩	138		137
ą	7518	TLATFDSRALLDKFLGALQVVINRHDIMRSSLRWQGLPQPVQVVHRQAQLPVIQLDTAPG	7577
⋩	138		137
ą	7578	EDALOMLRERTNTYHMRLDLQQAPLIAAYITYDTRQEKWLMALLDHHLISDNVTLRLIMG	7637
⋩	138		137
ą	7638	EIQAVMDGRADALPPSQPYRNFIARAACVSQAEHEAYFRQLLGDVDTTTAPYGVLDVRGG	7697
⋩	138		137
ą	7698	DATILRSVQDLSDDLSARIHSTARAQGVPTSVLFHAAWGLVVAATSGRDDGIFGTVLSGR	7377
⋩	138		137
ą	7758	SQGTSGANHALGMFINTLPMRIRLQQNSVRDIVQDAYQQLSGLLTHERAPLALAQRCSAV	7817
≿	138	DLOG-	141
ą	7818		7877
<i>≿</i>	142		141
ą	7578	SLTAQSIDGIDPHRIAAYLGQAVAELVNALEQDPARLASSLEVIPQAERQLLLNDFNDTA	7937
<u>``</u>	142		141
ą	7938	SDFAPAVPIHALFEDQVRRNPDAVALVYEDRQLSYRQLNRRANHVARQLLQLGVQPDERV	7997
ጽ	142		141

Ω	7998	AICAERSLDMIAGLLGVLKSGAAYVPIDPAHPADRMAFMLQUSQPRALLIQGALSLLVGD 803/	
>	142	141	
۾	8028	TPLMLLDSAESLLAADDQAFDANPVVDGLTAENLAYVIYTSGSTGQSKGVMVEHRSVFNF 8117	
≿.	142	141	
۾	8118	WNVLTRTTHQHCPTPATVALNAGFFFDMSIKGISQLFSGHKLVIIPQLLRANGSELLDFL 8177	
≿:	142	141	
ą	8178	EAHQVHAFDSTPSQLDTLLSAGLLERSSYQPVSVLLGGEAINASTWEKLRNCPTIRLYNM 8237	
≿	142	141	
ą	8238	YGPTECTVDATIDLIRDLGEKPSIGRPIANVQVHVLDARGEPAPLGVAGEIHIGGSGVAR 8297	
≿:	142	141	
ဂ္ဂ	8298	GYLNRDELSAERFIVDPFSDAANARLYKTGDLGRWLADGTLEYMGRNDFQVKVRGFRIEL 8357	
≿	142	141	
ą	8358	GEIENVLLAVPGIREVVVIARNDSQGDSDSQRLVAYVCGESVAAEHLRSELLRHLPEYMV 8417	
≿:	142	141	
ą	8418	PSAFVQLDALPLTANGKLDRRALPAPGQDALASKVYEAPQGETEEAIAEIWKALLHLDQV 8477	
≿:	142	141	
ရွ	8478	GRNDGFLELGGHSLLAVQLLSRLRRKLGTRITLRELFDAPTVRGLASLVNAAAPGEAQSI 8537	
≿	142	141	
ą	8538	PRANRSGRLPLSFSQQRLWFLDHLDHAAGAAYHLPWALRLTGALDTAALEATLDRLVARH 8597	
≿	142	141	
á	8538	ETLRTRFELVDGEPVQKIAPADSRLPLLKQDLRDLSGDERTSTLARLGGENATQLFDLTK 8657	
≿	142	141	
<u>Q</u>	8658	GPMLRGHLLRVADAEHVLLITLHHIVSDGWSNSVLAQEVSALYAAFSOGOKDPLPALPLO 8717	
≿	142	141	
a	8718	YVDYAAWQRQSLDGPALQAQIDFWRKHLEGAPSVLNLPLDRPRPAIQSYTGGMVEHVFSP 8777	
≿	142	141	
ą	8778	ALSADLRAFSGAQGSTPFMVLLAGWSMLMSHLSEQTDVVVGTPVANRQHPELEPMIGFFA 8837	
≿	142	141	
ရ	8838	NTLALRVATDRETRLNDMLDRIKSLTLAAYNHQDLPFEQVVSALQPTRNVSHSPLFQVML 8897	
≿	142	FDLGVTI 148	
ð	8838	SLDNTPPSLLQLPDLEVELLDSEHHTTQFDLSLSL 8932	

RESULT 6
T15789
hypochetical protein C41A3.1 - Caenorhabditis elegans
hypochetical protein C41A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 01-Dec-2000
C;Accession: T15789
R;Bentley, D.
R;Bentley, D.
Squbmitted to the EMBL Data Library, November 1995
A;Pescription: The sequence of C. elegans cosmid C41A3.

Qy         11           Db         991           EMAVKSIRECRKFALVATSQLIQSSKWLYSLKTLLDHHSTNSFSVDGSGFCRSDGVGVII         1050           Qy         11           Db         1051           LKTAEKGDSAVIKISSAKSHHCGAVMTPVVSSISQLLEEAGSFSYVEGHGTATSAGDSAE         1110           Qy         11           Db         111           SMAYQKLGSELIMSSVKAOFGHCEVASGLIQI,MKVQSTGRUGTTBGTANNTTSQUANTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTTSCTANNTS	OY 11	1231 KKACLSLIEMIDNSCESLYDISTTLOKQKTNFKWRTAVVGSSHADVVLKLKOFLTSEHNT 11LVAV 1291 SLTNWHISTSHHSIGGSTFFHNIPEFEDHYSMFCHRLRFEPHSNTNSIYHLLAVYALIR 15		Db 1411 NVKLLNLNGEPITTARQAVEATIDOKVKNVRLPETTLILSPSRAYEFASGLETIGDYYKL 1470  Qy 15	15 1531 15	1591 KIEEQDGLEKLVFGETDAISFKLTELQNFNPIPNERLNAEVHHTDNIYERFANSHLTYRN 15	न म	D 1831 KSNYPNASSTCVFDYPSIDLLSGYLSTLNDPQVTETSTGEDDIQKDLTEDHKPTRLAENP 1890  Y 15	15 1951 15 2011
282/ Db Oy	Length 7829; Gaps 27; Db	10 00 00 00 00 00 00 00 00 00 00 00 00 0	HGEGAA 330 Db		1. Oy Oy Db Db Db Db Oy Oy Oy Oy	ETFHSTVDKYCKLAETCGFPEARTALFFPFKLTLTPLTYNVSRLISSMATFELLVQYNTL 570  OY PNKLRGKGLGQIFCLAVAKVITFESAVQLIKGVVAEANLTDILGDIELKSSKIPIEIQHL 630  Oy OY	d o o o	10 00 00 00 00 00 00 00 00 00 00 00 00 0	ALECT 870  QY ALLFL 930  QY ATAL 990  Db
A;Accession: T15789 A;Status: preliminary; A;Molecule type: DNA A;Resdades: 1-7829 <be; a;cross-references:="" a;g<="" a;genetics:="" c;genetics:="" em="" td=""><td>Ouery Match Best Local Similarity 1.3 Matches 90; Conservative Oy 1 AAGGI</td><td>211</td><td>271</td><td>331</td><td>11 451</td><td>DS 511 ETFHSTVDKYCKLA OY 11 Db 571 PNKLRGKGLGQIFC OY 11</td><td>Db 631 KSTKKKILPIHISG Qy 11 Db 691 FRGRIVKTPTYSFL</td><td>751 11 11 811</td><td>Oy 11</td></be;>	Ouery Match Best Local Similarity 1.3 Matches 90; Conservative Oy 1 AAGGI	211	271	331	11 451	DS 511 ETFHSTVDKYCKLA OY 11 Db 571 PNKLRGKGLGQIFC OY 11	Db 631 KSTKKKILPIHISG Qy 11 Db 691 FRGRIVKTPTYSFL	751 11 11 811	Oy 11

ò	17		16
Q	2071 SKY	SKVIVAGVNLILNEKGQGLRTNGKMLSQHGMSLSFDSRASGYGRSDGCVVLMLELAKPNF	2130
ò	17	DVFQAH	22
g	2131 HYN	HYMSTIQSVNVNHGGRSVSLTAPNGVAHKMLLTSVINQSPSLAIDYWEAHGTGTPLGDPI	2190
ò	23		22
g	2191 EFN	EFNTLSSILONIIIGSVKASLGHGEASAGTCGLLKLFLMLTYQYVPTLIHFHVLNKDINA	2250
ò	23		22
셤	2251 GS	GSIRLPIIGEDSELVSAGISSFGVSGTNAAAIAFNDNNKLEPYIPIHKYYILPISAKNQI	2310
ò	23		22
Dp	2311 SL	SLDNLEKQILSVI PLTDVPI CNI ASALANNRSHFTI RNALI VSNSGI VNSKMEGKPHRVA	2370
ò	23		22
Ωp	2371 KK	KKDRYHVKLCDSLLDASLLQYDVINETYTVASLKNPQSFAMKFAIIKFLTSLSEYIEIVA	2430
ò	23		22
g	2431 SD(	SDGEELLAVLLANGSLKWENFNKTMIELPIGSLLTEFADHDLNSTTSSSIKSYQTQPESH	2490
ò	23		22
q	2491 NL	NLDSPMELMKLIMKLYITGYDVDWATVYSPVEQFIALPNYQFNKQTLWFEERLEIVDHYL	2550
ô	23		22
qq	2551 IG	IGTIDEESEDTLILKNQISELRHPQFFKGKPLDVGTMSEIAIEALKIRNEIPFSIQNLKT	2610
6	23		25
g	2611 EL	 ELITLTKPAWLETNVTRNEDDEGFNVSAYIDGQRLFSLNASSVEIQNIEVPAVEVQIPDK	2670
ò	26		. 25
QQ	2671 W	VVYLKECPNAVIRRHRNMVYVDSRAEQSPFRTANIVLNEIIGFAPTPSDMFIEILGVLPS	2730
ò	26		
đ	2731 VH	VHYMVQVDDGALWQFQMISQDKRVLSNIYVLKDAKGLEIPTIRMHKKSTLLSSQEASIVA	2790
ò	26		25
qq	2791 AK	aktlomavrhkvclavgdviesgldidesqlstgfselgidslatvdllnrlnokyfpei	2850
ò	26		25
q	2851 EL	ELTTSDLFONPSIIDLSIMIEQLLNEKGITEPSEPNTPKTSLRGRKLSIPAVRAQVLAQI	2910
ò	26		25
g	2911 EF	EFVENYNSKQKEVQAEAPSSSSECSNHLEESDATVDRTEIRRKVSLAVFDLATETLSAED	2970
ò	26		25
qq	2971 LQ	LQSKGFTELGMDSLSIVDFVNRLNDKYFPDDEITASDIFDYPTVDELSDHIVRKKSSSVP	3030
ò	26		25
g	3031 PA	PAASEIMKETMNGISTSVDAEHTKLENLSQSFMLLENQNSINPTLKMIWSNQTIKLVKPS	3090
ò	26		25
qq	3091 DG	DGNFLFELNANGGQEKEIQKHFTGPNNIIJDLKGFHEGSTETLYMSLLNLVKSISKLEIQ	3150
ò	26		25

g	3151	CRFGVSQEFGLGNSISRAFMKTVAAEKNPLISFAWYQNVQQVSFVDSDSPITGNWLITGG	3210
è			25
5 6	1211	.SGIGLEIGKETANNGAENVILISRROPTAKALRDILSTELTHIGLARKTIVLKLIKNIS	3270
3 8		A CORP.	90
3 8	3271	ISDLFSKKVTFFYNLLOSKCFSKHFHWLFEWLEVYLIKQWTV	3330
ò			43
원	3331		3390
ò	4		43
a	3391	LEEJEKHFNYKJENFIMMSSFTAACGNEGOLNYGVSNAYLEYOVQRRRRQGKSGCA10WG	3450
ò	4		43
qq	3451	NWIDTGMATDENVRKFLANLGFLGQHNKDALKYLRACILTKPELIMVANIDWNVILKNRK	3510
ò	4		43
g	3511	DLPKDLINTGILPFEDFTGKMNESEFPLSNGDFEKVSMNFSVEDEEEVLELIKEKVSSIL	3570
ઠે	4		43
q	3571	MCSPTKLKNNKNIMDMGLDSKLIVEFLNFINSTFKISVNLSDAYNHPTLEKLAAHIFEQM	3630
ò	4		43
g	3631	TIVDHPVNSVKSEEIFKSTDFCPIFGINIFFDNKNDFDKAKSTAVKLLENGEOLPTAGKY	3690
ò	4	PSLGAQ	49
සු	3691	AVSVVGKSIRDVVSKIKEAAPQQIKLCQESSKCVLMLTGQGSQYPMMGRQLVENYEIFRT	3750
ò	50		49
g	3751	TLQSCLKKCDEYLQGDVSLWEILFNTDHYKLLQLTKHMQPIMFCFGYATAQLWLSLGIVP	3810
ò	50	<u> </u>	20
OD	3811	DYYLGHSVGELVAGVLAGIMSIEDGLRLIVERGKAMENIAGLGALLAVQREIADEVLRKF	3870
ò	51	RVHLVKM	57
g	3871	KVSVATINSPKQVVFAGTKSVLDAALAFVKGQGKQATYVNQQYPFHSNLIQETHLVSLRQ	3930
ò	58		57
q	3931	CLADIKFSAGRTPLVSNVTGQIINTFSEAYIVKHTVSAVKFVDCVETLQAKGVTVWIDAG	399(
ઠે	58		53
qq	3991	SAAVLATFVKRIIQPTELSKHRIVQTCKEKESDVDNLVQACLELEQSGLPISWTTLYGCG	405(
ò	58		52
පු	4051	RNADERLVEFPMTHNDIIKNDEFELLEGHQLNGKIVVAGAYQLFKIDQLVKLKAAGMELM	411(
ò	58		52
8	4111	LKNVKFLKPWYIEDNREYQIQWNSDMTIELIVNSVIVCSLEVEPQNSVLKLETISENEKP	417(
ò	58		57
g	4171	FEVHDFYETLFRNGLQYDSGFRRIESARRSDKRCFSQIKSSPFAWPLIDSAMHSITASVV	423(
ò	28		57

۵	4231	PRRPDCYFLPVAMGSVTMKDTNSFTLPNLHAQTVITSETDKFIQVNVALLAGDTPICEVR	4290
≽	29	NIL/TEP	63
ā	4291	:         NMIIVVLKTEPVHTRIPNSIETVETPPKSEIEIVGFDISLPYNQISENSENWQHLKTNTV	4350
≿.	64		63
۾	4351	KQKLHNRSLKQDHARVALLDSDARYWDPEYFGIRPSEAKFIDPQQRLLLCSVAKLLDSLL	4410
≳	64		63
ထူ	4411	ITSLTSNTGVFIGCSANEFSHIVYAYGYKDPRAEWSGGTSNSALAGRIAHWLKLKGPVVT	4470
≥	64		63
စ္	4471	LDTACSSSFYALSAACDALRTGQCEYAIVGTVNLVMHEMTTDVLQNAKMTVDDFCKAFDV	4530
<u>≻</u>	64	EGAPNITA	71
ą	4531	DANGYKRSEAVCSMLLTKSPNIDSVATITNYATGHNGTSSSLFTPNGLSQLEVMQRATNP	4590
<u>≻</u>	72		79
g	4591	LEKILEIQTHCTGTKLGDPIEINAISKLVSSACKIGSVKSNIGHTEGSSGLVSLCSSLMS	4650
<u>&gt;</u>	80		79
ą	4651	FRSKYRVAQLHLKCPTNSIKTNKMICRFIGEDADENNSILINNFGFTGSNCSVVLKPKNA	4710
>	80		79
ڡۣ	4711	1SEHFVSSEVFYP1LLSSHSAKSLQKYVQVLCEF1SNSAKSLHDIMMSLFQKKIHVHRQF	4770
<u>≻</u>	80		79
ڡۣ	4771	IIFNFKRKIAVTSLDGFVEVRDERLEKLKHPCSVFLKEGVVHFDKDKSFQRVDLPSIVFN	4830
<u>≻</u> -	80		81
ō	4831	NTLHWALDSYRDEIDRHESQQMSFKNIFYEKVLLETPMPQQNPISKVVCIGRLDLIPKIE	4890
≥	82		81
. ي	4891	IDEVSSFANGIIVFHPISNSIFEYLKLAKVWSLISRNQNVFIIICCFENGTSHTEWTGTL	4950
<u>≻</u>	82		81
ð	4951	RSLASEKMI PYKFVSI DKVDALKLEFNHEYMFEAI FYSKRGRYVERLRKVNPTFKFAPQY	5010
≥-	82		81
۾	5011	EKCLISGGTGGIGSAIINELKPKSSVIITRKNIASEDGKTFLSSDITRLDISHKFNYVFH	5070
<u>≻</u>	82		81
ā	5071	LAGI VNNSLHENVKRDSLDEMVSI KLQGAKNLMKCCDETSHFVFSSSI ANVLGSYGQSNY	5130
ڃ	82	350	83
മ	5131	AFSNGLVTSFLETSSTKSTIIHWGPWKDVGMLAQPERREIVKQIESNGWKLLPNQDAISV	5190
≿	84		83
ą	5191	FYTQFMETHEQ11VFDGDFDT1VARQPHLQKLLSEVVEKTKVKEE1KKKSLNFEE1FFE1	5250
≿	84		83
Q	5251	VGITDISSKLNI PFMDLGI DSLCMENLRYSLNKNFDLELTVSEMFENATYQKLQTYVETL	5310
≿	8	SQTINPEDDTSQTINPEDDT	93
ð	5311	RKAKHSESLSHDRVSSQVSNKEDDTRVAVIGWSAEFSGSSNIHEYWENLMDGICSTGNNK	5370

ò	94	96
đ	5371	 YLLKNPFGFDNKFFNLTDEDARVLDPQVRKFIQHAYLALENSGYVKQKHELRCGVFAGAE 5430
ò	96	96
qq	5431	PSDYGRADDHDDAMRKLFVMNMNSYLASYCLDLKGEAVSVYSACSTALVAVANAVKS 5490
ò	96	56
q	5491	IQSGSMDYALVGAASIAEVSGALSGFDDQKKTMFSKSGVCRPFDKDSEGIVRGSGVGCFV 5550
ò	96	56
q	5551	LKRYSGALLDNDNVHFVIKDFAINNDGHSRASFMAPNPAGQLKCMTDVLARFTNKEKERI 5610
ò	96	86GHV
q	5611	SFVECHATGTTLGDTIEMNSLRTAYSFKNKLAIGSCKANIGHAYAASGLAALVKCAKMLQ 5670
ò	66	86
qq	5671	TGIIPPQVNFSEFRDGMGQFFTVNGKKSTISQNSLISIDSFGIGGTNVHMVIEFPARSQE 5730
ò	66	103
qq	5731	VVKISSENLILYDMIPISAKTEYSLDHTSEAISKYLQTDTNKIAQCSSTFIHSRVPMDSR 5790
ò	104	103
q	5791	TYLSVNNNNELLKIRTNKKTWFNGKSPKIALFFAPQGIQFTNILPNEYLKNSAYRREVEY \$850
ò	104	103
q	5851	LCELASSFGIPSLEGILYPTKNFDHLIHATOFAQIAIFVQCMAIFKAIKNVFNPTCLIGH 5910
ò	104	103
đ	5911	SVGEYAAAVISGALKTEEALKLLIKRSELIGKTEKARMLMVWNYEKQLPSHVHVSAIIDA 5970
ò	104	103
q	5971	NTKCVVGPVETIDNLEKYFINNHIKYRNIETKHGFHSKMFHCISKEFEFFCESFATKVPL 6030
ò	104	103
q	6031	IPMISSITGSEIKIFDSKYCTMHLTNPVNLELVVDHIMKLDIDIIVEVGPTGVLSNLLAK 6090
ò	104	103
q	6091	RNSKIVVVPTCGTKKHPKISLGECIGQLWSNGVDIRKLTPKLAVDGQVPGYCFDERQFGE 6150
ò	104	103
Q	6151	KNQKISQKLNRPSYYKESWKPVSSELEETKPVRFTVCDGSLNGISEPVLVYLLRKSEDIH 6210
ò	104	109
qq	6211	KNYFDVELFLKSSPRCSTVVFVGMDNSPSVHLSLGLIRCYQLVSRIDLKYVENFENIAMS 6270
ò	110	BLP112
Q	6271	IVIQKVLTANGLYFRIDSTGLCKHGFRTTEIPSRLHPVSRGHALVFGANGFIGSIVFRLL 6330
ò	113	112
g	6331	QEMGMNVIPISRASIPSCDITNIKDVQNVFKSLGFKKFSVVINCVGVETSAKMNKTSLEQ 6390
ò	113	112
Q	6391	EIVLSPKTFGSVNILKCLEEFSIEVDKLVNFSSLSSVVPLLGNFDYASANCFVEALTKQG 6450

m i	DD 5 GGSFRILLQEVVAALITILVVCLUTALQSGSGTISEFSSGVLFSSRANISGGFFVDDSNANGUA	DD 65 GIHVIDSHHIVRRDSYGRRGKRDVTSTDRRRRLQGVARDCGHACHLRLRSDDAVYIVHLH 124	6 vo	Db 125 RWNQIPDSHNKSVPHFSNSNFAPMVLYLDSEEEVRGGMSRTDPDCIYRAHVKGVHQHSIV 184	6 AQ	Db 185 NLCDSEDGLYGMLALPSGIHTVEPIISGNGTEHDGASRHRQHLVRKFDPMHFKSFDHLNS 244	9	245 ISVNETETTVATWQDQWEDVIERKARSRRAANSWDHYVEVLVVVADTKMYEYHGRSLEDYV	OY 31 LTNINIGAELERPSEGAQFRVHLVKMYILITEFEGAFNITANLISSELSVCGWSQTINFE 90  ON 306 LTTFEGATVASTYPHOSIPAGINESTONAVILITERPROPRITONAOTIODEFEMOOVYND9 364	505 DIEFOLVASTIRRQSERASTINVVVVALLVERTENAGFALLQUAQQLEQGFCKRQQLINGE	365 DDSSVQHHDVAILLTRKDICRSQGKCDTLGLABLGTMCDMQKSCAIIEDNGLSAAFTIAH	0y 126 125	Db 425 ELGHVFSIPHDDERKCSTYMPVNKVCKFQSTKFDKTQFQNNFHIMAPTLEYNTHPWSWSP 484	Qy 126 125	Db 485 CSAGMLERFLENNRGQTQCLFDQPVERRYYEDVFVRDEPGKKYDAHQQCKFVFGPASELC 544	Оу 126 125	Db 545 PYMPTCRRLWCATFYGSQMGCRTQHMPWADGTPCDESRSMFCHHGACVRLAPESLTKIDG 604	0γ 126 125	Db 605 QWGDWRSWGECSRTCGGGVQKGLRDCDSPKPRNGGKYCVGQRERYRSCNTQECPWDTQPY 664	Qy 126 125	Db 665 REVQCSEFNNKDIGIQGVASTNTHWVPKYANVAPNERCKLYCRLSGSAAFYLLRDKVVDG 724	Oy 126130	Db 725 TPCDRNGDDICVAGACMFAGCDHQLHSTLRRDKCGVCGGDDSSCKVVKGTFNEOGTFGYN 784	φγ 131 130	Db 785 EVMKIPAGSANIDIRQKGYNNMKEDDNYLSLRAANGEFLLNGHFQVSLARQQIAFQDTVL 844	Qy 131 130	DD 845 EYSGSDAIIERINGTGPIRSDIYVHVLSVGSHPPDISYEYMTAAVPNAVIRPISSALYLW 904	Qy 131TWS	Db 905 RVTDTWTECDRACRGQQSQKLMCLDMSTHRQSHDRNCQNVLKPKQATRMCNIDCSTRWIT 964	Qy 138 ED 139	Db 965 EDVSSCSAKCGSGQKRQRVSCVKMEGDRQTPASEHLCDRNSKPSDIASCYIDCSGRKWNY 1024	Oy 140 139	יים ביים יים יים יים יים יים יים יים יים
Oy 113 DGNRQVRGVT	123	6511 SSVNPADIATKSIAFHRTDENGSEVKAVESLKLPKSTSCEFVIAEIWKETLGISILNDAN	(V) 123	OSTI FWEFSEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	27. TOWNS TO THE TAMES OF THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE TAMES TO THE T	DO 0051 ALSIDALFUINSQUIQUEFULNETUL, ISRINLIFALISIELNET VWEFLANIOENS 0090	6691 YRTVFKSGNSPYQYICSLTESFHDFDKRCNLNNAISHEPNHLFEIGKSTPLRVRVAEDCD	Qy 132 140	Db 6751 NSRIHIVFNQHHILTDGWSMTVLSDTVSSLYAAYRGETSFPSKTKQTISQVAMGTKSSGD 6810	Ογ 141 140	6811 IKEALEYYQNTYHTIIPYDSETGNTSPSYVRISKLIPSKIWQKLVGLSKLYNTTMYNLAL	141	6871 SVFCDAVKSFIGQADILLAYALSGRNADNSELLGYFMNNALFKISLPFEILKLEEILNIV	UY 141	A DISCUSSION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O		1135313 1660	RESULT 7	1713/1 1720-1701 protein F25H8.3 - Caenorhabditis elegans C. 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Seature: prelimitaty; translated from GB/Embs/DDBU	A;Residues: 1-2165 <w1z> A;Cross-references: BBBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022; CESP:F25H8.3 A:Experimental anuxes. alone mittin</w1z>	Cybaptramentar acuted trong trong Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of the Comments of	634/3. 744/1.	; 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54/2; 54/2; 54/2; 54/2; 54/2; 54/2; 5	Query Match 29.6%; Score 229; DB 2; Length 2165;

ò	140	
<b>Q</b>	1085 SECSRSCDGGVKWRHAQCLDAADRETHTSRCGPAQTQEHCNEHACTWWQFGVWSDCSAKC 1144	30. Indeles
ò	140 139	01 18:14
셤	1145 GDGVQYRDANCTDRHRSVLPEHRCLKMEKIITKPCHRESCPKYKLGEWSQCSVSCEDGWS 1204	AGLDLAVEFSTELPDAGTVRALTERLLLLTOVAADPGVRLGDLDVLLPGEHHDL
ò	140 139	11.04
q <sub>Q</sub>	1205 SRRVSCVSGNGTEVDMSLCGTASDRPASHQTCNLGTCPFWRNTDWSACSVSCGIGHRERT 1264	1636 LVAANRPGTAPASPAPASPEPASPEPASPAPGTATLPELFERQAARHPDRTALTFEGTSL
ò	140 139	14
QQ	1265 TECIYREQSVDASFCGDTKMPETSQTCHLLPCTSWKPSHWSPCSVTCGSGIQTRSVSCTR 1324	1696 SYAELNARANRLARLLTARGIGPDALVALALPRSAELVVALLAVVKSGAAYVPLDPGYPA
ò	140 141	19
qq	1325 GSEGTIVDEYFCDRNTRPRLKKTCEKDTCDGPRVLQKLQADVPPIRWATGPWTACSATCG 1384	Db 1756 DRLAHALSDSAPAALLTDRATAGRLPAHEVPRIVLDAPAPADGGTTGGDPADAHPATDLA 1815
ò	142	Оу 19 18
q	NGTQRRLLKCRDHVRDLPDEYCNHLDKEVSTRNCRLRDCSYWKMAEWEECPATCGTHVQQ	18
ò	142	Оу 19 18
g G	1445 SRNVTCVSAEDGGRTILKDVDCDVQKRPTSARNCRLEPCPKGEEHIGSWIIGDWSKCSAS 1504	18
ò	142 143	Оу 19 26
ପୁ	1505 CGGGWRRRSVSCTSSSCDETRKPKMFDKCNEELCPPLTNNSWQISPWTHCSVSCGGGVQR 1564	::
ò	144	0y 27 30
qq	1565 RKIWCEDVLSGRKQDDIECSEIKPREQRDCEMPPCRSHYHNKTSSASMTSLSSSNSNTTS 1624	   Db 1996 AAASSASTIGVNIPDLRVYVLDDRLRPTAPGVTGEMYVAGAGLARGYLGRPALTADRFPA 2055
ò		Oy 31 30
a	1625 SASASSLPILPPVVSWQTSAWSACSAKCGRGTKRRVVECVNPSLNVTV 1672	Db 2056 DPYAALFGERGTRMYRTGDLARRRTDGGLDYLGRADQQVKIRGFRIEPGEIEAVLAAHPA 2115
RESULT	8 E1	Ογ 31 30
CDA	138249 CDA petide synthetase I - Streptomyces coelicolor - Specias Streptomyces coelicolor	Db 2116 VDDVAVVAREDVQGDPRLVAYVVTGSGATARALHDHAAGHLPDHMLPSAFVTLDVLPLTP 2175
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7, Sa	under, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A	Db 2176 NGKLDTKALPAPAHAGQVTGRAPRGPREBILCALFAEVLGVPRLTVDDSFFDLGGHSLLA 2235
Bubm A;Re	isted to the EMBL Data Library, March 1999 ference number: 221602	Qy 31 30
A; Ac	cession: T36248 atus: preliminary; translated from GB/EMBL/DDBJ	Db 2236 TRLAGRIRGTLGVELSVRRLFETPTVAGLSAALDGAERSGTGPTAGERPERLPLSYAQOR 2295
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A A S	OBS-TELETENCES: EMBL'ALUSS640; FIDN: CABS8518.1; GSFDB: GNUCO FO; SCUEDB: SCEOS. USC. perimental source: strain A3(2)	Db 2296 LWFLHQLEGPSPTYNITGALRLTGDLDPGALRAAFQDVVTRHESLRTVFSEDGHGARQTV 2355
A; Ge		Oy 31 42
C; Ke	perfamily: accenter-con ligase nomology; acyl caller protein nomology ywywode carrier protein; phosphopantetheine; bosphopotcein 6.101/man; carrier 100 14200 homology acyle; posphore atvairs 12011	Db 2356 LDAAGVRFELPVADVSEDRLDARLEEAARHCFDLTTDIPVRAELFRLGAREHVLLLMVHH 2415
F;31	.ypicai	Оу 43 42
F; 22	115-2184/Domain: acetate-CoA ligase nomology <acl2> 000-2268/Domain: acyl carrier protein homology <acp2></acp2></acl2>	Db 2416 IAGDGWSLGPLIRDLAAAYTARAARRAPDWAPLPVQYADFALWQRAALGDAADATSPAGR 2475
F; 28	104-1249/Domain: acetate-CoA ligase homology <acl3> 165-1332/Domain: acyl carrier protein homology <acp3></acp3></acl3>	φγ 43 42
F F F	123-4746/Domain: acetate-CoA ligase homology <acl4> 662-4836/Domain: acyl carrier protein homology <acp4></acp4></acl4>	Db 2476 QLAHWKEALAGLPDRLELPADRPLPAVASHRGGRVPLTVPAPLHSGVABLARESRTSVFM 2535
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	102-5870/Domain: acetate-com ligase nomology <acl5></acl5>	Qy 43 42
F F F 1		Db 2536 VLQAALAALLTRMGAGEDVPLGTPVAGRGDDAVDQVVGFFVNTLVLRTDTGGNPTFRALL 2595
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ò	43 -	42
g	2596 DI	DRVRDTDLTAYDHQDLPFEHLVDVLSPTRSLSHNPLFQVLLSLDTTQQDALAALSATGLG 2655
ò	43 -	42
엄	2656 VI	VRLLNVTTGVAKLDLALEIAEHRDADGAPAGLVGAAEYSADLFDEGTVTLLVERFLRLLD 2715
ò	43 -	45
a	2716 A	ALVADPSRRIGDVDVLGPRERERVLTEWNDTPRRPVQGTFADHVARHAAERPGHLAVETA 2775
ò	43 -	42
g	2776 G	gaaapggaliygelneranrlarallargagperfvavalprsadlvlsalaafkagaay 2835
ò	43 -	42
q	2836 L	LPVDPAHPAERITHLVSDAAPTLIVTTSALAASLPDTGTPVLLLDTPETAATLAALPGHD 2895
ò	43 -	. 45
g	2896 V	VTDADRPVPLRPEHPAYMIYTSGTTGRPKGVVVTHTGLPGLLDIFTRDCAAGPGSRILQH 2955
ò	43 -	DPSLGAQF 50
8	2956 L	LSPSFDASFWELAMGLLTGATLVVAPPETTPGPELAELATRHAATHLSLTTSVLGLLPPD 3015
ò	51 -	09
q	3016 S	SLPDGLTLVVGAEAIPPELVERWSPGRTMLNSYGPTETTVCSTMSGPLSGPAVPPIGSPV 3075
ò	51 -	09
Ωp	3076 A	ANSAVYVLDAALRPVPPGVPGELYAAGAHLARGYHDRRALTAERFVANPFGEPGSRLYRT 3135
ò	51 -	60
g	3136 G	GDLVRWRPDGQLEYLGRADTQVKIRGLRIEPTEIEAVITERPHLARAAVIVREDRPGDRR 3195
ò	61 -	
g	3196 L	LVAYVVPEPGATVDTAELRAALRETLPDHMIPTAFVVLDALPLTLNGKLDRKALPAPDYS 3255
ò	61 -	65
g	3256 #	
ò	99	9
g	3316 \	VRDVFEHQTPALLARSAAAAPAGDRTARDSDVPADGPAPRTPMMGWFAALGSDLAAFNQS 3375
ò	99	99
g	3376 1	LVLRVPAALDPDTLDTALRAVLDRHDALRMRVADDWTIEIPPPGSVTPADCLVRFDAVGL 3435
ò	99	9
Q	3436 I	DEAAVRSAVTEQARTARDRLAPADGRMLQAVWLDRGADRDGLLLLVANHLVVDGVTWRIL 3495
ò	. 99	59
q	3496 1	VPDLAAAYAGETLAPVGTPWRHWALSLSDLAGQPRTEEELDHWHSVLGDTPHTLRLDPAR 3555
ò	99	APNITANLTSSLLSVC
g	3556 1	DTHATAGEITAELDADTTEALLTWVPGVCHATVNDVFLSTFALAVAGWRRGRGEDADAPV 3615
ò	82	81
q	3616	VLDLESHGRHEEAVPGVELSRTAGWFTSMYPVRLAPPAGASGDGSALRALKAVKEQLRTV 3675
à	Ca	

q	3676 PGDGLGYGLLRHLNPRTRAALAALPLPEFGFNYLGRIGQEGTDEAPWTIEGGDVAGIDGA 373	38
ò	82 81	
g	3736 MPLAHPVDVNAVARETADGTRLRARWTYSRTALEPEDTQRLADTWFRLLRRLVEEARQPG 379	95
ò	82 81	
g	3796 AGGLTPSDIAHPALAQDEIEDLEHTVPGLQDILPLAPLQEGFLFLNLYDENARDVYVGQL 385	355
ò	82 61	_
Ор	3856 AFDLEGSFDGTRMRAAAGALLRRHANLRAGFRQTATGTWVQVVPAELEPDWRECDLTDRA 391	115
ò	82GWSQ 85	
qq	3916 DEAERDAEAGRLAAGDRERRFDLTSPPLMRFTAIRLSADRVRLVMTNHHILLDGWSMPLL 397	975
ò	98	٠,
qq	3976 WQELTELYVSGGDPVSLPPVRPYRDHLAWLGARDRAARDAWRRSLSGLDEATLLAPDAG 403	035
δ	58 98	
q	4036 PAEAAPLGIPFGLDRDATAALSAWARGRGVTWNTVVQGAWALALAQATGRDDVVFGATVS 405	960
ò	98	10
QQ	4096 GRPPELPGVESMIGLFINTLPVRARLDOAEPLGDLFRRLONEQARLLDHOWPGLADIOHW 41:	155
ò	98	ın
qq	4156 AGHGELFDTAMVFQNYPVSADTTSRQLDGLRVAGYDAVESTDFAVNLVAHTRDDALRLRL 42:	215
ò	98	'n
Q	4216 DYRADACAGDLVRSLADRMLRVLEALVTDSDRPVAHLDTLDPAVRERVLVEWNGAPTQLP 42°	275
ð,	98	ις.
qq	4276 GTPLHELISEQARLTPDAVAVVCDGTSLTYAELDGGANQLARHLLGEGLGAEDFVAIALA 43:	335
ò	98	'n
g	4336 KSLDAVISMLAVLKTGAAYLPIDPDYPAERITYMLDDARPALTLTEPVPVERYTGHSVTA 43	395
ò	98	S
q	4396 VIDEERRSPWSARHAAYMIYISGSTGRPKGVVIEHHALATYLHRARNTYTAMTGVTVLHS 44	455
ò	58 98	w
Q	4456 PLAFDLTITALWTPLTSGGTVHLTSLEESDTOPSLIKATPSHLPLLTTLPETASPSHTLI 45	515
ò	58 98	S
QQ	4516 LGGEALHTDHLVTWRTQHPGVQIINAYGPTESTVNITDHHVGEDTPDGPVPIGRPFANTQ 45	575
ò	06 98	0
q	4576 VYVLDSALRPVAPGVTGELYLAGEQLARGYLGRPALTAERFTANPHSSTPGARMYRTGDL 46	4635
ò	91	o
qq	4636 AHWNHHGHLTYDGRADHQIKLRGHRIEPGEIEATLTAQTGITQATVQLREDQPGDORLVA 46	695
ò	91 90	0
đ	4696 YLVVNDSTEYDEKTVRDALTSALPDYMVPSALVTLDALPLTPNGKLDRTALPAPAYSAST 47	755
ò	91	0

۵	4756	AGRAPRIPREEVLCTLFAEVLGVDLVTIDDNFFDLGGHSLLATRLVSRTRTALGVELSIR 4	4815
>	91	6	06
۵	4816	QLFETPTVAGLAEALDASGTVRTALTARPRPERIPLSYAQQRLWFLHQLEGPSATYNTVL 4	4875
<u>&gt;</u>	91	6	06
۵	4876	TLRLGGALDVDALRAAISDVVARHESLRTVFTEDERGAYQIVLPVEAASTPFTVVDVAEE 4	4935
≥	91	6	06
۵	4936	EIGDRLDEAVGHCFDLAQELPARTSLFRVSEREHVLLLLIHHIASDAWSRAPLAQDLTAA 4	4995
≥-	91	5	94
ڡ	4996	YAARVRSEAPMWAPLTVQYADYALWQQEILGDDTDADSLAGRQLAYWKQQLAGLPEQLDL 5	5055
≥.	95		94
Ω	5056	PTDRPRPAVAGYSGDRVPFTVPTELHTRLTELARATNTSAFMVIQAAVAVLLTRLGAGED	5115
≥	95	5	94
۾	5116	I PIGTPVAGRTDDAADDLIGLFINTLVLRTDTSGDPTFRRLLDRVRDTDLAAYAHQDLPF	5175
≥.	95		94
۵	5176	ERLVEALNPARTLSHHPLFQVLLTFNNTDHEGALKDISELPGLTVALREVQRTSSKFDLS	5235
≥.	95	5	94
Q	5236	FGFAESFDTSRRPQGIEAALDFSTELLDRRSAQAIADRFLRVLEAVTTAPDRPIGAVELM	5295
٠ ج	95		94
ā	5296	DPAERERVLVEWNGAPTQLPGTPLHELISEQARLTPDAVAVVCDGTTLTYAELDRRANQL	5355
<u>≽</u> -	95		94
۵	5356	ARHLLGEGLGAEDFVAIALAKSLDAVISMLAVLKTGAAYLPIDPDYPAERITYMLDDAQP	5415
≿	95		94
Q	5416	ALTLTAPIPPASYDSRPTSEITDVERRSPWSARHAAYMIYTSGSTGRPKGVVIEHHALAT	5475
≿.	95	5	94
Q	5476	YLHRARNTYTAMTGVTVLHSPLAFDLTITALWTPLTAGGTVHLTSLEEAEVQPSLIKATP	5535
≿	95		94
ð	5536	SHLPLLTTLPETASPSHTLILGGEALHTDHLATWRTQHPGAQIINAYGPTESTVNITDHH	5895
≿	95		94
ą	5596	VSEDTPDGPVPIGRPFANTQVYVLDSALRPVAPGVTGELYLAGEQLARGYLGRPALTAER	5655
≿	95		94
ð	5656	FTANPHSSTPGARMYRTGDLAHWNHDGHLTYDGRADHQIKLRGHRIEPGEIETTLTAQTG	5715
à	95		94
ဥ	5716	ITQTTVQLREDTPGDQRLVAYLVVNDSTEYDEPTLRDALASALPDYMRPSAYVTLDALPL	5775
⋩	95		94
ą	5776	TPNGKLDRTALPAPAYSASTTGRTPRTPREEILCTLFAEVLGVDLVTIDDNFFDLGGHSL	5835
⋩	95		94
ų	5836	LATRLVSRARTALGVELSVRQFFETPTIAGLSGAFDRAGRARAALTARPRPERIPLSYAQ	5895

ò	92	66
qq	5896	QRLWFLHQLEGPSATYNIPTTLRLTGTLDTDALQSALNDLLARHESLRTTYTEDGEGPRQ 5955
ò	95	86
Q	5956	VIHAWEPGMLPLGVVDTGEGELDAMLSAGVHHAFDLTAGIPVRATLFRISEQEHVLLLLI 6015
ò	95	96
QQ	6016	HHIATDAWSRTPLGHDLAAAYSARCAGDVPAWEPLPVQYADYALWQREVLGDEGDADAPA 6075
ò	95	6
q	6076	GRQLAYWTRQLADLPEQLDLPTDRPRPAVASQDGDRVAPSLDADLYVRLTELARATHSST 6135
ò	95	P6
g	6136	FMVVQAALAVLLTRLGAGEDIPIGTPVAGRTDDATENLVGFFVNTLVLRNDTSGNPTFRE 6195
ò	95	76
q	6196	LLEETRRTDLAAYAHQDLPFERLVEALNPARTLAHHPLFQVMLILSTAETDPDASLALPG 6255
ò	95	6
q	6256	LRVGAERSRLGAAKVDLAFALAEVRDGEGRSTGLTGALDFRTDLFDRSTARSLVERFVRT 6315
ò	95	66
g	6316	LEAVVADPGVRLSRVPVLTGSERRSLLDRGTGPLLEGLDATLPELFAEQALRTPGAPALV 6375
ò	95	6
q	6376	RGGTTVSYAELDLRTNRLARLLRQQGVRPGTPVVMLMERSPAHVVATLAIAKAGGAYVPL 6435
ò	95	76
q	6436	HDTYPLDRMRHVVADTAATLILTDRAEAARAGQLGARVMVVDEFGAAPSGSEADAAPGTG 6495
ò	95	6
g	6496	TGTGTGSRSGYVDDAPEVGLRPQDLAYVMYTSGSTGVPKGVAVTHRGVVDLVRDHCWRPG 6555
ò	95	99
දු	6556	VHERVLLHAPHAFDVSCYEMWVPLVSGGTVVVVAPPGHLDPAAITDLITAHDITAIHLTAG 6615
ò	100	102
q	6616	FFRVVAEEAPECFAGVREVLTGGDVVSPAAVARVLAHHPRIVLRHLYGPTETTLCVTQHE 6675
ò	103	102
qq	9499	VTAPYEARGSLPVGRATGNTRAYVLDRYLQPVPAGVPGELFISGSGLARGYLDRPDLTCE 6735
ò	103	YITR 106
QQ	6736	RFVADPYGGSGERMYRTGDLVRYNAAGELEYLARADDQVKIRGFRVELGEIEAVLATRPE 6795
ò	107	106
g	6796	LAQAAVVVREDRPGDRRLVGYVVAAAGRDGEVDPDALRAFSRQALPDYMVPSAFVVLGTL 6855
ò	107	109
q	6856	PLTANGKLDRKALPAPDYGAASTGRAARTPABELLCTLFAQVLGLSAVGVDDGFFDLGGD 6915
ò	110	109
Q	6916	SILSIQLVSRARAAGLALAVRDVFEHQSTARLAAALTDRDDAASVPEAEAVPPYGPAPLT 6975

Db         206 QERKRSTASPRPSSRGPGSRPSSPKKSMKSREGTPKRTLKPREGSPSKKLRSRTSTPVNE 265           Qy         9	38 33	4 10 10	OY 20	74 20 20 20 20 80	20	986 EVPENVTVVENETAILICKVSGSPAPTFRWFKGSREVISGGRFKHITDGKEHTVALALLK 24	Db 1106 GGGEKKPMTEAERROSLFPGKKVEKWDIPLPEKTVQQQVDKICEWKCTYSRPNAKIRWYK 1165 Qy 24
0y   110		Qy         145           Db         7216 VHDVLLTAFAFAVAGWRRGRGEDPDAPVVLDLESHGRHEEAVPGAELSRTAGWFTALHPV 7275           Qy         145           7276 RLAPDVTDWARLHQDGDALRDGLKQVKEQLRSVPGDGLGHGLLRHLNPTAGPRLARLPEP 7335           Qy         145           Db         7336 DFGFNYLGRRVTPATGTPEPWTVTGGGLAASRPTAPMAHAVELSAVVHEGADGPRLRAEW 7395	45	nge 11-Jan-2000		A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-7160 - M12> A; Cross-references: EMBL: 273899; PIDN: CAA98082.1; GSPDB: GN00022; CESP: ZK617.1b A; Experimental source: clone ZK829 C; Generics: A; Gane: CESP: ZK617.1b A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map position: 4 A; Map positio	Afintrons: 10/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3; 15/3/3/3/3; 15/3/3/3; 15/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3

g G	1286	EVEEDDQAEWTAR1TQDVFSKVQVYVEEPRHTFVVPMKSQKVNESDLATLETDVNDKDAE	1345
ò	EE.		32
요	1346	VVWWHDGKRIDIDGVKFKVESSNRKRRLIINGARIEDHGEYKCTTKDDRTMAQLIVDAKN	1405
ò	33	INTN	36
. g	1406	KFIVALKDTEVIEKDDVTLMCQTKDTKTPGIWFRNGKQISSMPGGKFETQSRNGTHTLKI	1465
ò	37	0	37
g	1466	; GKIEMNEADVYEIDQAGLRGSCNVTVLEAEKRPILNWKPKKIEAKAGEPCVVKVPFQIKG	1525
ò	38	ABLLR	42
Q	1526	TRRGDPKAQILKNGKPIDEEMRK	1585
ઠે	43	DPSLGA	48
g	1586	LAPFELFVKDKPKPPKGPLETKNVTAEGLDLVWGTPDPDEGAPVKAYIIEMQEGRSGNWA	1645
તે	49		48
q	1646	KVGETKGTDFKVKDLKEHGEYKFRVKALNECGLSDPLTGESVLAKNPYGVPGKPKNMDAI	1705
તે	4		48
q	1706	DVDKDHCTLAWEPPEEDGGAPITGYIIERREKSEKDWHQVGQTKPDCCELTDKKVVEDKE	1765
à	49		48
Q Q	1766	YLYRVKAVNKAGPGDPCDHGKPIKMKAKKASPEFTGGGIKDLRLKVGETIKYDVPISGEP	1825
à	49		48
g	1826	LPECLWVVNGKPLKAVGRVKMSSERGKHIMKIENAVRADSGKFTITLKNSSGSCDSTATV	1885
à	4		48
g G	1886	TVVGRPTPPKGPLDIADVCADGATLSWNPPDDDGGDPLTGYIVEAQDMDNKGKYIEVGKV	1945
ें	49		48
g G	1946	DPNTTTLKVNGLRNKGNYKFRVKAVNNEGESEPLSADQYTQ1KDPWDEPGKPGRPE1TDF	2005
à	49		48
g	2006	DADRIDIAWEPPHKDGGAPIEEYIVEVRDPDTKEWKEVKRVPDTNASISGLKEGKEYQFR	2065
ò	49		48
q	2066	VRAVNKAGPGQPSEPSEKQLAKPKF1PAWLKHDNLKS1TVKAGATVRWEVK1GGEP1PEV	2125
જે	49		48
අ	2126	KWFKGNQQLENGIQLTIDTRKNEHTILCIPSAMRSDVGEYRLTVKNSHGADEEKANLTVL	2185
à	49		48
g	2186	DRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVPCAKVKDTK	2245
ò	49		48
음	2246	AHIDGLKKGQTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKTGTPDVVDWDADRVS	2305
ò	49	OBRV	52
e G	2306	LEWEPPKSDGGAPITQYVIEKKGKHGRDWQECGKVSGDQTNAEILGLKEGEEYQFRVKAV	2365
ò	53		52
a a	2366	NKAGPGEASDPSRKVVAKPRNLKPWIDREAMKTITIKVGNDVEFDVPVRGEPPPKKEWIF	2425

ò	53	HLVKAVIL	
요	2426 1	/LGKPSSP	2485
ò	. 61		09
Ωp	2486	LGPLEVSNVYEDRADLEWKVPEDDGGAPIDHYEIEKMDLATGRWVPCGRSETTKTTVPNL	2545
ò	61		09
QQ	2546 (	QPGHEYKFRVRAVNKEGESDPLTTNTAILAKNPYEVPGKVDKPELVDWDKDHVDLAWNAP	2605
ઠે	61		09
g	2606	DDGGAPIEAFVIEKKDKNGRWEEALVVPGDQKTATVPNLKEGEEYQFRISARNKAGTGDP	2665
ò	61		9
qq	2666	SDPSDRVVAKPRNLAPRIHREDLSDTTVKVGATLKFIVHIDGEPAPDVTWSFNGKGIGES	2725
ò	61	_	65
qq	2726 1	KAQIENEPYISRFALPKALRKQSGKYTITATNINGTDSVTINIKVKSKPTKPKGPIEVTD :	2785
ò	99		65
a	2786	VFEDRATLDWKPPEDDGGEPIEFYEIEKMNTKDGIWVPCGRSGDTHFTVDSLNKGDHYKF	2845
ò	99		65
qq	2846	RVKAVNSEGPSDPLETETDILAKNPFDRPDRPGRPEPTDWDSDHVDLKWDPPLSDGGAPI	2905
ò	99		65
q	2906 1	EEYQIEKRTKYGRWEPAITVPGGGTTATVPDLTPNEEYEFRVVAVNKGGPSDPSDASKAV ;	2965
ò	99		65
q	2966	IAKPRNLKPHIDRDALKNLTIKAGQSISFDVPVSGEPAPTVTWHWPDNREIRNGGRVKLD ;	3025
ò	99		65
αg	3026 1	NPEYQSKLVVKQMERGDSGTFT1KAVNANGEDEATVK1NV1DKPTSPNGPLDVSDVHGDH	3085
ò	99		65
g	3086	VTLNWRAPDDDGGIPIENYVIEKYDTASGRWVPAAKVAGDKTTAVVDGLIPGHEYKFRVA	3145
ò	99	APNIT	70
g	3146 /	AVNAEGESDPLETFGTTLAKDPFDKPGKTNAPEITDWDKDHVDLEWKPPANDGGAPIEEY	3205
ò	71		7.0
q	3206	VVEMKDEFSPFWNDVAHVPAGQTNATVGNLKEGSKYEFRIRAKNKAGLGDPSDSASAVAK	3265
ò	71		20
a	3266 4	ARNVPPVIDRNSIQEIKVKAGQDFSLNIPVSGEPTPTITWTFEGTPVESDDRMKLNNEDG	3325
ò	71		20
g	3326 1	KTKFHVKRALRSDTGTYIIKAENENGTDTAEVKVTVLDHPSSPRGPLDVTNIVKDGCDLA	3385
ò	71		20
g	3386 1	WKEPEDDGGAEISHYVIEKQDAATGRWTACGESKDTNFHVDDLTQGHEYKFRVKAVNRHG	3445
ò	71		70
qq	3446	DSDPLEAREALIAKDPFDRADKPGTPEIVDWDKDHADLKWTPPADDGGAPIEGYLVEMRT ;	3505

ò	71	0/	
g	3506 1	PSGDWVPAVTVGAGELTATVDGLKPGQTYQFRVKALNKAGESTPSDPSRTWVAKPRHLAP 3565	
ò	7.1	0.2 70	
සු	3566	KINRDMFVAQRVKAGQTLNFDVNVEGEPAPKIEWFLNGSPLSSGGNTHIDNNTDNNTKLT 3625	
ò	. 11	0.2	
g	3626	TKSTARADSGKYKIVATNESGKDEHEVDVNILDIPGAPEGPLRHKDITKESVVLKMDEPL 3685	
ò	71	ANLT 74	
g	3686	DDGGSPITNYVVEKQEDGGRWVRCGETSDTSLKVNKLSEGHEYKFRVKAVNRQGTSAPLT 3745	
ò	75		
q	3746	  SDHAIVAKNPFDEPDAPTDVTPVDWDKDHVDLEWKPPANDGGAPIDAYIVEKKDKFGDWV 3805	
ò	9/	75	
Q	3806	ECARVDGKTTKAŢADNLTPGETYQFRVKAVNKAGPGKPSDPTGNVVAKPRRMAPKLNLAG 3865	
ò	16	. 52	
g	3866	LLDLRIKAGTPIKLDIAFEGEPAPVAKWKANDATIDTGARADVTNTPTSSAIHIFSAVRG 3925	
ò	76	82	
g	3926	::	
ò	83	85	
8	3986	LHYIVEKMDTSRGTWQEVGTFPDCTAKVNKLVPGKEYAFRVKAVNLQGESKPLEAEEPII 4045	
ò	83	88NILDSM	
요	4046	:	
ò	8	96	
q	4106	PGTTFSADNLKPGVEYEFRVIAVNAAGPSDPSDPTDPQITKARYLKPKILTASRKIKIKA 4165	
ò	96	56	
8	4166	GFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTTSIFFPSAKRADSGNYKLK 4225	
ò	96	56	
g	4226	VKNELGEDEAIFEVIVQDRPSAPEGPLEVSDVTKDSCVLNWKPPKDDGGAEISNYVVEKR 4285	
ò	96	ġ6	
g	4286	DTKTNTWVPVSAFVTGTSITVPKLTEGHEYEFRVMAENTFGRSDSLNTDEPVLAKDPFGT 4345	
ઠે	96	56	
සු	4346	PGKPGRPEIVDTDNDHIDIKWDPPRDNGGSPVDHYDIERKDAKTGRWIKVNTSPVQGTAF 4405	
ò	96	56	
g	4406	SDTRVQKGHTYEYRVVAVNKACPGQPSDSSAAATAKPWHEAPKFDLDLDGKEFRVKAGEP 4465	
ò	96	56	
g	4466	LVITIPFTASPQPDISWTKEGGKPLAGVETTDSQTKLVIPSTRRSDSGPVKIKAVNPYGE 4525	
ò	96	56	
g	4526	AEANIKITVIDKPGAPENITYPAVSRHTCTLNWDAPKDDGGAEIAGYKIEYQEVGSQIWD 4585	
ò	96	56	

Q C	4586 KVPGLISGIAYIVKGLEHGQQIRFKIRAENAVGLSDICQGVFVIANFFDFFOAFGLSF	
ò	96	95
qq	4646 TGYDTNQVSLAWNPPRDDGGSPILGYVVERFEKRGGGDWAPVKMPMVKGTECIVPGLHEN	4705
ò	96	97
q	4706 ETYQFRVRAVNAAGHGEPSNGSEPVTCRPYVEKPGAPDAPRVGKITKNSAELTWNRPLRD	4765
ò	86	97
q	4766 GGAPIDGYIVEKKKLGDNDWTRCNDKPVRDTAFEVKNLGEKEEYEFRVIAVNSAGEGEPS	4825
ò	98 ADLVL	102
q		4885
ò	103	102
qq	4886 ERTVVDVNPGEIVITTTGSKRSDAGPYKISATNKYGKDTCKLNVFVLDAPGKPTGPIRAT	4945
ò	103	102
셤	4946 DIQADAMTLSWRPPKDNGGDAITNYVVEKRTPGGDWVTVGHPVGTTLRVRNLDANTPYEF	5005
ò	103	102
q	5006 RVRAENQYGVGEPLETDDAIVAKNPFDTPGAPGQPEAVETSEEAITLGWTRPTSDGGAPI	5065
ò	103	102
đ	5066 QGYVIEKREVGSTEWTKAAFGNILDTKHRVTGLTPKKTYEFRVAAYNAAGQGEYSVNSVP	5125
ò	103	102
qq	5126 ITADNAPTRPKINMGMLTRDILAYAGERAKILVPFAASPAPKVTFSKGENKISPTDPRVK	5185
ò	103	102
g	5186 VEYSDFLATLTIEKSELTDGGLYFVELENSQGSDSASIRLKVVDKPASPQHIRVEDIAPD	5245
ò	103	102
qq	5246 CCTLYWMPPSSDGGSPITNYIVEKLDLRHSDGKWEKVSSFVRNLNYTVGGLIKDNRYRFR	5305
ò	103YITRFDLELP	112
q	: ::   :  5306 VRAETQYGVSEPCELADVVVAKYQFEVPNQPEAPTVRDKDSTWAELEWDRRFDGGSKIIG	5365
ò	113	112
g	5366 YQVQYRDTSSGRWINAKMDLSEQCHARVTGLRQNGEFEFRIIAKNAAGFSKPSPPSERCQ	5425
ò	113 DGNRQVRG	120
а	5426 LKSRFGPPGPPIHVGAKSIGRNHCTITWMAPLEDGGSKITGYNVEIREYGSTLWTVASDY	5485
ò	121	120
දු	5486 NVREPEFTVDKLREFNDYEFRVVAINAAGKGIPSLPSGPIKIQESGGSRPQIVVKPEDTA	5545
ò	121	120
q	5546 QPYNRRAVFTCEAVGRPEPTARWLRNGRELPESSRYRFEASDGVYKFTIKEVWDIDAGEY	5605
ò	121	120
Q	5606 TVEVSNPYGSDTATANLVVQAPPVIEKDVPNTILPSGDLVRLKIYFSGTAPFRHSLVLNR	5995
ò	121	120

121   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129   129	5725 120	5785	126	5845	126	5905	126	5965	126	6025	126	6085	126	6145	131	6205	131	6265	131	6325	131	6385	133	6445	133	6505	133	6565	133	6625	133	6685	137	5745	
5 6 6 6 6 6 6 8 6 8 6 8 6 8 6 8 6 8 6 8	EEIDMDHPTIRIVEFDDHILITIPALSVREAGRYEYTVSNDSGEATTGFWLNVTGLPEAP	QCPLHISNIGPSTATLSWRPPVTDGGSKITSYVVEKRDLSKDEWVTVTSNVKDMNYIVTG	1	LFENHEYEFRVSAQNENGIGAPLVSEHPIIARLPFDPPTSPLNLEIVQVGGDYVTLSWQR		PLSDGGGRLRGYIVEKQEEEHDEWFRCNQNPSPPNNYNVPNLIDGRKYRYRVFAVNDAGL		SDLAELDQTLFQASGSGEGPKIVSPLSDLNEEVGRCVTFECEISGSPRPEYRWFKGCKEL	1	VDTSKYTLINKGDKQVLIINDLTSDDADEYTCRATNSSGTRSTRANLRIKTKPRVFIPPK		YHGGYEAQKGETIELKIPYKAYPQGEARWTKDGEKIENNSKFSITTDDKFATLRISNASR		EDYGEYRVVVENSVGSDSGTVNVTVADVPEPPRFP11ENILDEAVILSWKPPALDGGSLV		TNYTIEKREAMGGSWSPCAKSRYTYTTIEGLRAGKQYEFRIIAENKHGQSKPCEPTAPVL		I PGDERKRRRGYDVDEQGKI VRGKGTVSSNYDNYVFDIWKQYYPQPVEI KHDHVLDHYDI		HEELGTGAFGVVHRVTERATGNNFAAKFVMTPHESDKETVRKEIQTMSVLRHPTLVNLHD		AFEDDNEMVMIYEFMSGGELFEKVADEHNKMSEDEAVEYMRQVCKGLCHMHENNYVHLDL	SM	KPENIMFTTKRSNELKLIDFGLTAHLDPKQSVKVTTGTAEFAAPEVAEGKPVGYYTDMWS		VGVLSYILLSGLSPFGGENDDETLRNVKSCDWNMDDSAFSGISEDGKDFIRKLLLADPNT		RMT1HQALEHPWLTPGNAPGRDSQIPSSRYTKIRDSIKTKYDAWPEPLPPLGRISNYSSL		RKHRPQEYSIRDAFWDRSEAQPRFIVKPYGTEVGEGQSANFYCRVIASSPPVVTWHKDDR		ELKQSVKYMKRYNGNDYGLTINRVKGDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEPLKF	LIND		BDTGF
	121	5726	121	5786	127	5846	127	5906	127	5966	127	6026	127	6086	127	6146	132	6206	132	6266	132	6326	132	6386	134	6446	134	9059	134	9959	134	6626	134	9899	138

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bacitracin C;Species:	nthetase 1 - Bacillus licheniformis cillus licheniformis
C;Date: 29-Oc C;Accession: R:Konz. D.: K	t-1999 #se T31677 Jens. A.:
Chem. Bic A, Title:	bacitracin biosynthesis of
Acces	on: T31677
Molec Resid	pressimilarly; crampraced from 65/2005/2005 type: DASS KXON> : 1-5255 kXON>
Cross	-references: EMBL:AF007865; NID:g4464275; PID:g2982194; PIDN:AAC06346.1 lics:
Super	aceta
⊀ eo ι	n: acetate-CoA ligase homology <acli></acli>
F;1134-15	;342-510/Domain: acyl carrier process sometagy carris; ;1134-1561/Domain: acetate-CoA ligages homology cACL2> :1683-1661/Anmain: acvl carrier protein homology cACD2>
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F;3195-36 F;3662-37 F;4712-51 F;5169-52	42/Domain: 29/Domain: 51/Domain: 37/Domain:
Query Match Best Local	itch 29.0%; Score 224; DB 2; Length 5255; al Similarity 1.6%; Pred. No. 47;
Matche	
	AGG
11	AGGAYLPIDPETPKDRIAFMLSDTKAAVLLTQGKAADGIDCEADIVQLDREASDGFSKEP
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Db 170	0 LSSVNDSGDTAYIIYTSGSTGTPKGVITPHYSVIRVVQNTNYIDITEDNVILQLSNYSFD 229
٠ م	ę
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۰ ک	5 8
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٠ ک	8
Db 350	O GSPLANTSVLIMDEAGKLVPIGVPGELCIAGDGLSKGYLNREELTAEKFIPHPFIPGERL 409
ò	8 6
Db 410	O YKTGDLAKWLPDGNIEFIGRIDHQVKIRGFRIELGEIESRLEMHEDINETIVTVREDEES 469
ò	8
Db 470	O RPYICAYITANREISLDELKGFLGEKLPEYMIPAYFVKLDKLPLTKNGKVDRKALPEPDR 529
۰ ک	9ELLVAVGPDVFQA
Db 530	O TAGAENEYEAPRNETEËKLAÅVÄQDVLHVEKAGIHDHFAQMGGHSLHAMELIAKIKEKMN 589
Qy 22	2 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10
Db 590	0 VEIPLHQLFKLATIKELSAPIEANHQEDKGDTLVTRAADPENIHEIFPLTGIQLAYLVGR 649
0y 26	6TER 28

g	650 DE	DETFEIGGVATNLTVEFEADVDLNRFQLTLQKLIDRHPILRTIVFENGTQKILEATQRYT 709	60
ò	29	28	_
g	710 IE	IETQDLRGFTEEEINVRILEQREKMTSKIIDPSVWPLFELKTFMLPGEKKYFFLNVDPLI 76:	69
à	29	36	
q	770 CD	CDDSSMKRLIREFKQLYENPGLQLPSLEYSFRDYVLASINFKQTSRYQKDQQYWLDKLDH 829	63
ò	37	36	10
g	830 FP	FPSAPELPLKSDPAHVAKPSFKKFSTFLDGHTWNELKKKARHHHLTPTSVLCAAYAYILA 889	39
ò	37	36	10
8	890 YW	YWSRQNHFAINLTVFNRIPFHPDVKNMIGDFTSLMLLDIHAEENMSSFWRFALNVQDTLL 949	6
ò	37	GAELLR	01
a C	950 EA	:::  EALEHRHYDGVDVIRNIAKKNGMNKKAVMPIVFTSVLSENPDDSFDSLVDFDNIHFFSTR 100	600
ò	43	42	63
g	1010 TS	TSQVYIDNQVYEINGGLYITWDYVEQIFEHEVIESMFDQYIAVIQKAVSGEDVSTIQMNE 106	690
ò	43	42	~
q	1070 KS	KSRQMISAYNDTDQSFDAKPLHELFTGQVKHGPDRMALKHHDEVMTYQELDEKSNQVARF 112	129
ò	43	44	-
g	1130 LI	LIGKGVEKGDYIGVIGKRSLGTIVNLLAVLKTGAAYIPLDPDYPEERKAYIQSKSNCKFF 118	189
à	45	44	€#
gg	1190 IS	ISHDVYDKEHIERFSKAPVDRKVDLDDMAYVIFTSGSTGKPKGVQITHVPQRNTILDINE 12	249
ò	45	SZLGAQFRV5LGAQFRV	0
a	1250 KF	KFNVTEQDNIMGISSLCFDLSVYDVFGALSSGASLVIIDDQRDVFSLKETAEKERITIWN 130	309
ò	53 -	60	٥
g	1310 SV	::::  SVPAIMGMTADVYPDNELNHHLRLILLSGDWIPLQLPATIKKTFKNAEVISLGGATEGSI 13	1369
ò	61	09	0
g	1370 WS	WSIYYPIQKVEEDWKSIPYGKPLANQKIYVLNQNKQLCPVGVEGELYIGGAGVASGYIHD 14	1429
ò	- 19	09	0
qq	1430 08	QEKTEHSFIQHQELGYIYKTGDYGVLKEDGYVEFLGRKDSQVKIRGYRVEMGEIENTLVS 14	1489
ò	61	TEPEGAPNITA71	1
g	1490 H(	HQEITKASVIDYTSPDGIKNLYAFVVAENAISQLDVKEFLQKTLPDYMIPAKFVQIEEIP 15	549
ò	72	71	т.
qq	1550 L	LTVNGKVDKRTLHDLAEQHTADEGQRGGRMLPENETQAMLLEIWKDIFGLDSINLDVSYY 16	1609
ò	72 -	71	
q	1610 E	EIGGDSLKAISIITEINKRMNVEMPISEIFKNDTIIALDHYLKNREESDMEHPIQKAREK 16	1669
ò	72 -	71	н
q	1670 E	eyyptspaqqrmymlsmlenergayhipmallvegrinamqlenalktflqrheilrtgf 17	1729
ò	- 21	57	ភេ.

g G	1730 E	EIQNNELIQKIYENVDFRLEYECLDASITDQHALMEITSRYCKESIKPFDLSRPPLMRAK 17	189
ò	. 92	75	ın
පු	1790 1	LĮKIDDIRHILVINFHHIISDGVSQGILMNEILELYSNVPLPEVNVQYKDYVEWNHTPNQ 18	849
ò	. 94	75	ß
đ	1850 8	SAAMKKQEAYWLDVYRDIPSKLDFPYDYKRHHIDTFEGSSVFLEMERELSDHIRKLAKHN 19	606
ò	. 94	75	S.
q	1910 (	GTTLYTVMLSAYYVLLNKYTNQTDIVVGTAAAGRLHPDLQDVFGVFVNTLALRNEVDTSY 19	696
ò	. 92	75	ß
q	1970	SFKEFLQQTKERTIAAFDNSEYPFDDLIRKLNGVRESNRNPLFDTMFVLEDARMFTKQKG 20	029
ò	16	75	.c
Q	2030	DVKLSPIIFELDNAKFDMIFNVLDFEQKIVLNIEYSTSLFKDETIQKIAEDYFRILEEVS 20	680
ઠે	9/	75	'n
qq	2090	ENLDVALHQIDMISRQEKRTLLESFNHTKTAYPKGKAIHQLFEEQAKRIPDHTAVVFEDQ 21	149
ò	94	75	ស
qq	2150	KLTYRQLNEKANQVARLLREKGVKPDTLVGIMMERSSDMIAAILGVLKAGGAYLPIDPEY 22	209
ò	16	22	ß
g	2210	PPERMRYMAFDSEVKVIISDVPLAEELTAESIELIHMDDERIAGODRSDIDNVNOSGDLA 22	269
ò	9/	8	S
g	2270	YVIYTSGSTGKPKGVMIEHQSLINLCSWHQSCFEVGQNDNSSIYASISFDAFVWELFPYI 23	329
ò	86	88	ស
qq	2330	TAGATVHVLNQETRLDVEKLNRYFHDHHITISFLPTPVCEQFTALDNHSLRTLLTGGDKL 23	389
ò	98	98	ស
Q	2390	NVFKEKSYQIVNNYGPTENTVVATSFPIDKSHQNIPIGKPIDNVKVYILNKDLOLCPLGA 24	2449
ò	86	98	S.
QQ	2450	SGELCIAGEGLARGYUNRPELTREKFIGNPFVPGERMYRTGDLAKMLPDGNIQFLGRVDQ 25	509
ò	98	58	ທ
QQ	2510	QVKIRGYRIEPGEIENRLLKYEKIEEAAVIAREDGDHDPYLCAYVTVKKEVEPEKIRAFL 29	869
ò	98		91
q	2570	KKSLPDYMIPQYFVQLDGLPLTVNGKVDKKSLPVPERSVTMDRRYEAPRÒMEEKLVSIW 20	629
ò	92	.6	덛
QQ	2630	EEALGINKIGINSHFFEAGGHSLKAAALVSTIHKELNVKLPLRQIFETPTIKGLRDISVR 20	2689
ò	92	.6	91
Q	2690	RRKCFYIDRKTEEKPYYRLSSAOKRLYILSOTGSHVAYNMPFAMTLEGDFDIRRFENTLK 2	2749
ò	95		91
qq	. 2750	NMVKRHESFRTSFVMIDGEVMQQIEKEIDFQVAYSDIGKESAEEKIKSFIRPFHLEKAPL 20	2809
ò	92	.6	91
q	2810	LRAEVVKLNEREHLLMFDMHHIISDGVSTDIFIQELGALYEGKSLKPFHIQYKDYAEWEN 28	2869

Page 45

ò	92	16	-
<b>Q</b>	2870	SHARSEELKRQEEYWLKTYKGDIPVLDLPIDHKRPLTKSSEGDTVTAAIESETFRKLQHM 29	929
ò	92	91	
g	2930	AKENGVTMYMLLLAGYTALLSKYTGQEDIIVGTPAAGRNHEDIQHLIGMFVNTLAIRNHP 29	. 686
ò	92	91	-
QQ	2990	EGKKT FRDY LQEVKENT LQAY ENQDY PPEELVEKVNI KRDMARNPLFDTMLVYHNT DVKP	3049
ò	92	91	
DP	3050	FEAEGLRSRLVEIKRGISKFDIT <b>V</b> TASEAADGLRLEVEYSTTLFNKERMERLSEHLISLL	3109
ò	92	91	
q	3110	EQAADHPDIAINQIDVLTKGERHRVLYDFNRTDGVFCKEMTIPELFEKQAEKTPDHPAVA	3169
ò	92	91	
qa .	3170	FGDETISYRELNERANSLAFTLRQKGVGPDVIAGILTERSIEMIVGIMGILKAGGAYLPI	3229
ò	92	9694QLLQ96	10
g	3230	DPAYPQERISYIVKDSDVSVLCAAGDVDPGEAYTGDIIRIDQTGQNDHVENLKHDIKPQH	3289
ò	97	96	
q	3290	LAYVIYTSGSTGKPKGVMIEHHSVNNLVHGLNERIYQHLDAHLNVALVAPYIFDASVKQI 334	149
ò	97	110	0
g	3350	FAALLFGHTLCIVPRETAWDAMSLIEYYSKNNINVSDMTPAHLNMLAYVDKTELEFDVKE 34	3409
ò	111	110	0
QQ	3410	LIVGGDALTPDVIGGLFHKFPNLSCNITNVYGPTECCVDAASHQIESGKVPQTPSIPIGR	3469
ò	111	110	0
qq	3470	PLLNTS1Y1 VDKELRPLPVG1AGELCIAGEGVARGYVNRPELTAEKFVDHPFEPGKKMYK	3529
ò	111	114	4
Q	3530	TGDLAMWLPDGQIEFLGRADHQVKIRGYRIELGEVEQQLLTHEKIKEAAVIAGKDQNGNS 3589	68
ò	115	114	4
g	3590	YLCAYIASDKELPAADVRQFLEREMPDYMIPSYFVKLDRLPRTPSGKVDRSALPEADGNV 364	49
ò	115	114	4
q	3650	NVMEGTGYDPPRNEIERKLVQVWREILGAEDIGISHHFFAAGGDSIKALQIVSRLAKMNL 3709	60
ò	115	124	4
Q	3710	KLEMKALFANPKIKDLSRFITEETRHRKHNKPVTGETELLPIQKRYFANNKEELDHFNQS 3769	69
ò	125	124	4
q	3770	FMLFRKDGYDENIVRTAFNKILEQHDALRMIYEEKDGDIIQYNRGYRENLFDLDVYDVRG 3829	29
ò	125	124	4
QQ	3830	FDSQEEKVFELATG1QKKSSIRKGKLVHLG1FRADEGDHLLIAIHHLVVDGVSWRILFED 3889	68
ò	125	124	4
g	3890	FETLYLQALKGEPLDIGYKTDSYQEFARQLKKYAQSRRLLKEREYWQKALEADVPFIPAE 394	94

ò	114111111111111111111111111111111111111	124
g	3950 KLERDTPEHSATLSIRIGPDVTAKLLRNAFKAYNTEINDILLTALIAAVRDITGENKLKV	4009
ò	. 125	124
q	4010 MMEGHGREDILDGVDITRTIGWFTTVYPVFIDLGEEKEISQNIKMVKEALRKIPNKGIGY	4069
ò	125	124
q	4070 GVLKYMTEBLQKIQTQAPLSFNYFGEMNNDMNRKVFSQSPFSPGESIGGKIVRHCAIEMN	4129
ò	125GGACSPT	131
qq	4130 AISLNGELTIYTTFNQDQYQTSTIEQLNQSFKENLEKIVDHCVDKEGSDMTPSDYGDVSL	4189
ò	132	131
qq	4190 GLEELELIKDKYSAFQIEKIYPLANMQKGMLFHNAMDQTSGAYFQOIVIKLKGRVHPDIL	4249
ò	132	131
qq	4250 EESFHEIVKRHEILRASFEYEITAEPRQIIARDRKTPFTSIDLTGENRTRQHRFIETYLK	4309
ò	132	133
q	4310 EDQEKGFDLSSEALMRVCLIKMSDESYRLIWSHHHILLDGWCLGIVLSELFSLYGKIMKG	4369
ò	134 ·····C	134
q	4370 ESRRLKEPKPYGDYIKWLEKQDQEEAVAYWKDYLKGYESRSELPAFNRGATSEEYCGKEK	4429
ò	135	134
a a	4430 VISFSKELTTKITRIAKQHHVTINTVLQGIWGMILAKYKNTDEVVFGTVVSGREAPVDGI	4489
ò	135	137
a		4549
ò		144
qq	4550 HVMAFQNYAFDEELFRSQSGETGFELGVHGKERTNYNFNLTGVLEDEQLKLKLTFNENV	4609
ò	145	144
g	.4610 YDNTIIETLEKHIITVAEQVAEDETQTLRDINLVSKEEQHRILHTFNDTKTGYPKDKPLH	4669
ò	145	144
q	4670 ELFEEQAMKTPDHTALVFGAQRMTYRELNEKANQTARLLREKGIGRGSIAAIIADRSFEM	4729
ò	145	144
q	4730 IIGIIGILKAGGTYLPIDPETPRDRIDYMLKNSGAALLVTTDSLLKPFDIKTVDLCSDEL	4789
ò	145GVTI 148	
g	4790 HLLSEENLPRVNRSSDTAYIVYTSGSTGTPKGVVI 4824	
RES 1117 1117 0,50 0,00	RESULT 11 T17428 FX506 polyketide synthase - Streptomyces sp. (strain MA6548) C;Species: Streptomyces sp. A;Variety: strain MA6548 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-;C;Accession: T17428	2000
A P P E E E E E E E E E E E E E E E E E	otamedi, H.; Shafiee, A J. Biochem. 256, 528-534, 1998 itle: The biosynthetic gene cluster for the macrolactone ring of the eference number: 218779; MUID:98451508; PMID:9780228 ccession: T17428	îmmunosuppres

A;Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA	δ	40
A;Residues: 1-7576 <mot> A:Cross-references: RMRL.APA82100: NID.AJ788623: DID.AJ788624: DIDN.AAC888E :</mot>	Dp 4	711 AHVFGLVQDAFRRSVVADRRLVARIPRGHSFPVAASVPIVFATAWYGLVDAGQVRPGQKV 770
Experimental source: strain MA6548	ó	40 39
	Db 7	771 LIHAATGGVGSAARQIARHMGADVYATASPAKQHLLLADGFDADHVANSRTTAFADAFPP 830
Construction: involved in synthesis of the backbone of the immunosuppressant FK506 p	ò	96
Johnson Street process (1907)   Carital Process   Synchage   Domos Keywords   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carital Process   Carita	Db 8	831 VDVVLNSLTGEFLDASVELLAPGGRFIEMGKTDIRHDVQQPFDLSDVDPARLREILELLL 890
1095-1166/Domain: acetate-tow ligase nomology (ACL)	ò	9639
F;1639-1959/Domain: 3-oxoacyi-(acyi-carrier-protein) synthase i homology <oasi> F;1682-1953/Domain: (acyi-carrier-protein) S-malonyltransferase homology <amti></amti></oasi>	<b>8</b>	191 ELFDRDELRPLPVRPWDIRRARDAFGWMSQARNTGKTVLTVPRPLGPDAPVLVTGEGADA 950
. 2804-3198/Domain: acyl carrier protein homology <acp2></acp2>	ò	40LRDP 44
3295-3569/Domain: [acyl-carrier-protein] S-malonyltransferase homology 4320-4391/Domain: acyl carrier protein homology <acp3></acp3>	. qa	
14435-483U/DOMBIN: 3-OXOBCYI-CBTTIET-PROTEIN SYNTHBSE I HOMOLOGY 59903-594/Dombin: 8CY Carrier protein homology <acp4></acp4>	ò	45SLGAQ49
513-6412/DOMBIN: 513-6785/DOMBIN: 450-7521/DOMBIN:	DP 10	
20 09. 00000 000 000 000 000 000 000 000	ò	5049
Similarity 1.3%; Pred. No. 1.75; Conservative 17. Mismarrhe	Db 10	1071 GRAEPGAAGPEWGSRLAAADADRENVLLDLVRDSVATVLGLPGAERCAPDRTFRENGLDS 1130
PAGOTI I TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRA	ò	50
	Db 11	1131 LTTVEFANTVAARTGLRVPASTAFDHPTPRSFAAHLAGSVAAPAAKAALGSGEPVAIVGM 1190
6 I HI FI I VAVGDD	ò	60LIEPEG 65
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11 IDDMINGTON VALAGENERGE VALAGENERGE FRAFRANDEGENERARMENTOS COMPANION TO THE TRANSPORTED VALAGENERARMENTOS COMPANION TO TRANSPORTED VALAGENERARMENTOS COMPANION TO TR	ò	99
121 TTGRPKGVVSAORSG	Db 12	:   1251 ATGFDAAFFGISPNEALAMDPQQRLVLETSWEAFEHAGIVPDTLRESDTGVFMGAFHQGY 1310
	ò	69 TTANLTS 75
23 ARILGGEVARDVI.DALAEHPCTVI.VGVPTWYRVI.I.GAVGGEDOTTBALDVAI.VAGGTEDAS	Db 13	
	'n	76 75
291 LTAGFEAAFGVPLLDTYGCTETTGSLTANTLTDTRVPGSCGLPVPGLSLRFVDPVTGADV	Db 13	1371 LALAGGVTVMATPGSFVEFSRQRGLSPDGRCKAFADAADGTGFAEGVGVLVVERQSDAER 1430
	ò	76
351 RRGDEGELWASGPSLMLGYHAQTEATAQVLADGWYRTGDLARQAETGHVTITGRVKELII	Db 1431	31 NGHTVLAVVRGSAVNQDGASNGLSAPNGVAQQRVIRQALANAGLSGADVDAVEAHGTGTV 1490
Qy 32 31	λo	7675
Db 411 RGGENIHPREIESVAQEVPGVRDAAAAGRPHPVLGEIPVLYVVPEGPVVPADAILAECRR 470	Db 1491	91 LGDP1EAQAVLASYGQEREVPLLLGSVKSNVGHTQAAAGVAGVIKMVMAMRHGLLPKTLH 1550
0y 32	Vo	76 75
Db 471 QLAYFKVPDEILHVTTVPRTASGKVRRGELAGLPARLVGTGSGEAALCELVWERRELPDT 530	15	51 VDEPSSHVDWSAGAVEVVTETRPWPESGGARRAGVSSFGVSGTNAHVILEGVAESSVRDG
Oy 32TNLNIGA 38	ò	76 75
Db 531 VSQVQAVVTRRAVGIGPAEVPDADQALRMDEALVRQAAEPGSFVLVDTDTDTDTDTDANNGD 590	DP 16:	GSSGLVPLPVSARTESSLALQVERLGEYVRGGADAAAVADGLVRGRAVFDRRAVLLGESA
Oy .39 E39		
Db 591 EADELVAAAAALGEPQVALRSGVAYVPRLVRADTTPLPASQWALRPPASGTLRDLAVAPS 650	-	VAGVAVEGARTVFVFPGQGSQWVGMGRELMGASEVFAARMRECAAVLEPHTGWDLLDVLG
Ογ 40 39	ò	83 82
Db 651 DAPPRPLAAGEVRVDVRAAGLNFRDVLIALGTYPGDGAMGGEAAGIVTEVGPGVDDLVPG 710	Db 1731	31 EAVVVDRVEVLQPASWAVAVSLAALWQAHGVVPDAVVGHSQGEIAAACVAGALSLEDAAR 1790
	ò	83 82

VVALRSQAIAARLAGRGAMASIAVPASAVETVEGVWIAARNGPESTVVAGDPAAVERVLA 1850	RYEAEGVRVRRIAVDYASHTPHVEAIEAOLADALEGTTGSTDGVDWWGGNVDGCWNTGTDG	0101 524917 1999 1999 1999 1999 1999 1999 1999	DAYWYRNLRQPVAMDTAVSELDGSLFIECSAHPVLLPALDQERTVASLRTDDGGWDRFLA 1970	5.00	:     ALAQAWTGGADVDWTTLIEPAPHRVLDLPTYPFDHKRYWLQPAPVTGAGIGHPFLSSAAV 2030	78TI	LPGSDGVLLTGKLSLATHPWLADHTVQEVVLLPGTAFLELVVRAGDEVGCDTIDELVIET 2090		PHSLPASGAVDLTVTVDQPDDTGHRPVSVHARPAGTDTWTRHATGTLGRTEDTAPDTNSF 2150		POWPPTGAQPASLDEFYERLAGAGYTYGPAFQGLRAAWRAGDTVYAEVALDGAADVDRFG 2210		VHPALLDAALHAGRLDAGDELELPFSWTGVRLHATGAAAVRVAHSRGPAGVAVQVADLDG 2270	26 UDBOD 83		6	PTNPHNTPTRTHTQTTRVLTALQHHLTTTNHTLIVHTTTDPPGAAVTGLTRTAQNEHPGR 2390	85	IHLIETHHPHTPLPLTQLTTLHQPHLRLTNNTLHTPHLTPITTHHNTTTTTPNTPPLNPN 2450	TDP95	   HAILITGGSGTLAGILARHLNHPLTYLLSRTPPPPTTPRTHIPCDLTDPTQITQALTHIP 2510		QPLTGIFHTAATHDDATLTNLTPQHLTTTLQPKADAAWHLHHHTQNQPLTHFVLYSSAAA 2570		TLGSPGQANYAAANAFLDALATHRHTQGQPATTIAWGMWHTTTTLTSQLTDTEROOVRDG 2630		FRPLTEAEGNHFLDASLATDAPFVVAAIPAEPARRRVERRTARTGEDSGRDLLAVVCVAT 2690		   AAVLGHADASEIGAATAFKDLGIDSLSGIRLRNSLAEATGVRLSATAVFDHPTPDALabr		LAEELRGDDDSQGAAAAAAAAGTVPTVAAAGDEPLAIVAMACRMPGGVDTPEDLWSLVES 2810		GGDAITEFPTDRGWDLAALYDPDPDAIGKVSVRHGGFLSGAADFDAEFFGISPREALAMD 2870	105
	RYEAEGVRVRRIAVDYASHTE		DAYWYRNLRQPVAMDTAVSEL	WSO	:   ALAQAWTQGADVDWTTLIEPA		LPGSDGVLLTGKLSLATHPWL	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PHSLPASGAVDLTVTVDQPDD		POWPPTGAQPASLDEFYERLA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VHPALLDAALHAGRLDAGDELI		RPVVSVDALVLRPRSVAPSGPN		PTNPHNTPTRTHTQTTRVLTAL		ІНЬІЕТННРНТРЬРЬТОСТТСН		aailitggsgtlagilarhlnh		<b>PLTGIFHTAATHDDATLTNLT</b>		'LGS PGQANYAAANA FLDALAT		RPLTEAEGNHFLDASLATDAP	GHAD	{    AVLGHADASEIGAATAFKDLG:		AEELRGDDDSQGAAAAAAPG;		GDAITEFPTDRGWDLAALYDPI	LVLYIT
1791	1851	83	1911	83	1971	86	2031	88	2091	88	2151	88	2211	88	2271	93	2331	93	2391	6	2451	96	2511 (	96	2571 7	96	2631 F	- 96	2691 A	100	2751 L	100	2811 G	- 00τ
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đ	Db 2871 PQORLVLEVSWEAFERAGILPASVRGSDAGVFMGAFTQGYQAGVDLGGFGATGTPTSVI.	GATGTPTSVIS 2910
.ò	106	105
ପ୍ର	Db 2931 GRLSYYFGLEGPSVTVDTACSSSLVALHQAARSLRSGECSLALVGGVTVMATTTGFVEFS	
ò	106	105
q	Db 2991 RQRGLAPDGRAKAFADTADGTSFAEGAGVLIVERLSDATRLGHPVLAVVRGSAVNSDGAS	
ò	106	
g	Db 3051 NGLSAPNGPAQQRVIERALDDAGLAPGDIDAVEAHGTGTRLGDPIEAQALEAAYGLDRLH	
ò	106	
Q	Db 3111 PLLIGSLKSNFGHTQAAAGVAKVIKMVLAMRHGVLPRTLHVDEPSRHVDWGGDVRLLRRN	
ò	106	105
Q	Db 3171 EPWPVTGRVRRAGVSSFGISGANAHVVLEAGPPAAFAPLPAADPVPEDVVWPVSARTPDG	WPVSARTPDG 3230
ò	106	
q	Db 3231 VRDVAGRLTALTAPAAAIGHSLATTRTAMRHRAVVPARDAEAFARGEEVPGVVRGTADVT	
ò	Qy 106Qy	105
QQ	Db 3291 DTRAVFVFPGGGSQWDGMGAELLATEPVFARRLGECAEALAPYTGWDLLDVIARRPGAPE	
à	Ογ 106	105
g	Db 3351 LDRVDVVQPASFAMMVALAELWRAHGVAPAAVVGHSQGEVAAACVAGVLTLDDAAKVVAL	
ò	106	
gg	Db 3411 RSRLVATERAGHGGMVSVPPADFDAAAWAGRLEVAAVNGPASIVVAGAADAVEELLAATP	AVEELLAATP 3470
ò	Oy 106	105
qq	Db 3471 HARRIAVDYASHTAHVESIRGALLDALADLTPGAPEIPFFSTVDEAWLDRPADAAYWYDN	
ò	106	
<b>අ</b>	Db 3531 VRCPVRFGAAAARLAELGHRVFVEASPHPVLTTALADTLAGHPNTAVTGTLRRGDGGARR	
ò	107	
q	Db 3591 FTRSLAELWVRGVPVSWPFGELRGVPLPTYPFRRDRYWVDAEPAGTSGHPLLGSLVERAD	
ò	Qy 108	107
qq	Db 3651 GEGAFATALFSVRRQPWLADHEVDGRIIVPGSALVELLAEAGARLGTPTIAELTIVAPVV	ELTIVAPUV 3710
ò	Ογ 108	107
QQ	Db 3711 VDEERDTEIQLTVATEVSGRRAVRLHSRTGAGPWTVGATGALSADTRDPE	PVEWPPADAE 3770
ò	Ογ 108	107
qq	Db 3771 PVDLTGFYDTLPISYGPAFRAMTAMWAGQGRAYASVRLGEQLTDARYGLHPVLLDAAVHA	
ò	108	107
q	Db 1831 LGTLFADPERRRLAFSWSGVRIHARAATTQRVLLERADGDTIRILATDEHGAPVLDVDGL	
ò	Qy 108	107
a	Db 3891 TVRAAEPGTEALFEVAWVSVPASPVPGWTHLADVPEGDVLEGDAGEGDVGESDPPVVVL	SDPPPVVVL 3950
ò	Оу 108	107
qq	Db 3951 AVEPGDPDSSPGVRARELGRDLLATVRTWLAAPRWAESRIVVVTRTGDPAQEALGGLVRT	EALGGLVRT 4010

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. 6	102	GTVI VITCOTCCI CBI I VITHI I TALBAA PIANA COCCO DOCA DA DOUGANAA DISTRIBUTA	
}	108		
, q	4131	AALVDGVAERLCAVVHMAGIVDDAVVATMRPOOMDAVLRVKADVAMOLHELTRDLELAAF	
ò	112		
g	4191	VLYSSISATFGGAGQANYATGNÄFLDALARHRRDQGLPAVSLAWGLWDEADGMGGRLAAT	
ò	112	111	
g	4251	DLTRIARGGMIPMTAEQGLELFDAALHSDRAALVPVRLDLAAVAASDQVPPILRDLVPNA 4310	
ò	112	111	
g	4311	RRAAAPTAARDMLELVRTSAALVLGHRDAHAVEPTRAFKEVGFDSLTGVELRNRLADATG 4370	
ò	112	111	
අ	4371	LTLPATLVFDHPTAQALAAHLDELAGARTATRRRTPAPARRHDEPLAIVGMACRLPGGVA 4430	
ò	112	111	
g	4431	SPDDLWRLLESGGDGITAFPADRGWDVDALYDPDPEHSGTSTVRHGGFLTGAGDFDAGFF 4490	
à	112	111	
q	4491	GISPREALAMDPQQRVVLETSWEALEHAGIDPHTLRGTETGVFMGGYFYGYGSGADRGDF 4550	
તે	112	111	
q	4551	GATSTQTSVLSGRLSYFYCLEGPAVTVDTACSSSLVALHQAGQSLRTGECSLALVGGVTV 4610	
à	112	115	
g	4611	MASPSGFVDFSQQRGLAPDGRCKAFAEAADGTAFAEGSGVLVVERLSDAERHGHRVLAVV 4670	
ጵ	116	115	
ą	4671	RGSAVNQDGASNGLSAPNGPSQERVIRQALANAGLQPSDVDAIEAHGTGTRLGDPIEATA 4730	
ጵ	116		
ရ	4731	LLATYGQDRATPLLLGSLKSNIGHTQAAAGVAGIIKMVLAMRHGTLPPTLHVDTPSSHVD 4790	
à	116	115	
q	4791	WSAGTVELLTDARTWPETGRPHRAAVSSFGVSGTNAHVIIESHPRPTPAPDTGSSTHPVP 4850	
à	116	115	
g	4851	LLISARTPEALDEHTTRVRAFLDAEGEDERAVASALLTRTAFTHRAALIGTDLITGTAEP 4910	
à	116	115	
q	4911	DRRLVWLFSGQGSQRPGMGDELAAAYDVFARTRRDVLDALQVPAGLDVHDTGYAQPAVFA 4970	**
ጵ	1.16	115	
ð	4971	LQVALSAQLDAWGVRPDVLVGHSIGELAAAYVAGVWSLDDATELVSARARLMQALPPGGA 5030	
ጵ	116	115	
g	5031	MAAVSASERDALPLLCEGVEIAAVNGPASIVLSGDEDAVLDVAARLGRFTRLRTSHAFHS 5090	

ò	911	ATT
QD	5091	 ARMEPMLDEFRDVAERLTYHEPKLPMAAGADCATPEYWVROVRDTVRPAEQVAAYDGAAL 5150
ò	120	119
qq	5151	LEIGPDRNLARLVDGIPVLHGEDEARSAMTALARLHTGGVAVDWPEVIGAAPTDLPHLPT 5210
ò	120	119
QQ	5211	YPFERTRYWLGSRAAGDAAPAGGLPVAHPVLTAAVMVPGTGDLVLTGRVEATDPLATRVR 5270
ò	120	119
Q	5271	HPGAARAVLLDLRSRRATKRAAAPWRRSPWTPRSALPQSGGLALSVTVAAPGEDGRRAVA 5330
ò	120	119
QQ	5331	VHARPGTGEWTEHATGILARVARVASAVPETPSPWPPATARPFDVGELADRLARAGHTDG 5390
ò	120	119
QQ	5391	PALPRPRAAWADDDAVHAEVALADEQHADAERYGLHPALLGAALALAGEGADLPSAFDDV 5450
ò	120	119
q	5451	RVHATGATTVRVAVTATGIHLADETGSPVATVGAVRRRPLTVEGAVPGLLRPDLAEIAEL 5510
ò	120	119
qq	5511	PPTTATTGGLDDPVVPDVVILPAHGTGGGPLGETRDLGARVLAALRSFLTDDRYADAVLA 5570
ò	120	119
qq	5571	VHTGPGLAPAAAAGLVRTAQAEHPRRIVVVDAEPDTAAPLLAAAAGLGEPQVVLREGRAY \$630
ò	120	119
QQ	5631	ARRLTPAVPSGDAPELDPDGTVLITGGSGTLAGIVARHLVGHYGVRRLLMLSRGGTASDV 5690
ò	120	119
QQ	5691	PGAEVTAVACDIADRDELASALAGIDPAHPLTAVVHTAAVIDDGVLTALTPERLDTVLRP 5750
ò	120	119
qq	5751	KADGAWHLHELIKDQDLAALCSTPRPPECSATRDRATTPRRTLLDELAEQRRAGGLPALS 5810
ò	120	124
qq	5811	VAWGLWEPESGLTAGAGDRMRRDGVTALSTERGLALLDAALRSPEAALVAADPGGLGSSA 5870
ò	125	124
g	5871	LLRAPHRGPRRRAAGASALADRIAGLSAADAEKAALAVVRECAAAVLGHEGPARIEATAT 5930
ò	125	124
qq	5931	FKELGVDSLTAVRLRNAFTEATDVRLPATAVFDFPTPQAVAAKLTAALTGRVPARARATK 5990
ò	125	130
qq	5991	AVGGHDEPLAIVGMACRLPGGVASPDDLWRLLESGGDGITAFPADRGWDVDALYDPDPEH 6050
ò	131	135
g	6051	SGTSTVRHGGFLTGAGDFDAGFFGISPREALAMDPQQRVVLETSWEALEQAGIVPGTLRG 6110
ò	136	1401TEDT140
q	6111	SDTGVFMGAFSDGYGLGTDLGGFGATGTQTSVLSGRLSYFYGLEGPAVTVDTACSSSLVA 6170
è	141	

		λ	143
		qa	7311 VIHH
	SGVLVVERLESDAERHGHRVLAVVRGSAVNQDGASNGESAFNGFSQERVIRQALANAGLQF 6230	٥	143
		qq	7371 LRRTE
6291 SDVDAIEAHGTGTRLGDPIE	SDVDAIEAHGTGTRLGDPIEATALLATYGQHRTTPLLLGSLKSNIGHTQAAAGVAGIIKM 6350	ò	143
141	140	· 6	7431 SDGG
6351 VLAMRHGTLPPTLHVDTPSS	VLAMRHGTLPPTLHVDTPSSHVDWTTGDVELLTQPRPWPQTNRPHRAGISFGVSGTNAHV 6410		
141	140	RESULT	SULT 12
6411 IIEAHVAAEPPALNSPGPDS	IIEAHVAAEPPALNSPGPDSPVAEPGASLFATERTPLPVSARTSEAVDGQVQRLREHLAA 6470	H C	-toxin synthe
141	140	O'S D'S D'S D'S D'S D'S D'S D'S D'S D'S D	re: 10-du
6471 HPRDDPRAVAAALLATRTDF	HPRDDPRAVAAALLATRTDFPHRAVLLGDDVVTGTALTAPRTVFVFPGQGSQWLGMGREL 6530	24 (2) (2) (3) (4) (5) (6)	R, Scott-Craig,
141	140	A;Ti	tle: The
6531 MAESPVFAARMRQCADALAE	MAESPVFAARMRQCADALAEHTGRDLIAMLDDPAVKSRVDVVHPVCWAVMVSLAAVWEAA 6590	A;AC	cession:
141	140	0 W. (4	lecule ty
6591 GVRPDAVVGHSQGEIAAACV	GVRPDAVVGHSQGEIAAACVAGAISLEDGARLVALRSALLVRELAGRGAMGSIAFAAAAR 6650	A A ; EX	perimenta
141	140	200	perfamily
6651 IDGVWVAGRNGTATTIVSGR	IDGVAVAGRNGTATTIVSGRPDAVETLIADYEARGVAVTRLVVDCPTHTPFVDPLYDELQ 6710	F 2 . 2 . 2 . 2 . 2 . 2 . 2 . 2 . 2 . 2	7-743/DOM
141		0 E	#2-2366/D
6711 RIVAATTSRAPEIPWFSTAD	RIVAATTSRAPEIPWFSTADERWIDAPLDDEYWFRNMRNPVGFAAAVAAAREPGDTVFIE 6770	1 E E	36-3526/D
143	142	7. F. F.	86-4655/D
6771 VSAHPVLLPAINGTTVGTLR	VSAHPVLLPAINGTTVGTLRRGGGADRVLDSLAKAHTVGVAVDWSTVVAATGAADDAASV 6830	F;81	8,3583,47
143	142	70 8	Query Match
6831 TAHDTGTAHDLPTYAFHHER	TAHDTGTAHDLPTYAFHHERYWIEPATGTDASGLGLDAVDHPLLAASVALPDSDEVLLTG 6890	Ma	tches 87
143	142	۸۵	2 AGGI
6891 RLSLATHPWLAGHTVDGEVL	RLSLATHPWLAGHTVDGEVLLPGPVFVELAGRGADEARCDLLDELVIETPLALPATGAVQ 6950	qa	304 AGGV(
143	142	<i>δ</i> ο	9
6951 VRVTVAAADDAGRRAVRIHA	VRVTVAAADDAGRRAVRIHARAHGGRTWTRHASGIAAIATTESATADGPWPPARAERIDI 7010	qa	364 SDTV
143	142	% 0%	9
7011 ADFYRRLDEARTSSAPSSGM	ADFYRRLDEARTSSAPSSGMSAAWSHGDTLFAEVALDGTLARDAARYTLHPALLVTALQA 7070	qq	424 SYTFI
143	142	λo	9
7071 GSLAAGSEDAGVRLPFAFTG	GSLAAGSEDAGVRLPFAFTGVRVHSSGATKARVTFAAGDGGARVHIADELGQPVAEIGSF 7130	qa	484 KDFI
143	142	ò	9
7131 VTRPLAEADRGGDVRLYRRT	VTRPLAEADRGGDVRLYRRTWTGVRAPAAPGTTAVRYADLGDGATSDATSPDAASPDVVL 7190	qa	544 TRTW
143	142	ò	9
7191 MRASDPAEVRAALDDPRTAD	MRASDPAEVRAALDDPRTADATLVVSAEAGSVAGAVAALLDAAEPGRLVLVQTADTVTPR 7250	qa	604 RGRRI
	4. ,		

Db 7251	1 RAAALARLDEPHLRLTGGRLEAPRLVPAPTTTTAAPYGDVVLLDGGSEBLARRLGEHGAE 7310
 Qy 143	3 142
Db 7311	1 VIHHKPGKLPETPVSAVVHAHGAADSPWELHRLTRDLPLTAFVLLVPPGEAAGPWEALAE 7370
Qy 143	3 142
Db 7371	1 LRRTEGLPAVAFTATEDRQTDLLDVACATGEAVVVATAPPRRGDPSPLWRPVQRPARRSA 7430
 Qy 143	3DLGV 146
Db 7431	1 SDGGSLLERLFDLSPKDQEQVLLDVVRDTAATLLGHADARAVTATTAFKDLGV 7483
 RESULT 1	8
 A45086 HC-toxin	synthetase - fungus (Cochliobolus carbonum)
 C;Specie C;Date:	s: Cochliobolus carbonum 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 03-Nov-2000
 C, Access R, Scott-	ion: A45086 Craig, J.S.; Panaccione, D.G.; Pocard, J.A.; Walton, J.D.
 J. Biol. A, Title:	Chem. 267, 26044-26049, 1992 The cyclic peptide synthetase catalyzing HC-toxin production in the filament
A;Refere	nce number: A45086; MUID:93100328; PMID:1281482 ion: A45086
A; Status	: preliminary; not compared with conceptual translation
A; Residu	es: 1-5232 <8CO>
A; Experi	31 backbone (NCBIP:120884)
C; Superf	um HC-toxin
F; 277-74	se homology <a(< td=""></a(<>
F; 784-85 F; 1882-2	4/Jomain: acyl carrier procein nomocogy cacks. 366/Jomain: acetate-CoA ligase homology cacks.
 F; 2397-2	464/Domain: acyl carrier procesu nomology carres 526/Domain: acetate-CoA ligase homology caCL3>
 F;3549-3 F;4186-4	F;3549-3618/Jomain: acyl carrier procein nomology carrier F;4186-4655/Jomain: acetace-Coa ligase homology carrier
F;4680-4 F;818,35	750/Domain: acyl carrier protein homology «ALV4» 83,4715/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
Query	Match 28.7%; Score 222, DB 2; Length 5232;
Best Loc Matches	Local Similarity 1.8%; Pred. No. 59; hes 87; Conservative 20; Mismatches 36; Indels 4702; Gaps 27;
ò	2 AGGI5
Db 304	: 4 aggvcvpidprypverirdiirttnatialvgagktaalpksadtavqti <b>bl</b> tkdiphgl 363
 ò	9
 Db 364	4 SDTVVQSNTKIDDPAFGLFTSGSTGVPKCIVVTHSQICTAVQAYKDRFGVTSETRVLQFS 423
 <i>⁄</i> o	5
Db 42	4 SYTFDISIADTFTALFYGGTLCIPSEEDRMSNLQDYMVSVRPNWAVLTPTVSRFLDPGVV 483
γ̈́	5
 Db 48	4 KDFISTLIFTGEASREADTVPWIEAGVNLYNVYGPAENTLITTATRIRKGKSSNIGYGVN 543
 ò	5
Db 544	4 TRTWVIDVSGACLVPVGSIGELLIESGHLADKYLNRPDRTEAAFLSDLPWIPNYEGDSVR 603
 ò	59
 Db 604	4 RCRRFYRTGDLVRYCDDGSLICVGRSDTQIKLAGQRVELGDVEAHLQSDPTTSQAAVVFP 663
 į	

ā	664	RSGPLEARLIALLVTGNKDGTPHNQQSLPKPAFAQCPPDLVKYATSSLQQRLPSYMVPSV 723	
2		5	
۾ ج	724	724 WLGIDFLPMSVSGKLDRAVLQDQLESLSPSDYAEILGTTGLEVDPGGAASSVASDSDLRD 783	
<u>≻</u>	9	5	
ā	784	784 MNDDSLLLTACSRVLNLPAGKISYSQSFIHAGGDSITAMQVSSWMKRFTGKRIGVKDLLV 843	
ڃ	φ	5	
ရွ	844	SPSISTAASCIKSAQDGSRNFVAVRPGQRIPVSPIQKLFFQTAEASKSWNHYHQSFLFRI 903	
≿	9	5	
ą	904	904 DQPIKPQTIEDAISLVMQRHPMLQARFERTEEGDWYQYIPIDVERRASVEVIGSLSTDDR 963	
≿	9	5	
ą	964	964 EAAMLRARQSIDLTEGPLIRCQLFNNNVDEASRLFFVVIHHAVVDLVSWRIIMEELEAHL 1023	
⋩	ø	5	
ą	1024	1024 ATDSTPDRGEAYQESVPFLAWCQVQAEAVKDIPVDRTVPLIPKIPTADFGYWGLKHDENV 1083	
⋩	v	7	
ą	1084		
۶		7	
ą	1144	1144 GREPGGEDAVDLSRTVGWFTTISPVYVPEVSPGDILDVVRRVKDYRWATPNNGFDYFSTK 1203	
⋩	σ,	8 7	
ą	1204	1204 YLTQSGIKLFEDHLPAEILFNYEGRYQAMESEQTVLKPESWHAGEASKDQDPGLRRFCLF 1263	
à	σ	ELLVANGED	
ą	1264	:          1264 EISTAVLPDGQLHLTCSWNKNMRHQGRIRLWLDTLLPAAIGEIVSSLALASPQLTLSDVE 1323	
à	18	17	
g	1324	LLRLYDYSSLDILKKKSILSIPAVQTLDDLEGVYPGSPMQDALFLSQSKSQDGAYEVDFTW 1383	
à	18	VFQAHQED 25	
ą	1384	RVATSLQNSQPAVDIGCLVEAWKDTVALHAALRTVILESSLPATGILHQVVLRSHDPDIV 1443	
à	26		
g	1444		
à	28	30	
g	1504	TDKIIQDLSKAYTCRHSNKLPDHSESKLHDGTYGNRPTKPPLAEFIRYIRDFQRKQDSIN 1563	
ò	31	37	
QC Op	1564	YWKNALRGATTCSFPPLFDQITSEKAMPRQSWASVPIPLCVD	
à	38	37	
g	1624	FQTVWAIVLRIYSQNGQSVFGYLTSGRDAPVDGIDSAVGNFIAMLVCFFDFDDDGVHTVA 1683	
ò	38	37	
q	1684	DMARKIHNASANSISHQACSLAEIQDALGLSTSTPLFNTAFTYLPKRPTNVKAGEPEHHL 1743	
ờ	38		
g	1744	CFEELSMSDPTEFDLTLFVEPTQESNEVSAHLDFKLSYISQAYATSIASTVAHILSELVH 1803	

<u>≻</u>	43	Dp
ą	1804	 DPYRALNTLPIVSEHDTAIIRSWNDHLFPPATECIHETFSRKVVEHPQREAICSWDGSLT 1863
≿	45	SLGAQFRVHLVKM ST
ą	1864	YAELSDLSQRLSIHLVSLGIKVGTKIPICFEKSMMTIVTILAVVQAGGVFVLLEPGHPES 1923
<u>&gt;</u>	28	64
ð	1924	RLSGIIKQVQAELLLCSPATSRMGALQNISTQMGTEFKIVELĖPĖFIRSLPLPPKPNHOP 1983
≿	65	67  67
ð	1984	MVGLNDDLYVVFTSGSTGVPKGAVATHQAYATGIYEHAVACGMTSLGAPPRSLQFASYSF 2043
≿	68	73
ą	2044	DASIGDIFTTLAVGGCLCIPREEDRNPAGITTFINRYGVTWAGİTPSLALHLDPDAVPTL 2103
≿	74	73
ą	2104	KALCVAGEPLSMSVVTVMSKRLNLINMYGPTEATVACIANQVTCTTTTVSDIGRGYRATT 2163
⋩	74	73
ą	2164	WVVQPDNHNSLVPIGAVGELIIEGSILCRGYLNDPERTAEVFIRSPSWLHDLRPNSTLYK 2223
⋩	74	73
ą	2224	TGDLVRYSADGKIIFIGRKDTQVKMNGQRFELGEVEHALQLQLDPSDGPIIVDLLKRTQS 2283
à	74	73
ą	2284	GEPDLLIAFLFVGRANTGTGNSDEIFIATSTSSLSEFSTVIKKLODAQRAMEVLPLFMVP 2343
à	74	79
ą	2344	QAYIPIEGGIPLTAAGKIDRRMLRKLCEPFNRNDLISFTSKALSTSVKDAETTDTVEDRL 2403
à	80	64
g	2404	ARIWEKVLGVKGVGRESDFFSSGGNSMAAIALRAEAQRSGFTLFVADIFTNPRLADMAKL 2463
à	80	62
q	2464	FSHGQSVSPSSSTLRTKVPISSLQKRSSGLQTAAPVSNGSPVRRCQKENIIDCPVAFEYE 2523
à	80	82 82
q	2524	:   EGPSDTQLKEASRICGISSRSIEDVFPCTPMQEALVALSLIPGAQASYALHAAFELRPGL 2583
ò	83	82
g	2584	DRNRFRSAWESTVKAQPILRSRIISGSNGSSVVVTSATDSIPQLDVSGLDTFLEQQLQVG 2643
ò	83	85 111
g	2644	FAPGAPLFRLAFVYSKADDCDYFVISAHHAIYDGWSLNLIWSQVLALYTNGELPPPGPSF 2703
ò	98	98
Op	2704	KHFARNLNLVQSKLDSEDFWRKLLVKPDQESFRFPDVPVGHKPATRCTTNFHFPFSWQSK 2763
ò	98	88
QQ	2764	I IGTTANTCINAAWAITLAQYSSNKTVNFGVTLWGRDFPMIDIEHWTGPTIVTVPRQVNVI 2823
ò	89	88
ţ	,	PESSIVATE OF ORSTAND PHOHIST HAT DALGP TAROACDFSTLL VVNHGSSISWSEL 2883

≿	83		88
ð	2884	EAADI VPVPLRSSDLYAYPMVVEVENASSDTLDIRVHSDPDCI EVQLLERLMEQFGHNLQ	2943
≿	89		88
ą	2944	TLCRAASFDPGKRIAELMDDTATTHLRTLFSWNSRVKDSPDVAAIAVHKLLEETAQSQPA	3003
ج	89		88
ą	3004	ESAIVAHDGQLSYMQMDRCADVLARQIRKTNMISAQSPFVCIHLLRSATAVVSMLAVLKA	3063
≿	89	BED	91
ð	3064	GGAFMPVDISQPRSRLQNLIEESGAKLVLTLPESANALATLSGLTKVIPVSLSELVQQIT	3123
≿	92	DTDP	95
ą	3124	DNTTKKDEYCKSGDTDPSSPAYLLYTSGTSGKPKGVVMEHRAWSLGFTCHAEYMGFNSCT	3183
≿	96		95
ą	3184	RILOFSSLMFDLSILEIWAVLYAGGCLFIPSDKERVNNLODFTRINDINTVFLTPSIGKL	3243
≿	96		95
ą	3244	LNPKDLPNISFAGFIGEPMTRSLIDAWTLPGRRLVNSYGPTEACVLVTAREISPTAPHDK	3303
⋩	96	GHA	86
ð	3304		3363
⋩	6	DLVLYIT	105
ą	3364		3423
≿	106		105
ą	3424	FHEASVQLYNPATDPDRDATVDVQMREPYLAGLLVLDLVSLMRSWDSMHVLNIANTSENL	3483
≿	106		105
ą	3484	QTLVTELKKSLRGVLPHYMVPLHFVAVSRLPTGSSGKLDHAFVRACLRELTAPLDGNFPK	3543
⋩	106		105
ą	3544	VEQVLTTNESVLRQWWGTVLAMDPHSIQRGDDFFSLGGSSISAMRLVGLARSSGHKLQHE	3603
⋩	106		109
ą	3604	DIFMCPRLADMAGQISFVQEASVSPTTSPTIKFDLLDDCEVDEVIDHILPQLDMNKELIE	3663
⋩	110		109
ą	3664	DVYPCTPLQESLMAATARHGEAYTMIQSITVLAAQLAQLKKAMDVVFRDFEVLRTRIALG	3723
à	110		109
ą	3724	PSOQALQVVVKHEELSWESFPSIQSFKDHFYRSLGYGKPLARLAVITQALDTKQPISHGT	3783
à	110		109
ą	3784	REARTKNSQDTVMVVVGAHHSIYDAHVLSMIWRRLYREFIGSQADGILEAETSRSEGVVP	3843
ጽ	110		113
g	3844	FKSYVEKLLRGKDNDESLLFWKEKLRGVSSSQFPPASWPRVLEHQPSATQTLITKVSLPT	3903
à	114	GNRQVRGVT	122
q	3904	: i :	3963
ે	123		122

q	3964 VPLR	LRIIIDFQTVVSDFLSTLQKDIVRAAYFGQMMGLNSIAHIDNDCRDACGFKSIIVVQV 402	023
ò	123	122	22
qq	4024 PD	PDEGENHVGRAANPFQMSLESIGHFPAPLVVEVEQSESTDVLIRMAYDPVLVPEKLAHFI 408 <sup>.</sup>	083
ò	123	123	22
qq	4084 SDT	TFTTTMSNLSAANPKAKVESIPALSEAHLAELDVTCPEWILGKAKDEKIRTESHQCLQ 414	143
ò	123	125 	52
Dp	4144 DE	DLVCRRAQQSPNSQAIDSWDGSISYHELDGLSSILAEHLSQLGVRPEAPVCLLFEKSKWA 420	203
ò	126	125	25
qq	4204 VV	VVAMIGIIKAGGCFVPLDPSYPHERLEHIISETGSSVIVTSAAYSKLCLSLSVRGIVCDG 426	263
ò	126	125	25
qq	4264 SV	SVESSTKKPLPSTADSPPSFSVRPNQAAYILFTSGSTGKPKGVVMEHHSVCSALIALGKR 432	323
ò	126		28
qq	4324 MG	MGLGPQSRVLQFNSYWFDVMLLDIFGTLVYĞGCLCIPKEEQRMSNLSGWVQKFKVNTMLL 438	383
ò	129	128	28
qq	4384 ST	SVSRLMQPADTPSLETLCLTGEAVLQSDVDRWAPKLHLIAGYGPTETCIMSVSGELTP 44	443
ò	129	128	28
qq	4444 SS	PANLIGKPVSCQAWVINPLKETELAPYGATGELYIQGPTVARGYLHDDVLTSKAFIVD 450	503
ò	129	128	28
d G	4504 PQ	PQWLTGYKTNENOWSRRAYKTGDLVFWGPQSNLYYVRRKDSSQVKIRGORVELAEIEEVI 456	563
ò	129	128	28
g	4564 RQ	RQHIPPDVTVCVDLLSSDDQNTRIILGAVLGIGDRALGGPEDLEVIGYMDDLKSHIIPAL 462	623
ò	129	131 11	33
Ωp	4624 EA	EASLPHHMIPEAYVPFVQLPTLGSGKLDRKTVRRVAGPLAFSLPQASARHPNQPTVTHTO 468	683
ò	132	131	31
QC	4684 KL	LRQLWCKILPQLDESAVNKQDNFLGIGGDSIAAIKLVALLRQHGISLAWAEIFTRPTL 474	743
ò	132		31
q	4744' EA	EAMSSLIDEHNFVVSHAGILSDVTRNTSGVMRQTTNLIAGRHSMAVEKSRECDNSTLPCT 480	803
ò	132	131	31
QC	4804 EY	EYQQMFLAGTEAFTGAHSAQFIFRLPEKIDLDRLQAAFDHCADWYPNLRTQIHKDADTGR 486.	863
ò	132	13	34
qq	4864 LL	LLHDISPIGVKVPWSCHYSDDLNTVLSHDKKPPGLDGPLHRVTIMRHRDPTESMLVWTL 492	923
ò	135	140	0
qq	4924 NH	TKEASRSFWSSYLSDVK 4	983
ò	141	140	40
<b>a</b>	4984 PA	PARLMFNYNLVSNPRQDRLYEARINIPKRVLSQATAATVLLAGLTLLVARVCDTRDVILA 504	043
ò	141	140	40

DE SAME HILTOPHI PLACTENCPOPTITKUPLEI PLANDOBLUTLELDSVAKKITAELMRVMPHEHS 5103	Oy 16
	Db 746 SDNGLDFRAMLKHRESQAGFOKDGEGGAGGGGEKKPMTEAERRQSLFPGKKVEKWDIP
141 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	16
;	w
RESULT 13	18
n unc-22 (imported) - Caenorhabditis elegans es: Caenorhabditis elegans	Db 866 VDDTGKYTCEANGVPTHAQLTVLEPPMKYSFLNPLPNTQEIYRTKQAVLTCKVNT
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C;Accession: A88852	Ογ 33
	Db 921 PRAPLVHYRGSKAIQEGDPRFIIEKDAVGRCTLTIKEVEEDDQAEWTARITQDVFSKVQV
lattorm for investigating bid	Ογ 33
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and	DD 981 YVEEPRHTFVVPMKSQKVNESDLATLETDVNDKDAEVVWWHDGKRIDIDGVKFKVESSNR
A,Accession: A88852 A,Status: preliminary	Оу 33
TO	Db 1041 KRRLIINGARIEDHGEYKCTTKDDRTMAQLIVDAKNKFIVALKDTEVIEKDDVTLMCQTK
A;Cross-references: GB:chr_IV; PIDN:CAA98081.1; PID:g3881830; GSPDB:GN00022 C;Genetics:	Oy 33
Gene: unc-22 :Map position: 4	Db 1101 DTKTPGIWFRNGKQISSMPGGKFETQSRNGTHTLKIGKIEMNEADVYEIDQAGLRGSCNV
witchin, fibronectin type III repeat homolog	Oy 38AELLR
atch 28.6%; Score 221; DB 2; Length 6831; cal Similarity 1.3%; Pred. No. 1.7e+02;	Db 1161 TVLEAEKRPILNWKPKKIEAKAGEPCVVKVPFQIKGTRRCDPKÅQILKNGKPIDEEMRKL
Conservative 28; Mismatches 32; Indels elsi; daps	Qy 43
	Db 1221 VEVIIKDDVAEIVPKNPQLADTGKWALELGNSAGTALAPFELFVKDKPRPPKGPLETKNV
Db 146 GGLYHAIFSDLGDQTYLCQLEIRGPSSSDAGQYRCNIRNDQGETNANLALNFEEPDPSER 205	Oy 43DPSLGA
	Db 1281 TAEGLDLVWGTPDPDEGAPVKAYIIEMQEGRSGNWAKVGETKGTDFKVKDLKEHGEYKFR
Db 206 QERKRSTASPRPSSRGPGSRPSSPKKSMKSREGTPKRTLKPREGSPSKKLRSRTSTPVNE 265	ον 49
8 6 VO	Db 1341.VKALNECGLSDPLTGESVLAKNPYGVPGKPKNMDAIDVDKDHCTLAWEPPEEDGGAPITG
Db 266 EVSQSESRRSSRTDKMEVDQVSGASKRKPDGLPPPGGDEKKLRAGSPSTRKSPSRKSASP 325	ον 49
8 6 VO	Db 1401 YIIERREKSEKDWHQVGQTKPDCCELTDKKVVEDKEYLYRVKAVNKAGPGDPCDHGKPIK
Db 326 TPSRKGSSAGGAASGTTGASASATSATSGGSASSDASRDKYTRPPIVLEASRSGTGRIGG 385	δγ γο
8 6	Db 1461 MKAKKASPEFTGGGIKDLRLKVGETIKYDVPISGEPLPECLWVVNGKPLKAVGRVKMSSE
Db 386 SVVLEVQWQCHSSTIIEWYRDGTLVRNSSEYSQSFNGSIAKLQVNKLTEEKSGLYKCHAK 445	Qy 49
!	Db 1521 RGKHIMKIENAVRADSGKFTITLKNSSGSCDSTATVTVVGRPTPPKGPLDIADVCADGAT
Db 446 CDYGEGQSSAMVKIEQSDVEEELMKHRKDAEDEYQKEEQKSQTLQAETKKRVARRSKSKS 505	Qy 49
Oy 9BLL 11	Db 1581 LSWNPPDDDGGDPLTGYIVEAQDMDNKGKYIEVGKVDPNTTTLKVNGLRNKGNYKFRVKA
DD 506 KSPAPQAKKSTISESGRQEASEVEHKRSSSVRPDPDEESQLDEIPSSGLTIPEERRRELL 565	νο 49
Qy 12 VAVG 15 ,	Db 1641 VANEGESEPLSADQYTQIKDPWDEPGKPGRPEITDFDADRIDIAWEPPHKDGGAPIEEYI
Db 566 GQVGESDDEVSESISELPSFAGGKPRRKTDDKPKKVSIAPVSTNKSSDDEPSTPRRKSSI 625	Оу 49
Qy 1615	Db 1701 VEVRDPDTKEWKEVKRVPDTNASISGLKEGKEYQFRVRAVNKAGPGOPSEPSEKQLAKPK
Db 626 DMRRESVQEILEKTSTPLVPSGASGSAPKIVEVPENVTVVENETAILTCKVSGSPAPTFR 685	Oy 49
Oy 16 15	Db 1761 FIPAMLKHDNLKSITVKAGATVRWEVKIGGEPIPEVKWFKGNQOLENGIOLTIDTRKNEH
Db 686 WFKGSREVISGGRFKHITDGKEHTVALALLKCRSQDEGPYTLTIENVHGTDSADVKLLVT 745	Qy 49

ရ	1821	TILCIPSAMRSDVGEYRLTVKNSHGADEEKANLTVLDRPSKPNGPLEVSDVFEDNLNLSW 1880	
≿	4.9	48	
Q	1881	KPPDDDGGEPIEYYEVEKLDTATGRWVPCAKVKDŢKAHIDGLKKGQTYQFRVKAVNKEGA 1940	
≿	49	48	
ą	1941	SDALSTDKDTKAKNPYDEPGKTGTPDVVDWDADRVSLEWEPPKSDGGAPITQYVIEKKGK 2000	
≿	49		
ą	2001	HGRDWQECGKVSGDQTNAEILGLKEGEEYQFRVKAVNKAGPGEASDPSRKVVAKPRNLKP 2060	
à	53	52	
ą	2061	WIDREAMKTITIKVGNDVEFDVPVRGEPPPKKEWIFNEKPVDDQKIRIESEDYKTRFVLR 2120	
⋩	53		
ą	2121	GATRKHAGLYTLTATNASGSDKHSVEVIVLGKPSSPLGPLEVSNVYEDRADLEWKVPEDD 2180	
≿	61	09	
ą	2181	GGAPIDHYEIEKMDLATGRWVPCGRSETTKTTVPNLQPGHEYKFRVRAVNKEGESDPLTT 2240	
ጵ	61	09	
ą	2241	NTAILAKNPYEVPGKVDKPELVDWDKDHVDLAWNAPDDGGAPIEAFVIEKKDKNGRWEEA 2300	
⋩	61	09	
ą	2301	LVVPGDQKTATVPNLKEGEEYQFRISARNKAGTGDPSDPSDRVVAKPRNLAPRIHREDLS 2360	
≿	61	09	
ą	2361	DTTVKVGATLKFIVHIDGEPAPDVTWSFNGKGIGESKAQIENEPYISRFALPKALRKQSG 2420	
à	61		
q	2421		
à	99	9	
ą	2481	. EIEKWNTKDGIWVPCGRSGDTHFTVDSLNKGDHYKFRVKAVNSEGPSDPLETETDILAKN 2540	
ጵ	99	99	
g	2541	. PFDRPDRPGRPEPTDWDSDHVDLKWDPPLSDGGAPIEEYQIEKRTKYGRWEPAITVPGGQ 2600	
à	99	99	
ą	2601	. TTATVPDLTPNEEYEFRVVAVNKGGPSDPSDASKAVIAKPRNLKPHIDRDALKNLTIKAG 2660	
ठे	99	99	
g	2661	. QSISFDVPVSGEPAPTVTWHWPDNREIRNGGRVKLDNPEYQSKLVVKQMERGDSGTFTIK 2720	
à	99	9	
g	2721	I AVNANGEDEATVKINVIDKPTSPNGPLDVSDVHGDHVTLNWRAPDDDGGIPIENYVIEKY 2780	
ઠે	99	9	
g	2781	L DTASGRWVPAAKVAGDKTTAVVDGLIPGHEYKFRVAAVNAEGESDPLETFGTTLAKDPFD 2840	
ò	99	5 APNIT 70	
g	2841		
ò	7.1	0.2 1	

g	2901	ATVGNLKEGSKYEFRIRAKNKAGLGDPSDSASAVAKARNVPPVIDRNSIQEIKVKAGQDF	2960
ò	11		70
g	2961	SLNIPVSGEPTPTITWTFEGTPVESDDRMKLNNEDGKTKFHVKRALRSDTGTYIIKAENE	3020
à	7.1		20
g	3021	NGTDTAEVKVTVLDHPSSPRGPLDVTN1VKDGCDLAWKEPEDDGGAE1SHYV1EKQDAAT	3080
ò	7.1		20
g	3081	GRWTACGESKDTNFHVDDLTQGHEYKFRVKAVNRHGDSDPLEAREAIIAKDPFDRADKPG	3140
ò	71		70
q	3141	TPEIVDWDKDHADLKWTPPADDGGAPIEGYLVEMRTPSGDWVPAVTVGAGELTATVDGLK	3200
ò	71		20
g	3201	PGQTYQFRVKALNKAGESTPSDPSRTMVAKPRHLAPKINRDMFVAQRVKAGQTLNFDVNV	3260
à	71		70
Dp	3261	EGEPAPKIEWFLNGSPLSSGGNTHIDNNTDNNTKLTTKSTARADSGKYKIVATNESGKDE	3320
ò	71		70
g	3321	HEVDVNILDIPGAPEGPLRHKDITKESVVLKWDEPLDDGGSPITNYVVEKQEDGGRWVPC	3380
ò	71	ANLTS	75
g	3381	GETSDISLKVNKLSEGHEYKFRVKAVNRQGTSAPLTSDHALVAKNPFDEPDAPIDVIPVD	3440
ò	16		75
g	3441	WDKDHVDLEWKPPANDGGAPIDAYIVEKKDKFGDWVECARVDGKTTKATADNLTPGETYO	3500
ò	16		75
q	3501	FRVKAVNKAGPGKPSDPTGNVVAKPRRMAPKLNLAGLLDLRIKAGTPIKLDIAFEGEPAP	3560
ò	16	78	77
g	3561	VAKWKANDATIDTGARADVTNTPTSSAIHIFSAVRGDTGVYKIIVENEHGKDTAQCNVTV	3620
ò	78	rsycg	82
ap	3621	LDVPGTPEGPLKIDEIHKEGCTLNWKPPTDNGGTDVLHYIVEKMDTSRGTWOEVGTFPDC	3680
ò	83		82
qq	3681	TAKVNKL VPGKEYAFRVKAVNLQGESKPLEAEEPI I AKNQFDVPDPVDKPEVTDWDKDR I	3740
ò	83	WICON	88
g	3741		3800
ò	89	PEDDTDP	95
g	3801		3860
ઠે	96		95
g	3861	SGAALAPELLVDAKSSTTSIFFPSAKRADSGNYKLKVKNELGEDEAIFEVIVQDRPSAPE	3920
ò	96		95
g	3921	GPLEVSDVTKDSCVLNWKPPKDDGGAEISNYVVEKRDTKTNTWVPVSAFVTGTSITVPKL	3980
ò	96		95
g	3981	TEGHEYEFRVMAENTFGRSDSLNTDEPVLAKDPFGTPGKPGRPEIVDTDNDH1D1KWDPP	4040

,		0y 113 DGNRQVRG 120
ò	Ch	DD 5121 TITWMAPLEDGGSKITGYNVEIREYGSTLWTVASDYNVREPEFTVDKLREFNDYEFRVVA 5180
g	4041 RDNGGSPVDHYDIERKDAKTGRWIKVNTSPVQGTAFSDTRVQKGHTYEYRVVAVNKAGPG 4100	121
ò	56 96	121
ф	4101 OPSDSSAAATAKPMHEAPKFDLDLDGKEFRVKAGEPLVITIPFTASPQPDISWTKEGGKP 4160	סופן זואיאפרניניסטרטינים איני איני איני פייטאיטיעני זי לפטעסטרני פייטאיטיעני איני פייטאיטיעני פייטאיטיני פייטאיט
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g	4221 SRHTCTLNWDAPKDDGGAEIAGÝKIEYQEVGSQIWDKVPGLISGTAYTVRGLEHGQQYRF 4280	5301 LEKDVENTILFFSGDLVKLKIRFSGIAFFRASLVLNREEIUMDRFIIKTVBFUUNLIFIF
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A;Status: preinminary; translated trom objects bush book A;Molecule type: DNA
A,Residues: 'MGTPGKKCKO'.19-6819 <w12> A,Crose-references: EMBL:271899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a A:Experimental source: clone ZK629</w12>
C;Comment: Lack of unc-22 leads to a constant twitching of the body muscles. C;Genetics:
A,Gene: unc-22; CESP:ZK617.1a A,Map position: 4
A;Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 152/3; 6591/3; 610/4; 610/4; 610/4; 1776/1; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4; 610/4
C; Reywords ATP: Unicular Distriction; diplication; muscle; phosphotransferase; sering F; 806-898, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-24; 96-5790, 6263-6356, 6386-6478, 6541-6635, 6649-6742, 6745-6838/Region: motif 2
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F;5940-6197/Domain: protein kinase homology <kin> ;5948-5956/Region: protein kinase ATP-binding motif F;5971/Active site: Lys #eratus predicted</kin>
Query Match 28.6%; Score 221; DB 2; Length 6839;
Best Local Similarity 1.3%; Fred. No. 1.74*/2; Matches 81; Conservative 28; Mismatches 32; Indels 6181; Gaps 25;
Qγ 3 GGILHL
Db 154 GGLYHAIFSDLGDQTYLCQLEIRGPSSSDAGQYRCNIRNDQGETNANLALNFEEPDPSER 213
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Ω	874	:   :  VDDIGKYTCEANGVPTHAQLTVLEPPMKYSFLNPLPNTQEIYRTKQAVLTCKVNT	928
>	33		32
Ω	929	PRAPLVMYRGSKAIQEGDPRFIIEKDAVGRCTLTIKEVEEDDQAEWTARITQDVFSKVQV	988
<u>&gt;</u>	33		32
۵	989	YVEEPRHTFVVPMKSQKVNESDLATLETDVNDKDAEVVWWHDGKRIDIDGVKFKVESSNR	1048
≽	33		32
۵	1049	KRRLIINGARIEDHGEYKCTTKDDRTMAQLIVDAKNKFIVALKDTEVIEKDDVTLMCQTK	1108
<u>&gt;</u>	33	SINTN	37
ফু	1109	DTKTPGIWFRNGKQISSMPGGKFETQSRNGTHTLKIGKIEMNEADVYEIDQAGLRGSCNV	1168
≿	38	ABLLR	42
ą	1169	TVLEAEKRPILNWKPKKIEAKAGEPCVVKVPFQIKGTRRGDPKAQILKNGKPIDEEMRKL	1228
ڃ	43		42
ā	1229	VEVIIKDDVAEIVFKNPQLADTGKWALELGNSAGTALAPFELFVKDKPKPPKGPLETKNV	1288
<u>&gt;</u>	43	DSLGA	48
۾	1289		1348
2	4		48
Q	1349	VKALNECGLSDPLTGESVLAKNPYGVPGKPKNMDAIDVDKDHCTLAWEPPEEDGGAPITG	1408
≿	4		48
Q	1409	YIIERREKSEKDWHQVGQTKPDCCELTDKKVVEDKEYLYRVKAVNKAGPGDPCDHGKPIK	1468
≿	4		48
ð	1469	MKAKKASPEFTGGGIKDLRLKVGETIKYDVPISGEPLPECLWVVNGKPLKAVGRVKMSSE	1528
≿	4		48
ą	1529	RGKHIMKIENAVRADSGKFTITLKNSSGSCDSTATVTVVGRPTPPKGPLDIADVCADGAT	1588
à	49		48
ą	1589	. LSWNPPDDDGGDPLTGYIVEAQDMDNKGKYIEVGKVDPNTTTLKVNGLRNKGNYKFRVKA	1648
ጵ	4		48
ą	1649	VNNEGESEPLSADQYTQIKDPWDEPGKPGRPEITDFDADRIDIAWEPPHKDGGAPIEEYI	1708
À	49		48
ą	1709	I VEVRDPDTKEWKEVKRVPDTNASISGLKEGKEYQFRVRAVNKAGPGQPSEPSEKQLAKPK	1768
ል	4		48
ą	1769	FIPAMLKHDNLKSITVKAGATVRWEVKIGGEPIPEVKWFKGNQQLENGIQLTIDTRKNEH	1828
ጽ	4 0		48
ą	1829	) TILCIPSAMRSDVGEYRLTVKNSHGADEEKANLTVLDRPSKPNGPLEVSDVFEDNLNLSW	1888
ઠે	4		48

qq	1889	KPPDDDGGEPIEYYEVEKLDTATGRWVPCAKVKDTKAHIDGLKKGQTYQFRVKAVNKEGA 19	948
ò	4	48	60
đ	1949	SDALSTDKDTKAKNPYDEPGKTGTPDVVDWDADRVSLEWEPPKSDGGAPITQYVIEKKGK 20	800
ò	4	52	Ŋ
g	2009	 HGRDWQECGKVSGDQTNAEILGLKEGEEYQPRVKAVNKAGPGEASDPSRKVVAKPRNLKP 20	068
ઠે	53	52	آن ا
QQ	2069	WIDREAMKTITIKVGNDVEFDVPVRGEPPPKKEWIFNEKPVDDOKIRIESEDYKTRFVLR 21	128
ò	53	09	0
qq	2129	GATRKHAGLYTLTATNASGSDKHSVEVIVLGKPSSPLGPLEVSNVYEDRADLEWKVPEDD 21	2188
ò	61	99	0
QQ	2189	GGAPIDHYEIEKMDLATGRHVPCGRSETTKTTVPNLQPGHEYKFRVRAVNKEGESDPLTT 22	248
ò	61	)9	09
g	2249	NTAILAKNPYEVPGKVDKPELVDWDKDHVDLAWNAPDDGGAPIEAFVIEKKDKNGRWEEA 23	308
ò	61	)9	0
Q	2309	LVVPGDQKTATVPNLKEGEEYQFRISARNKAGTGDPSDPSDRVVAKPRNLAPRIHREDLS 23	2368
ò	61	)9	0
qq	2369	DTTVKVGATLKFIVHIDGEPAPDVTWSFNGKGIGESKAQIENEPYISRFALPKALRKQSG 24	1428
ò	61	9	SS
qq	2429	KYTITATNINGTDSVTINIKVKSKPTKPKGPIEVTDVFEDRATLDWKPPEDDGGEPIEFY 24	488
ò	99	39,	ις.
q	2489	EIEKMATKDGIWVPCGRSGDTHFTVDSLNKGDHYKFRVKAVNSEGPSDPLETETDILAKN 25	548
ò	99	59	S.
q	2549	PFDRPDRPGRPEPTDWDSDHVDLKWDPPLSDGGAPIEEYQIEKRTKYGRWBPAITVPGGQ 26	2608
ò	99	39	55
QQ	2609	TTATVPDLTPNEEYEFRVVAVNKGGPSDPSDASKAVIAKPRNLKPHIDRDALKNLTIKAG 26	8998
ò	99	39	52
qq	2669	QSISFDVPVSGEPAPTVTWHWPDNREIRNGGRVKLDNPEYQSKLVVKQMERGDSGTFTIK 2°	2728
ò	99	19	S.
qq	2729	AVNANGEDEATVKINVIDKPTSPNGPLDVSDVHGDHVTLNWRAPDDDGGIPIENYVIEKY 2°	2788
ò	99	9	9
QQ	2789	DTASGRWVPAAKVAGDKTTAVVDGLIPGHEYKFRVAAVNAEGESDPLETFGTTLAKDPFD 2	2848
ò	99	7APNIT.	70
g	2849	KPGKTNAPEITDWDKDHVDLEWKPPANDGGAPIEEYVVEMKDEFSPFWNDVAHVPAGQTN 2	2908
ò	71	L	20
q	2909	ATVGNLKEGSKYEFRIRAKNKAGLGDPSDSASAVAKARNVPPVIDRNSIQEIKVKAGQDF 2	2968
ò	71	6	20
g	2969	SLNIPVSGEPTPTITWTFEGTPVESDDRMKLNNEDGKTKFHVKRALRSDTGTYIIKAENE 3	3028

10.29 NGTDTAEVKUTVLDHPSSPRGPLDVTNIVKDOCDLAMKEPEDDOGGEISHYVIEKQDAAT 71 72 7309 GRWTACGESKUTNFHYDDLTGGHEVKENVKANNRHGDSDPLEAREALIAKUPFDBADKPG 73 7309 PGGTYOPRVKALNKAGESTBSDPÅRIMVAKFBHLAPKINRDMFVATVGAGELTATVDGLK 73 7309 PGGTYOPRVKALNKAGESTBSDPÅRIMVAKFBHLAPKINRDMFVATVGAGELTATVDGLK 73 7309 PGGTYOPRVKALNKAGESTBSDPÅRIMVAKFBHLAPKINRDMFVATVGAGELTATVDGLK 73 74 75 75 76 77 77 78 78 78 78 78 78 78 78 78 78 78	į	5	C
10'29 NGTDTAEVKNTVLDHPSSEPRGELDVTNIVKDGCDLAMKEPEDDGGAEISHYVIEKQDAAT  7.1  7.1  7.2  7.1  7.1  7.2  7.3  7.3  7.4  7.4  7.5  7.5  7.5  7.5  7.6  7.7  7.7  7.7	ŝ	1/	
119 TPEIUDMDCDHADLTQCHEYKERVAANNRHGDSDELEAREAIIAKDFEDRADKPG 11	ð		308
119 TREIVUMDEDHADLKWIPPADDGGAPIEGYLUSHWITPSGDWVPATVGAGELTATVGGLK 11 TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA	તે	71	10
119 TPEIVDWDKDHADLKWTPPADDGGAPIEGYLUBMTPSGDWVPAYTVGAGELTATVDGLK 71 72 COTTOER CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED	g		314
1149   TPEIUDMOKDHADLKWTPPADDGGAPIBCYLUSHRTPSGDWVPAUTVGAGELTATVDGLK	ते	7.1	10
1329   PGOTYOFRUKALNKAGESTPSDP\$RTWVAKPRHLAPKINRDMFVAGRYKAGOTLNFDVNV   71	q		
3209 PGGTYOFRVKALNKAGESTPSDP\$RTWVAKPRHLAPKINRDMFVAGRYKAGGTLNFDVNV 71 72 7329 FGEPAPKIEWFLANGSPLSSGGNTHIDNNTDNNTKLTTKSTARADSGKYKIVATNESGKDE 73 7329 HEVDWILLDIPGAPEGPLRHKDITKESWULKMDEPLDDGGSPITNYVVEKQEDGGRAWPC 73 74	à	71	10
1269   EGEPARKIEWELNGSPLSSGGNTHIDNNTRLITKSTARABGECKYKIVATNESGKDE   1329   HEVDWILLDIPGAPEGPLRKEUTKESVVLKWDEPLDDGGSPITNYVVEKQEDGGRWYPC   1	ရှ		326
326   GGEPAPKIEWFLNGSPLSSGGNTHIDNNTDNNTKLTTKSTARADSGKYKIVATNESGKDE	à	11	10
71	ą	3269	332
3329   HEVDVNILDIPGAPEGPLRHKDITKESVVLKWDEPLDDGGSPITNYVVEKOEDGGRWVPC	ጵ	71	10
11	ရ		338
3389 GETSDTSLKVNKLSEGHEYKFRVKAVNRQGTSAPLTSDHAIVAKNPFDEPDAPTDVTPVD 76 76 776 777 78 LOVCA 78 LOVCA 79 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGTPIKLDIAFGGEPAP 76 77 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGTPIKLDIAFGGEPAP 77 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 78 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 79 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 70 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 71 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 71 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 71 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 71 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYIVEKGNTAQCNVTV 71 LOVPGTPECPLKIDETHKEGCTLNWKPPTDNGGTDVLHYINGFDVPDPTATWTVGD 71 LOVPGTPECPLKIDETHKEKGSAIWTEAGKTPRTNTWVPVSAFVTGTPGTPFSAVIAVN 70 LOVPGTPECPLKIDETHKARYLKPKILTAASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGD 71 LOVPGTPECPLKIDETHKARYLKPKILTAASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGD 71 LOVPGTPECPLKIDETHKARYLKPKILTAASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGD 71 LOVPGTPECPLKIDETHKARYLKPKILTAASRKIKIKAGFTHNTWVPVSAFVTGTSITVPKL 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBDRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGEBRAIFEVIVODDRFSAPE 71 LOVPGTPECPLKYDAKSSTTSIFFPSAKRADSGNYKLKVKNYBLGTPGTPGRPEIVUTDDNDHIDIKNDPP 71 LOVPGTPECPLKYDAKSSTTSIFFROM LIKVNTSPVQGTPFSDTRVVVKGTTYFYTYTYPVCL	⋩	7.1	
149   WDKDHVDLEWKPPANDGGAPIDAYIVEKKDKFGDWVECARVDGKTTKATADNLTPGETYQ   16	ą		344
349 WDKDHVDLEWKDPANDGAPIDAYIVEKKDKFGDWVECARVDGKTTKATADNLTPGETYQ  76	⋩	96	75
1569	ą	449	
3509 FRVKAVNKAGPGKPSDPTGNVVAKPRRNAPKLNLAGLLDLRIKAGTPIKLDIAFEGEPAP 76	⋩	16	ż
1569 VAKWKANDATIDTGARADVTNTPTSSAIHIFSAVRGDTGVYKIIVENEHGKDTAQCNVTV	ą	509	356
3569 VAKWKANDATIDTGARADVTNTPTSSAIHIFSAVRGDTGVYKIIVENEHGKDTAQCNVTV  78 LSVCG	à	16	
18.0	ą	569	362
3629 LDVPGTPEGPLKIDEIHKEGCTLNWKPPTDNGGTDVLHYIVEKMDTSRGTWQEVGTFPDC 83	≿	78	
83	ą	629	C 368
3689 TAKYNKLVPGKEYAFRVKAVNLQGESKPLEAEEPIJAKNQFDVPDPVDKPEVTDMDKDRI  83WSQTIN	≿	83	
83WSQTIN	ă		374
3749 DIKWNPTANNGGAPVTGYIVEKKEKGSAIWTEACKTTPGTTFSADNLKPGVEYEFRVIAVN 89PEDDTDP 1	≿	83	
99	ð		380
3869 AAGPSDPSDPTDPTTXARYLKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGD 96	≿	8	
96	ð		
3869 SGAALAPELLVDAKSSTTSIFFPSAKRADSGNYKLKVKNELGEDEAIFEVIVQDRPSAPE 96	⋧	96	56
96	ą		392
3929 GPLEVSDVTKDSCVLNMKPPKDDGGAEISNYVVEKRDTKTNTWVPVSAFVTGTSITVPKL 96	⋧	96	56
96	ક		398
3989 TEGHEYEFRVMAENTFGRSDSLNTDEPVLAKDPFGTPGKPGRPEIVDTDNDHIDIKWDPP 96	à	96	56
96	8		
4049 RDNGGSPVDHYDIERKDAKTGRWIKVNTSPVQGTAFSDTRVQKGHTYEYRVVAVNKAGPG	ጵ	96	56
	g		

à	96	AD
đ	4109	QPSDSSAAATAKPWHEAPKFDLDLDGKEFRVKAGEPLVITIPFTASPQPDISWTKEGGKP 4168
ò	96	56
QQ	4169	LAGVETTDSQTKLVIPSTRRSDSGPVKIKAVNPYGEAEANIKITVIDKPGAPENITYPAV 4228
ò	. 96	56
qq	4229	SRHTCTLNWDAPKDDGGAEIAGYKIEYQEVGSQIWDKVPGLISGTAYTVRGLEHGQQYRF 4288
ò	96	56
gg	4289	RIRAENAVGLSDYCQGVPVVIKDPFDPPGAPSTPEITGYDTNQVSLAWNPPRDDGGSPIL 4348
ò	96	9797
q	4349	GYVVERFEKRGGGDWAPVKMPMVKGTECIVPGLHENETYQFRVRAVNAAGHGEPSNGSEP 4408
ò	86	6
	4409	VTCRPYVEKPGAPDAPRVGKITKNSAELTWNRPLRDGGAPIDGYIVEKKKLGDNDWTRCN 4468
ò	8	102 102 1111
g	4469	DKPVRDTAFEVKNLGEKEEYEFRVIAVNSAGEGEPSKPSDLVLIEEQPGRPIFDINNLKD 4528
ò	103	102
q	4529	ITVRAGETIQIRIPYAGGNPKPIIDLFNGNSPIFENERTVVDVNPGEIVITTTGSKRSDA 4588
ò	103	102
g	4589	GPYKISATNKYGKDTCKLNVFVLDAPGKPTGPIRATDIQADAMTLSWRPPKDNGGDAITN 4648
ò	103	102
q	4649	YVVEKRIPGGDWYTVGHPVGTILRVRNLDANIPYEFRVRAENQYGVGEPLETDDAIVAKN 4708
ò	103	102
qq	4709	PFDTPGAPGQPEAVETSEEALTLQWTRPTSDGGAPIQGYVIEKREVGSTEWTKAAFGNIL 4768
ò	103	102
qq	4769	DTKHRVTGLTPKKTYEFRVAAYNAAGQGEYSVNSVPITADNAPTRPKINMGMLTRDILAY 4828
ò	103	102
QQ	4829	AGERAKILVPFAASPAPKVTFSKGENKISPTDPRVKVEYSDFLATLTIEKSELTDGGLYF 4888
ò	103	102
q	4889	VELENSQGSDSASIRLKVVDKPASPQHIRVEDIAPDCCTLYWMPPSSDGGSPITNYIVEK 4948
ò	103	108
q	4949	LDLRHSDGKWEKVSSFVRNLNYTVGGLIKDNRYRFRVRAETQYGVSEPCELADVVVAKYQ 5008
ò	109	LELP
g	5009	:    FEVPNOPEAPTVRDKDSTWAELEWDPPRDGGSKIIGYQVQYRDTSSGRWINAKWDLSEQC 5068
ò	113	112
අධ	5069	HARVTGLRONGEFEFRIJAKNAAGFSKPSPPSERCQLKSRFGPPGPPIHVGAKSIGRNHC 5128
ò	113	120
g	5129	: :     ::   TITWMAPLEDGGSKITGYNVEIREYGSTLWTVASDYNVREPEFTVDKLREFNDYEFRVVA 5188
ò	121	120

ţ			Q	6269 IVKPYGTE
9	SIBY INAMGRAIFSEFINIQESGGSRFQIVVRFEDIAQFINKKAVFICEAVGRFEFINKNI SZY		ò	134
ò	, 121 120		qq	6329 КСООКСЕХ
g	5249 RNGRELPESSRYRFEASDGVYKFTIKEVMDIDAGEYTVEVSNPYGSDTATANLVVQAPPV 5308			
ò	, 121 120			алнашааа оосу
qq	5309 IEKDVPNTILPSGDLVRLKIYFSGTAPFRHSLVLNREEIDMDHPTIRIVEFDDHILITIP 5368			
ò	, 121 120			NAN
셤	5369 ALSVREAGRYEYTVSNDSGEATTGFWLNVTGLPEAPQGPLHISNIGPSTATLSWRPPVTD 5428			
ò	, 121		RESULT	T 15
g	5 5429 GGSKITSYVVEKRDLSKDEWVTVTSNVKDMNYIVTGLFENHEYEFRVSAQNENGIGAPLV 5488		polyketide	polyketide synthas C.Species: Strepto
ò	y 121 126 126		A; Var.	A;Variety: strain C:Date: 22-Oct-199
qq	5489 SEHPIIARLPFDPPTSPLNLEIVQVGGDYVTLSWQRPLSDGGRLRGYIVEKQEEEHDEW 5548	•	C; Agg	C; Accession: T3028
ò	γ 127 126		Eur.	J. Biochem. 2
q	D 5549 FRCNONPSPPNNYNVPNLIDGRKYRYRVFAVNDAGLSDLAELDQTLFQASGSGEGPKIVS 5608		A; Ref	A;Reference number
ò	γ 127 126		A;Sta	Status: prelimin
đ	5 5609 PLSDLNEEVGRCVTFECEISGSPRPEYRWFKGCKELVDTSKYTLINKGDKQVLIINDLTS 5668			Residues: 1-6420 Cross-references
ò	γ 127 126		C, Gen	Genetics:
QQ	o 5669 DDADEYTCRATNSSGTRSTRANLRIKTKPRVFIPPKYHGGYEAQKGETIELKIPYKAYPQ 5728		C,Sup	erfamily: 3-c
ò	y 127 126		F;51-	433/Domain: 3
d	5729 GEARWIKDGEKIENNSKFSITTDDKFATLRISNASREDYGEYRVVVENSVGSDSGTVNVT 5788		F,339	,3391-3462/Domain
ò	γ 127 126		F;398	3393-4254/Domain 3983-4254/Domain 5307-5378/Domain
q	5789 VADVPEPPRFPIIENILDEAVILSWKPPALDGGSLVTNYTIEKREAMGGSWSPCAKSRYT 5848		F,543	5307-5375/20main 5431-5831/Domain 5932-6206/Domain
ò	y 127 131			3-6364/Domair
q	b 5849 YTTIEGLRAGKQYEFRIIAENKHGQSKPCEPTAPVLIPGDERKRRRGYDVDEQGKIVRGK 5908		One	Query Match Rest Local Simil
ò	y 132 131		Mat	ches 88; C
qq	b 5909 GTVSSNYDNYVFDIWKQYYPQPVEIKHDHVLDHYDIHEELGTGAFGVVHRVTERATGNNF 5968		ò	1 AAGGI
ò	y 132 131		qq	360 AAAGVAGI
q	5969 AAKFVWTPHESDKETVRKEIQTMSVLRHPTLVNLHDAFEDDNEMVMIYEFWSGGELFEKV 6028	. <del>:</del>	ò	10
ò	y 132131		QQ	420 SSFGVSG1
Q	b 6029 ADEHNKMSEDEAVEYMRQVCKGLCHMHENNYVHLDLKPENIMFTTKRSNELKLIDFGLTA 6088		ò	15
ò	y 132 133		QQ	480 GADRVTVA
qq	L 6089 HLDPKQSVKVTTGTAEFAAPEVAEGKPVGYYTDMWSVGVLSYILLSGLSPFGGENDDETL 6148		ò	19
ò	γ 134 133		q	540 TYSVFADA
QQ	b 6149 RNVKSCDWNMDDSAFSGISEDGKDFIRKLLLADPNTRMTIHQALEHPWLTPGNAPGRDSQ 6208		ò	19
ò	γ 134133		qq	600 GVLSIGDA
q	b 6209 IPSSRYTKIRDSIKTKYDAWPEPLPPLGRISNYSSLRKCHRPQEYSIRDAFWDRSEAQPRF 6268		ò	19
ò	у 134 133		q	660 GDEGPVLD

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ex protein
3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier protein
3-oxoacyl-[acyl-carrier-protein] synthase I homology «OASI»
n: 3-oxoacyl-[acyl-carrier-protein] synthase I homology «OAS2»
n: acyl carrier protein homology «ACPP)
n: acyl carrier protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein homology and protein p
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144, 74-80, 1997
Il organization of a multifunctional polyketide synthase involved in
12 220806; MUID:97217427; PMID:9063448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                TVRAKNSYGTKEEIVFLNVTRHSEPLKFEPLEPMKKAPSPPRVEEFKERRSA 6388
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRLIQKNHQCKLTCSLQGNPNPTIEWMKDGHPVDEDRVQVSFRSGVCSLEIF 6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : EMBL:Y10438; NID:e1014806; PID:e290681; PIDN:CAA71463.1
VGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRV 6328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALLAARSRLMDELPTGGAMVTVLTSEENALRALRPGVEIAAVNGPHSVVLS 659
                                                                                                                                                                                                                                                                                                                                          QTLARRTPFEHRAVLLGDTLITADPNAGSĠPVVFVYSGQSTLHPHTGHQLAA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGEVLGHLNADQGPATHFAHQIALTALLRSWGITPHAVIGHSLGEISAACAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||::
IKMVLAMRHGTLPPTLHVDTPSSHVDWTTGDVELLTQARPWPQTNRPHRAGI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | ::
NAHVIIESHPRPTPAPDTGSSTHPVPLLISARTPEALDEHTTRIRAFLDDNP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVAQQLGIHHRLPTRHAGHSARMDPLVAPLLEAASGLTYHQPHTAIPEDPTTA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.5%; Score 220; DB 2; Length 6420;
arity 1.5%; Pred. No. 1.5e+02;
conservative 25; Mismatches 35; Indels 5843; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     se - Streptomyces sp. (strain MA6548)
omyces sp.
MA6548
)9 #sequence revision no C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| :
TYTVTATNDLGVDV 6470
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19	FOAHQE	24
720 4	AYWARQVRDQVRFQAHAERYPGATFLEIGPNQDLSPVVDGIPTQTGTPEEVQALHTALAR	. 624
•		4.
	780 LHTRGGVVDWPTVLGSDRAPVALPTYPFQHKDYWLRATAQVDVTGAGQEKVAHPLLGAAV	839
25		24
840	ALPGTGGTVLTGRVSLASHPWLGGHAVNGTVLLPGAAFLELAVRAGDETGSDLLHELVVE	899
	DIER	28
900	TPLTLPATGSVAISVEVAEPDDTGRRAVTVHARADGAALWTRHATGFLGKAAATTAETGD	959
29		28
960	PAPWPPAGARQVDVGDVYERFAGIGYAYGSSFQGLLAAWRDGDTVHAEVALPDEQVPDAA	1019
		28
	1020 RFTLHPALLDAAFQAGALSALDAPGEAARLPFSFQDVRIHAAGATRARVTVSRDGDRSTV	1079
29		28
	1080 RMTGEDGQPVAEVGSVVSRPYAGGSGSDDELLRPVWTELPMPAPSAADPRVEVLDADPLD	1139
29		28
	1140 GEPAAATRELTARVLDSLQHRLSATDDVTLVVRIGTGLAAAATAGLVRSAQAENPGRFVL	1199
29		28
	1200 VEAPPDTPADLLTACAALDEPQLAVRDGVLFAPRLVRMSDPVHGPLPLPDGDWLLAHSAS	1259
29		28
1260	GVLQDVTLAADGTPRRALEAGEVRVDVRAAGLNFRDVLIALGTYDGATALGGEAAGVVVE	1319
	TJVY	32
1320	TGPGVADLAPGDRVFGLTRGGIGPTAVTDRRWLARIPDGWTFATAASVPIAFATAWYGLV	1379
		0.4
1380	:   ; DLAGLRAGEKVLVHAATGGVAMAATQVARHLGAEVYATAGTGKQHVLRAAGLPGTHVADS	1439
	LRDP	44
1440	RTTAFRIDFPRMDVVLNSLIGEFIDASLELLDADGRFVEMGRAELRDPATIAPAYLPFDL	1499
	SLGAOFR	51
1500	LDAGTDRIGEILGELLRLFDAGALTPLPVRAWDIRQARDALGVMSRARHIGKNVLTLPRP	1559
52	THA.	54
1560	LDPEGAIVITGGSGTLAGILARHVSAQHVYLLSRSAPPEGTPGIHLPCDVSDRQQLAAAL	1619
		54
1620	RRIDRP1TAVVHTAGALDDGTLPSLTPGRFDTELRPKADGAWHLHELTKDQDLAAFVLYS	1679
		54
	1680 SAAGVLGNAGQGNYAAANAFLDALAEQRRAAGLPALSIAWGLWEDASGLTAELSEADRQR	1739
55		54.
	1740 MRRSGFRTITARQGMRLYEAARRTGSPVVVAAALDDAPDVPLLRGLRRTTVRRAAVRERS	1799
22		54

임	1800 LADRSPCCPTTSAPTPPSRSSWNSTATVLGHLGAEDI	PATTTFKELGIDSLTAVOLRNAL 1859
ò	ολ 25	\$5
q	1860 TTATGVRLNATAVFDFPTPRALAARLGDELAGTRA	PVAARTAATAAAHDEPLAIVGMACR 1919
ò	Qy 55	54
q	Db 1920 LPGGVASPQELWRLVASGTDAITEFPADRGWDVDALYDPDPDA	PDPDAIGKTFVRHGGFLDGATG 1979
ò	Ογ 55	54
q	Db 1980 FDAAFFGISPREALAMDPQQRVLLETSWEAFESAGITPDAARGSDTGVFIGAFSYGYGTG	DAARGSDTGVFIGAFSYGYGTG 2039
ò	Ογ 55	54
q	2040 ADTNGFGATGSQTSVLSGRLSYFYGLEGPSVT	VDTACSSSLVALHQAGOSLRSGECSLAL 2099
ò	Oy 55	95 84
QQ	Db 2100 VGCVTVMASPGGFVEFSRORGLAPDGRAKAFGAGADGTSFAEGAGALVVERLSDAERHGH	SFAEGAGALVVERLSDAERHGH 2159
ò	Qy 55	95 84
q	Db 2160 TVLALVRGSAANSDGASNGLSAPNGPSQERVIHQALANAKLTPADVDAVEAHGTGTRLGD	AKLTPADVDAVEAHGTGTRLGD 2219
ò	Ογ 55	VKMV 58
đ	Db 2220 PIEAQALLATYGQDRATPLLLGSLKSNIGHAQAASGVAGIIKMVQAIRHGELP	311KMVQAIRHGELPPTLHADE 2279
ò	Oy 59	85
q	2280 PSPHVDWTAGAVELLTSARPWPGTGRPRRAAVS	SFGVSGTNAHIILEAGPVKTGPVEAGA 2339
ò	Оу 59	85
q	Db 2340 IEAGPVEVGPVEAGPLPAAPPSAPGEDLPLLVSARSPEAL	ALDEQIGRLRAYLDTGPGVDRA 2399
ò	Ολ 59	89
qq	Db 2400 AVAQTLARRTHFTHRAVLLGDTVIGAPPADQADELVFVY	/SGQGTQHPAMGEQLAAAFPVF 2459
ò	Оу 59	85 28
qq	2460 ADAWHDALRRLDDPPDPPTRSQHTL	FAHQAAFTALLRSWDITPHAVIGHSLGEITAAYA 2519
ò	69	62
q	2520 AGILSLDDACTLITTRARLMHTLPPPGAMVTVLTSEE	EARQALRPGVEIALFGPHSVVL 2579
ò	Оу 63	62
g	Db 2580 SGDEDAVLDVAQRLGIHHRLPAPHAGHSAHMEPVAAELLATTRELRYDRPHTA	JATTRELRYDRPHTAIPNDPTT 2639
ò	Оу 63	62
අ	Db 2640 AEYWAEQVRNPVLFHAHTQRYPDAVFVEIGPGQDLSPLVDGI	/DGIALQNGTADEVHALHTALA 2699
ò	Оу 63	62
d d	Db 2700 RLFTRGATLDWSRILGGASRHDPDVPSYAFQRRPYWIESAPPATADSGHPVLGTGVAVAG	SAPPATADSGHPVLGTGVAVAG 2759
ò	Оу 63	62
QQ	Db 2760 SPGRVFTGPVPAGADRAVFIAELALAAADATDCATVEQLDVTSVPGGSARGRATAQTWVD	LDVTSVPGGSARGRATAQTWVD 2819
ò	Qy 63	62
QQ	Db 2820 EPAADGRRRFTVHTRVGDAPWTLHAEGVLRPGRVPQPEA	AVDTAWPPPGAVPADGLPGAWR 2879
ò	ογ 63	7

g	2880	RADOVFVEAEVDSPDGFVAHPDLLDAVFSAVGDGSRQPTGWRDLAVHASDATVLRACLTR	2939
ጽ	63		62
ą	2940	RDSGVVELAAFDGAGMPVLTAESVTLGEVASAGGSDESDGLLRLEWLPVAEAHYDGADEL	2999
à	63	PEG	65
ą	3000	  PEGYTLITATHPDDPPDPTNPHNTPTRTHTQTTRVLTALQHHLITTNHTLIVHTTTDPPG	3059
à	99		65
ą	3060	AAVTGLTRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQPHLRLTNNTLHTPHLTPITT	3119
ጵ	99		65
ą	3120	HHNTTTTTPNTPPLNPNHAILITGGSGTLAGILARHLNHPHTYLLSRTPPPPTTPGTHIP	3179
ጵ	99		65
ą	3180	CDLTDPTQ1TQALTH1PQPLTG1FHTAATLDDATLTNLTPQHLTTTLQPKADAAWHLHHH	3239
۶	99		65
ď	3240	TONOPLTHFVLYSSAAATLGSPGOANYAAANAFLDALATHRHTQGQPATTIAWGMWHTTT	3299
≿	99		65
ą	3300	TLTSQLTDSDRDRIRRGGFLP1SDDEGMRLYDAAVGSGEDFVLAAAMDPAQPMAGDVPP1	3359
≿	99		65
ą	3360	LSGLRKSARRTARTGQTFAQRLAELPAADRDTALVTLVSDATAAVLGHADASGIAPTTTF	3419
≿	99		65
ą	3420	KDLGIDSLTAIELRNRLAEATGLRLSATMVFDHPTPRVLAAELRTDLFGTAAPLPARTAR	3479
≿	99		65
ą	3480	TRHDEPLAIVGMACRLPGGVTSPEDLWRLVASGTDAITEFPTORGWDIDRMFDPDAPG	3539
≿	99		65
ą	3540	KTYVRHGGFLSEAAGFDAAFFGISPREAWAMDPQQRVILETVWEAFENAGIVPDTLRGSD	3599
ڿ	99		65
ð	3600	TGVFMGAFSHGYGAGDDLGGFGATATQNSVLSGRLSYFFGMEGPAVTIDTACSSSMVALH	3659
≿	99		65
ą	3660	QAAQSLRDGECSLALAGGVTVMPTPLGYVEFCRQRGLAPDGRAKAFAEGADGTSFSEGAG	3719
≿	99	APN	. 89
q	3720	VLVVERLSDAERNGHTVLALVRSSAVNQDGASNGISAPNGPSQQRVIRQALDKAGLAPAD	3779
≿	69		68
ą	3780	VDVVEAHGTGTPLGDP1EAQAIIATYGQDRDTPLYLGSVKSNIGHTQTTAGLAGVIKMVM	3839
≿	69		68
ð	3840	AMRHGLLPKTLHVDEPSSHVDWSAGAVELLTEARPWPDSDRPRRAGVSSLGISGTNAHVI	3899
≿	69		68
ą	3900	LEGVAESSYRSVESSGLVPLPVSARTESSLALQVERLGEYVRGARDLAAVADGLVRGRTV	3959
≿	69		89
ą	3960	FGHRAVLLGESTVAGVAGAESRTVFVFPGQGSQWVGMGRELMGCSEVFAARMRECAAVLE	4019

ò	69		B 9
g	4020	pytgwdlldvlgeavvaervevlqpaswavavslaalwqahgvspdavighsqgeiaaac	4079
ò	69		89
. <u>a</u>	4080	VAGALSLEDAARIVALRSQTIAAHLAGRGAMASIALPATAVETVEGVWVAARNGPESTVV	4139
ò	69	TANLTSELSVCGWS	84
QO.	4140 /	AGDPSAVERVLARYEAEGVRVRRIAVDYASHTPHVEAIQEQLADVLGDITSSAPSVPWWS	4199
ò	85		84
g	4200	TVDGGWVTEPAGDDYWYRNLRQPVAMDTAIGELDGSLFIECSAHPVLLPALDQERTVASL	4259
ò	85		8
qq	4260 1	RTDDGGWDRFLTALAQAWTQGADVDWTTLIAPAPDRLLDLPTYPFDHKRYWIBATGAADL	4319
ò	. 82		84
QQ	4320	TALGLTDTAHPMLAATAALPTNDGTVLTGRISLRTHPWLADHTIODTVLLPGTAFLELVM	4379
ò	85	OTIN	88
qq	4380 }	 RAGDEVGCDTIDELVIETPLTLPVTGAVDLTVTVEQADATGHRPVSVHARPAGTDTWTRH	4439
ò	89		88
g	4440	atgtlgrtedtapdtnsfpqwpptgptaldvtefyaqlaalgyrfvptfrglraawragd	4499
ò	68	9ED	91
g	4500 7	TVYAEVALPEDRAADADHFGVHPALLDAALQSGSLLMLESDGEQGVQLPFSWHGVRFHAT	4559
ò	95		91
qq	4560 (	GATSLRVAI VPGPDGLRLRAADSENHPVATI DALVTRPPADLAPSDPVLRVGWTAVPVPA	4619
ò	92		16
Q	4620	EVRPSDADVLMLHSDDADP1QETRDLTTRVLDALLTTEGTL1VQVTGGLAAMAAAGLVRT	4679
ò	92 .	OUTDPG	96
đ	4680 7	AQSEQPGRFFLVETDPGEVLDGARCDMIAALGEPRLRLRGNRFEAARLVRAAAALTPPDT	4739
ò	. 76		96
q	4740 (	GSWQLRQSATGSLDDVAIVPTGEPDRPLGAGEVRIAVRAAGLNFRDDTVALGVVADDRPL	4799
ò	. 46		96
qq	4800	GSEAAGVVLETGPGVHDLAPGDRVLGMLAGAFGPVAITDRRLLGRMPDGWTFPQAASVVT	4859
ò	- 16	HADLVLYITR	106
q	4860 \	VFATTWYGLVDLAELRPGEKVLIHAAATGVGAAAVQIARHLDADVYATASTPKQHLLDLE	4919
ò	107 -		107
q	4920 E	PTHIADSRTTAFADTFPPADVVLNSLTGPLLDASAQLLTPGGRFIEMGKTDIRHHVQQPF	4979
ò	108 [	DLSL	111
đ	4980	DLMVAGPDRLQQIITQLLDLFANGTLHPLPVHAMDVRQAREAFGWMSSGRHTGKLVLTVP	5039
ò	112	PDG	114
g	5040 F	RPLDPEGAVIITGGSGTLAGHLARHLDHPHTYLLSRTPPPDTTPGTHLPCDVSDPTQLAT	5099

ò	115	114
đ	5100	ALAQIPQPLTGIFHTAATLDDALLHNLTPQRIDTVLQPKADAAWHLHHHTHTHTHATDLAAF 5159
ò	115	NRQVRG120
8	5160	VLYSAVAGVMGSPGQGNYVAANAFLDALAEHRQAMGLPAQSLAWGMWADVSALTAKLTDA 5219
ò	121	VTQLGG
q	5220	DRGRIRRGGFPPLSAADGMRLFDSAARTRSRSSRRPSDVTRLDGPVAPLLRGLVAHRSG 5279
ò	127	126
g	5280	PVRAVARNADDEPLAARLAGHTAAEQRRVMQEVVLRQAAAVLAYGLGEQVAADRPFRDLG 5339
ò	127	
8	5340	FDSLTAVDLRNRLAAETGLRLPTTVVFSHPTAEALATHLLELLDAPAALTTGAPLPAVTA 5399
ò	127	126
a	5400	APGTAARDQDEPIAIVAMACRLPGGVTSPEELWRLVESGTDAITTAPGDRGWDLDALYDP 5459
ò	127	126
g	5460	DPDAVGKAYSLRGGFLEGAAEFDAAFFDISPRESLGMDPQQRLLLETAWEAIERGRINPA 5519
ò	127	129
g	5520	SLHGREIGVYVGAAAQGYGLGAEDTEGNAITGGSTSLLSGRLAYVLGLEGPAVTVDTACS 5579
ò	130	129
q	5580	SSLVALHLACQGLRLGECELALAGGVSVLSSPAAFVEFSRQRGLAADGRCKSFGSGADGT 5639
ò	130	129
8	5640	TWAEGVGVLVLEQLSDAERLGHTVLAVVRGSAVTSDGASNGLTAPNGLAQQRVIRKALAA 5699
ò	130	PTW132
8	5700	AGLTAADVDLVEGHGTGTRLGDPVEADALLATYGQNRGEPVWLGSLKSNIGHATAAAGVA 5759
ò	133	132
얺	5760	GVIKTVQAIGAGTMPRTLHADEPSPAVDWTAGQVSLLTGNRPWPMTSVPGERPSPRSGSA 5819
ò	133	
යු	5820	- GRTLTSSLNSTVRSPWRRDRLARNPGRCLGCCPRGPLPPCGRRPPVCAIIWRPSGPDPLD 5879
ò	136	135
ය ර	5880	IGYAQATSRAQFTHRAAEEAASPDGFRAGLDSVADGAEAPESSAEPPRSARRFLFDGQGA 5939
ò	136	135
g	5940	QRVGMGRELHGRFPVFAAAWDEVSDAFGKHLEHSPTDVFHGEHGDLAHDTLYAQVGLFTL 5999
ò	136	135
අ	0009	EVALLRILEHWGVRPDVVVGHSVGEVTAAYAAGVLTLADATTLIVARGRALRALPPGAMT 6059
ò	136	135
g	0909	AVEGSPAEVGAFTDLDIAAVNGPSAVVLTGAPDDVAAFEREWAAAGRRAKRLDVGHAFHS 6119
ò	136	135
q	6120	RHVDGALDDFRGVLESLAFGAARLPVVSTTTGRDAAGDLATPEHWLRHARRPVLYADAVR 6179
ò	136	

Š

6239	135	6539		
6180 ELADLGVNMFVAVGPSGALASAASENTGGSAGTYHAVLRARTGEESAALTAVAELHAHGA 6239	136 135	6240 PVDLAAVLAGGRPVDLPVYPFQHRSYWLAPAVGGGSPTAVPDTGRPTEPDPDDLTVAEIV 6299	136ITEDIGVTI 148	6300 RRRAAALLGIADPGDVDADTTFFALGFDSLAVQRLRNQLTAATGLDLPTAV 6350
QQ	ò	q	ò	Д

Search completed: March 20, 2003, 12:41:52 Job time : 204 sec8

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DYHG\_CHLRE DYHC\_MOUSE

09nyc9 P98164 09h251 P19712 P36022 P363 07513 039575 099hu4

SEOID\_1\_15FUSED Perfect score: Title:

Run on:

773 \_ - 1 1 AAGGILHLELLVAVGPDVFQ......SPTWSCLITEDTGFDLGVTI 148 BLOSUM62 Gapop 10.0 , Gapext 0.0 Scoring table: Sequence:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homod	P58397 homo sapien	homod	b bac			homod	ens (	088277 rattus norv		b tyr		P33450 drosophila		Q14517 homo sapien		P37276 drosophila								Q15413 homo sapien	ratt	P21530 hog cholera		homo	param	Ogazo mus musculu	P97857 mus musculu	Q9ukps homo sapien
SUMMARIES	ΩΙ	ATS7 HUMAN	AT12 HUMAN	EPPL_HUMAN	BACA_BACLI	HTS1_COCCA	BIR6 HUMAN	FAT2_HUMAN	RYR1_PIG	FAT2 RAT	RYR1_HUMAN	TYCC_BACBR	ACVS_NOCLA	FAT_DROME	PKD1 HUMAN	FATH HUMAN	RYR2_RABIT	DYHC_DROME	ATS8_HUMAN	RYR1_RABIT	RYR2_HUMAN	BACC_BACLI	ATS9_HUMAN	POLG_BVDVN	RPOA_LELV	RYR3_HUMAN	ATS1_RAT	POLG_HCVB	PGCV_HUMAN	PRKD_HUMAN		ACF7_MOUSE		ATS6_HUMAN
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	Length		1593	2065	5255	5217	4829	4349	5035	4351	5038	6486	3649	5147	4303	4590	4969	4639	890	5037	4967	6329	1629	3988	3829	4870	967	3898	3396	4128	4540	5327	968	860
<b></b>	Query	0.7	σ	O	29.0	æ	7	27.8	7	~	27.2	~	7	7	ø	ø	w	ø	ø	ø	ø	S.	w	to i	Ω.	Δ.	ın.	n	in	ī	ß	25.6	2	S
	Score	237	229	226	224	. 222	216	215	212	211	210	210	209	209	208	207	206	205	204	204	203	203	202	202	200	200	199	199	198	198	198	198	197	196
	Result No.	н	7	m	4	ស	ø	7	æ	0	10	11	12	13	14	15	16	17	18	19	50	21	25	23	57.0	52	26	27	28	29	30	31	35	33

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 ARPGHAQPHVVYKRQAPERLAQRGDSSAPSTCGVQVYPELESRRERWEQRQGWRRPRLRR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 KMVILTEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P58397,
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24.-) (A disintegrin and
metalloproteinase with thrombospondin motifs 12) (ADAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 -----TERYVLTNLNIGAELLRDPSLGAOFRVHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 LHQRSVSKEKWVETLVVADAKMVEYHGQPQVESYVLTIMNMVAGLFHDPSIGNPIHITIV
                      rkosITE; PS00427; DISINTEGRIN 1; FALSE NEG.
Hydrolase; Metalloprotease; Zinc; Signāl; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                         CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
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ZINC (CATALYTIC)
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(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                . score 237; DB 1; Length 997; Pred. No. 0.026; 24; Mismatches 62; Indele 17
                                                                                                                                                                                                                                                                               6587044ED02FC104 CRC64;
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MEDLINE=21264577; PubMed=11279086;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
                                                                                                                                                               ZINC (CATALYTIC)

* DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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ADAMTS-7.
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  ZINC_PROTEASE; 1.
ADAM_MEPRO; 1.
TSP1; 1.
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Mammalia, Eutheria, Primates;
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 PS500142; PS50215; PS50092;
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les 61; Conserv
           PROSITE, PS50215,
PROSITE, PS50092,
PROSITE, PS00427,
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P58397;
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SEQUENCE
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                                                               matrix (By similarity).
-!- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                  origin.
-!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                R InterPro; IPR00126; Disintegrin.
R InterPro; IPR001280; Rep_M12B_propep.
R InterPro; IPR001280; Reprolysin.
R InterPro; IPR001290; Reprolysin.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R Pfam; PP01421; Reprolysin; 1 6
R Pfam; PP01421; Reprolysin; 1 7
R PR031TE; PS50125; DISINTEGRN 1; R PR031TE; PS50092; TSP1; 2
R PR031TE; PS50092; TSP1; 2
R PR051TE; PS50092; TSP1; 2
R PR051TE; PS00142; ZNC_PR0TEASE; 1
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
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                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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BY SIMILARITY.
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
SPACER 2.
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ADAMTS-12.
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TSP TYPE-1 6.
TSP TYPE-1 7.
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CYS-RICH.
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           EMBL, AB051895; BAB40803.1; -
Genew, HGNC:15577; EPPK1.
Pfan; PF00681; Plectin_repeat.
Pfan; PF00681; Plectin_36.
SMART; SM00250; PLEC; 65.
Colled coll; Repeat. Structural protein
REPEAT 9 46 PLECTIN 1
REPEAT 123 160 PLECTIN 3
REPEAT 165 200 PLECTIN 6
REPEAT 253 290 PLECTIN 6
REPEAT 253 290 PLECTIN 6
REPEAT 350 356 PLECTIN 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE CERVICAL CARCINOMA;

TISSUE Cervical Carcinoma;

MEDLINE-2101183; PubMed-11278896;

MEDLINE-2101183; PubMed-11278896;

MA Sasaki M., Mateuo N., Khaleduzaman M., Yoshioka H.;

Tuppilakin, a novel member of the plakin family originally identified as a 450-kDa human epidermal autoantigen: structure and tissue to localization.;

Tuppilakin, a novel member of the plakin family originally identified as a 450-kDa human epidermal autoantigen: structure and tissue to localization.;

Tuppilakin, MIDELY EXPRESSED WITH HIGHEST LEVELS IN LIVER, SMALL INTESTINE, COLON, SALIVARY GLANDS, STOMACH AND APPENDIX.

SMALL INTESTINE, COLON, SALIVARY GLANDS, STOMACH AND APPENDIX.

SIMILARITY: CONTAINS 65 PLECTIN REPEATS.
                                                                                                                                                                                   124 GNLSHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDFF1EPVKKHP 183
                                                                                                                                                                                                                              243
                                                                                                                                                                                                                                                       244 KERWVETLVVADTKMIEYHGSENVESYILTIMMWYTGLFHNPSIGNAIHIVVVRLILLEE 303
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                         184 LVEGGYHPHIVYRROKVPETKEPTCGLKDSVNISQKQELWREKWERHNLPSRSLSRRSIS
                                                                                                                                                                                                                                              -----QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTE
                                                                                                                                                                                                                                                                                 63 PEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRG
                                                                                                                                                                                                                                                                                              304 EEQGLKIVHHAEKTLSSFCKWQKSINPKSDLNPVHHDVAVLLTRKDI-CAGFNRPCETLG
                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
EPPRI OR EPIPL.
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18.3%; Pred. No. 0.26
:ive 35%; Mismatches
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1031 HHLPM 58 V	1091 PESAP	59		P. A.		V2.190 1.501		۵ :	1331 LQVQL		1391 QLRER	67	1451 EYVGA	29	1511 AQLIS		1571 LRPGT	69	1631 YTGQQ	29	1691 RILADI	74	1751 VLQSR	74	1811 EETET	74	1871 SDCIAC	82	1931 DVGLVP	82	1991 VIDPQ	82 GW	2051 EDTGWN	84	2111 KLQLVF
d yo	g	ò 4	3 8	3 8	ò	3 6	3 3	Ŝ i	සි .	ò i	QC O	ò	a	ò	g	ò	g	ò	g	ò	ල ි	ò	q	ò	Op	ò	අු	ò	q	ò	g	ò	g	ò	đ
FT DOMAIN 2593 2624 COLLED COIL (POTENTIAL). FT DOMAIN 3127 3158 COLLED COIL (POTENTIAL). FT DOMAIN 3661 3692 COLLED COIL (POTENTIAL). FT DOMAIN 4195 4226 COLLED COIL (POTENTIAL).	DOMAIN 4729 4760 SEQUENCE 5065 AA; 553078	29.2%; Score 226; DB 1; Le imilarity 1.9%; Pred. No. 11;	87; Conservati		131 ATGGLVDPAQGVLVAPEPACHQG	6 9 AO	Db 191 ERCVRAPGSGLALLPLKITFRSMGGAVSAAELLEVGILDEQAVQGLREGRLAAVDVSARA 250	0y 6	Db 251 EVRRYLEGTGSVAGVVLLPEGHKKSFFQAATEHLLPMGTALPLLEAQAATHTLVDPITGQ 310	Oy 6 LHLELLVA		Qy 14 13	Db 371 DAQLATGGLVCPARRLRLPLEAALRCGCLDEDTQRQLSQAGSFSDGTHGGLRYEQLLALC 430	Ογ 14	Db 431 VTDPETGLAFLPLSGGPRGGEPQGPPFIKYSTRQALSTATATVSVGKFRGRPVSLWELLF 490	0y 14 13	Db 491 SEAISSEQRAMLAQOYQEGTLSVEKLAAELSATLEQAAATARVTFSGLRDTVTPGELLKA 550	0, 14	Db 551 EIIDQDLYERLEHGQATAKDVGSLASAQRYLQGTGCIAGLLLPGSQERLSIYEARCKGLL 610	Qy 14 18	:     611 RPGTALILLEAQAATGFIIDPKANKGHSVEEALRAAVIGPDVFAKLLSAERAVTGYTDPY 6	FOAHO		24	731 ILLDPSDDTKGFFDPNTHENLTYLOLLERCVRDPETGLYLLPLSSTOSPLVDSATOOAFO		791 NLLLSVKYGRFOGORVSAWELINSEYFSEGRRROLLRRYROREVTLGOVAKLLEAETORO		851 ADIMLPALESRYTVHOLIEAGIIDOOLLDOWLAGTISBEALLIAMGWBRYLGGLGAVGGV		911 RLLPSGORLSLYOAMROKLLGPRVALALLEAGAATGTIMDPHSPESISVDEAVBRGVVGP	and defined to the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second seco	971 ELYGRIKRAEGAIAGREDPESGKOVSVEOAMKKGLIPWEOAABLLEAOVATGGIIDPTSH	CHINK 5	: : : : : : : : : : : : : : : : : : : :

Q	1031 H	HHLPMPVAIQRGYVDQEMETALSSSSETFPTPDGQGRTSYAQLLEECPRDETSGLHLLPL 1090
ò	58 V	85
qq	1091 P	PESAPALPTEEQVQRSLQAVPGAKDGTSLWDLLSSCHFTEEQRRGLLEDVQEGRTTVPQL 1150
ò	- 65	85
ф	1151 L	LASVQRWVQETKLLAQARVMVPGPRGEVPAVWLLDAGIITQETLEALAQGTQSPAQVAEQ 1210
ò	59	66
gg	1211 P.	PAVKACLWGTGCVAGVLLQPSGAKASIAQAVRDGLLPTGLGQRLLEAQVASGFLVDPLNN 1270
ò	- 49	99
qq	1271 0	QRLSVEDAVKVGLVGRELSEQLGQAERAAAGYPDPYSRASLSLWQAMEKGLVPQNEGLPL 1330
ò	- 49	99
QQ	1331 L	LQVQLATGGVVDPVHGVHLPQAAACRLGLLDTQTSQVLTAVDKDNKFFFDPSARDQVTYQ 1390
ò	- 49	99
Op	1391 0	QLRERCVCDSETGLLLLPLPSDTVLEVDDHTAVALRAMKVPVSTGRFKGCSVSLWDLLLS 1450
ò	- 49	99
q	1451 E	EYVGADKRRELVALCRSGRAAALRQVVSAVTALVEAAERQPLQATFRGLRKQVSARDLFR 1510
ò	- 49	99
qq	1511 A(	AQLISRKTLDELSQGTTTVKEVAEMDSVKRSLEGGNFIAGVLIQGTQERMSIPEALRRHI 1570
ò	- 49	99
g	1571 LI	LRPGTALVLLEAQAATGFIIDPAENRKLTVEEAFKAGMFGKETYVKLLSAERAVTGYTDP 1630
ò	- 69	99
qq	1631 Y	YTGQQISLFQAMQKDLIVREHGIRLLEAQIATGGIIDPVHSHRVPVDVAYRCGYFDEEMN 1690
ò	- 49	73
ය ය	1691 RJ	RILADPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLYLLQIIKKGENYVYINEATRH 1750
ò	74	73
qq	1751 VI	VLQSRTAKMRVGRFADQVVSFWDLLSSPYFTEDRKRELIQEYGAQSGGLEKLLEIITTTI 1810
ò	74	Š
QQ	1811 EE	EETETQNQGIKVAAIRGEVTAADLFNSRVIDQKTLHTLRVGRTGGQALSTLECVKPYLEG 1870
ò	74	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
g	1871 SI	SDCIAGVTVPSTREVMSLHEASRKELIPAAFATWLLEAQAATGFLLDPCTRQKLSVDEAV 1930
ò	82 -:	
gg	1931 DA	DVGLVNEELRERLLKAERAATGYRDPATGDTIPLFQAMQKQLIEKAEALRLLEVQVATGG 1990
ò	82	81
g	1991 VI	VIDPQHHHRLPLETAYRRGCLHKDIYALISDQKHMRKRFVDPNTQEKVSYRELQERCRPQ 2050
ò	82	GW
Q	2051 EI	EDTGWVLFPVNKAARDSEHIDDETRRALEAEQVEITVGRFRGGKPTLWALLNSEYVTEEK 2110
ò	84	87 87
5	2111 171	Ot to an impromine the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continu

ò	88		87
qq	2171	MLQDLETGRSTTQELMEDDRVKRYLEGTSCIAGVLVPAKDQPGRQEKMSIYQAMWKGVLR	2230
ò	88		87
qq	2231	PGTALVLLEAQAATGFVIDPVRNLRLSVEEPVPAGVVGSEIQEKLLSAERAVTGYTDPYT	2290
ò	88		87
g	2291	GQQISLFQAMQKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRV	2350
ò	88	NPEDDT	93
엄	2351	:          Ladpsdotkgffdpnthenltyv&llarcvpdpdtglymlqlagrgsavhQlseelrcal	
ò	94		93
g	2411	RDARVTPGSGALQGQSVSVWELLFYREVSEDRRQDLLSRYRAGTLTVEELGATLTSLLAQ	2470
ò	94		93
엄	2471	AQAQARAEAEAGSPRPDPREALRAATMEVKVGRLRGRAVPVWDVLASGYVSRAAREELLA	2530
ò	94	5d0	96
g	2531	EFGSGTLDLPALTRRLTAIIEEAEEAPGARPQLQDARRGPREPGPAGRGDGDSGRSQREG	2590
ò	97		9,6
g	2591	QGEGETQEAAAAAAARRQEQTLRDATMEVQRGQFQGRPVSVWDVLFSSYLSEARRDELL	2650
ò	97	HADLVLXITR	106
qq	2651	AQHAAGALGLPDLVAVLTRVIEETEERLSKVSFRGLRRQVSASELHTSGILGPETLRDLA	2710
ò	107		106
g	2711	QGTKTLQEVTEMDSVKRYLEGTSCIAGVLVPAKDQPGRQEKMSIYQAMWKGVLRPGTALV	2770
ò	107		106
q	2771	LLEAQAATGFVIDPVRNLRLSVEEAVAAGVVGGEIQEKLLSAERAVTGYTDPYTGQQISL	2830
ò	107		106
g	2831	FQAMQKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSD	2890
ò	107	FD	108
q	2891	DTKGFFDPNTHENLTYVQLLRRCVPDPDTGLYMLQLAGRGSAVHQLSEELRCALRDARVT	2950
ò	109		108
셤	2951	PGSGALQGQSVSVWELLFYREVSEDRRQDLLSRYRAGTLTVEELGATLTSLLAQAQAQAR	3010
ò	109		108
셤	3011	AEAEAGSPRPDPREALRAATMEVKVGRLRGRAVPVWDVLASGYVSGAAREELLAEFGSGT	3070
ò	109	LELP	115
g	3071	   LDLPALTRRLTAIIEEAEEAPGARPQLQDAWRGPREPGPAGRGDGDSGRSQREGQGEGET	3130
ò	116		115
a	3131	QEAAAAAAAARRQEQTLRDATMEVQRGQFQGRPVSVWDVLFSSYLSEARRDELLAQHAAG	3190
ò	116	RQV	118
a	3191	ALGLPDLVAVLTRVIEETEERLSKVSFRGLRRQVSASELHTSGILGPETLRDLAQGTKTL	3250

ò	119	118
QQ	3251	QEVTEMDSVKRYLEGTSCIAGVLVPAKDQPGRQEKMSIYQAMWKGVLRPGTALVLLEAQA 3310
ò	119	122
q	3311	ATGEVIDPVRNLRLSVEEAVAAGVVGGEIQEKLLSAERAVTGYTDPYTGQQISLFQAMQK 3370
ò	123	122
g	3371	DLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFF 3430
ò	123	122
q	3431	DPNTHENLTYVQLLRRCVPDPDTGLYMLQLAGRGSAVHQLSEELRCALRDARVTPGSGAL 3490
ò	123	122
d	3491	QGQSVSVWELLFYREVSEDRRQDLLSRYRAGTLTVEELGATLTSLLAQAQAQARAEAEAG 3550
ò	123	0LGGACSPTW
qq	3551	SPRPDPREALRAATMEVKVGRLRGRAVPVWDVLASGYVSGAAREELLAEFGSGTLDLPAL 3610
ò	133	132
q	3611	TRRITAIIEEAEEAPGARPQLQDAWRGPREPGPAGRGDGDSGRSQREGQGEGETQEAAAA 3670
ò	133	132
g	3671	AAAARRQEQTLRDATMEVQRGGFQGRPVSVWDVLFSSYLSEARRDELLAQHAAGALGLPD 3730
ò	133	132
q	3731	LVAVLTRVIEETEERLSKVSFRGLRRQVSASELHTSGILGPETLRDLAQGTKTLQEVTEM 3790
ò	133	SCL
QQ	3791	:  DSVKRYLEGTSCIAGVLVPAKDQPGRQEKMSIYQAMWKGVLRPGTALVLLEAQAATGFVI 3850
ò	136	135
q	3851	DPVRNLRLSVEEAVAAGVVGGEIQEKLLSAERAVTGYTDPYTGQQISLFQAMQKDLIVRE 3910
ò	136	135
g	3911	HGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFFDPNTHE 3970
ò	136	135
qq	3971	NLTYVQLLRRCVPDPDTGLYMLQLAGRGSAVHQLSEELRCALRDARVTPGSGALQGQSVS 4030
ò	136	139
qq	4031	VWELLFYREDERGOLLSRYRASTLTVEELGATLTSLLAQAQAQARAEAEAGSPRPDP 4090
ò	140	139
g	4091	REALRAATMEVKVGRLRGRAVPVWDVLASGYVSRAAREELLAEFGSGTLDLPALTRRLTA 4150
ò	140	139
g	4151	IIEBAEEAPGARPQLQDAWRGPREPGPAGRGDGDSGRSQREGQGEGETQEAAAAAAAA 4210
ò	140	139
qq	4211	QEQTLRDATMEVQRGQFQGRPVSVWDVLFSSYLSEARRDELLAQHAAGALGLPDLVAVLT 4270
ò	140	139
đ	4271	RVIEETEERLSKVSFRGLRRQVSASELHTSGILGPETLRDLAQGTKTLQEVTEMDSVKRY 4330
ò	140	142

seqid 1 15fused.rsp

		the European Ric
Oy 143 142	388	use by non-pro
Db 4391 RLSVEEAVAAGVVGGEIQEKLLSAERAVTGYTDPYTGQQISLFQAMQKDLIVREHGIRLL 4450		entities requir
Oy 143 142		or seine an emar
Db 4451 EAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFFDPNTHENLTYVQ 4510	22.5	HSSP; P14687;
Oy 143 142	388	InterPro; IPR001
Db 4511 LLRRCVPDPDTGLYMLQLAGRGSAVHQLSEELRCALRDARVTPGSGALQGGSVSVWELLF 4570	<u> </u>	Pfam; PF00501; P
Oy 143	ž	Pfam; Fr00550 Pfam; PF00668 pprvms: pp001
Db 4571 YREVSEDRRODLLSRYRAGTLTVEELGATL 4600	588	PROSITE: PS00013
RESULT 4	KA DE	PROSITE; PS5007 Ligase; Isomera
BACA_BACLI ID BACA_BACLI STANDARD; PRT; 5255 AA.	FT	ncti
O68006; 15-JUL-1999 (Rel. 38,	T.H.	
15-JUL-1999 (Rel. 38, 15-JUN-2002 (Rel. 41,	FT	
	FT	
	FT	DOMAIN 15
(Glutamate activase), ATP-dependent isoleucine adenylase (11eA)  (Inchincine activase), Glutamate racemase (FC 5 1.1.3)	- E	DOMAIN 3664
	F	o ċ
OS BACITIUB ILCHENITOTMIB. OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. OX NCBI TaxID=1402;	FT	
	FT	ш
STRAIN-ATCC 10716; MEDLINE-98089193; Pubmed=9427658;		
	n 2	Best Local Similar Matches 77; Conf
	λõ	. 2 AGG
<pre>\tag{L} Chem. Biol. 4:927-937(1997). CC -!- FUNCTION: ACTIVATES FIVE AMINO ACIDS, INCORPORATES TWO D-AMINO</pre>	Q 	   110 AGGAYLPIDP
	٥ م	3
<del>!</del>	qa	170 LSSVNDSGDT
<del>+ +</del>	ò	
<del>!</del>	QC	230 GSVFDIFGAL
CC THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS CC RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION	ò	2 5
	qa	290 SNLRKILFGG
CC -1- MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC. CC DODECAPEPTIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST	ò	6
	qa	350 GSPLANTSVL
	ò	6
CC HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C- CC TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT	QQ ——	410 YKTGDLAKWL
•	δ	6
<u>:</u> .	ପ୍	470 RPYICAYITA
CC I SIMILARITY: CONTAINS 5 ACYL CARRIER DOMAINS.	2	6

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GERASIPHVRKVLNHVGRDKLIHVYGPTESTVYATYYFINBIDDEAETIPI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLNGASLVMIEKEALLNINRLGSAINEEKVSVMFITTALFNMIADIHVDCL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIMDEAGKLVPIGVPGELCIAGDGLSKGYLNREELTAEKFIPHPFIPGERL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPDGNIEFIGRIDHQVKIRGFRIELGEIESRLEMHEDINETIVTVREDEES 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETPKDRIAFMLSDTKAAVLLTQGKAADGIDCEADIVQLDREASDGFSKEP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAYIIYTSGSTGTPKGVITPHYSVIRVVONTNYIDITEDNVILQLSNYSFD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------BLLVAVGPDVFQA------21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANREISLDELKGFLGEKLPEYMIPAYFVKLDKLPLTKNGKVDRKALPEPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN 1 (ISOLEUCINE-ACTIVATING).

DOMAIN 2 (CYSTEINE-ACTIVATING).

DOMAIN 3 (LEUCINE-ACTIVATING).

DOMAIN 4 (GLUTAMINE-ACTIVATING).

DOMAIN 5 (ISOLEUCINE-ACTIVATING).

CYCLIZATION (POTENTAL).

ACYL CARRIER (ACP) 1.

ACYL CARRIER (ACP) 2.

ACYL CARRIER (ACP) 3.

ACYL CARRIER (ACP) 5.

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             4; AMPBINDING.
12; PHOSPHOPANTETHEINE; 3.
55; AMP BINDING; 5.
75; ACP DÓMALIN; 5.
age; AnTibiotic blosynthesis; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels 4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 224; DB 1; Length 5255;
Pred. No. 15;
34; Mismatches 36; Indels 4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2651 PHOSPHOPANTETHEINE (BY SIMI)
3694 PHOSPHOPANTETHEINE (BY SIMI)
5201 PHOSPHOPANTETHEINE (BY SIMI)
5201 PHOSPHOPANTETHEINE (BY SIMI)
5201 PHOSPHOPANTETHEINE (BY SIMI)
5201 PHOSPHOPANTETHEINE
                                                                                                                                                                                                                           000073; AMP-bind.
001242; Condensatn.
003880; Ppantne attach.
AMP-binding; 5.
pp-binding; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l enzyme; Repeat.
                                                                                                                                                                                  ; AAC06346.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arity 1.6%;
onservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2689
3732
5249
1037
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Ωp	530	TAGAENEYEAPRNETEEKLAAVWQDVLHVEKAGIHDHFAQMGGHSLHAMELIAKIKEKMN	589
ò	22	- GaoH	25
a	590	 VEI PLHQLFKLATIKELSAFIEANHQEDKGDTLVTRAADPENIHEIFPLTGIQLAYLVGR	649
ò	26	-TER	28
g	650	DETFEIGGVATNLTVEFEADVDLNRFQLTLQKLIDRHPILRTIVFENGTQKILEATQRYT	709
ò	29		28
a	710	I ETQDLRGFTEEEINVRI LEQREKMTSKI I DPSVWPLFELKTFMLPGEKKY FFLNVDPLI	692
ò	29	- AVLTNLNI	36
QQ	770	CDDSSMKRLIREFKQLYENPGLQLPSLEYSFRDYVLASINFKQTSRYQKDQQYWLDKLDH	829
ò	37		36
a	830	FPSAPELPLKSDPAHVAKPSFKKFSTFLDGHTWNELKKKARHHHLTPTSVLCAAYAYILA	889
ò	37		36
g	890	YWSRQNHFAINLTVFNRIPFHPDVKNMIGDFTSLMLLDIHAEENMSSFWRFALNVQDTLL	949
ò	37	GAELLR	42
a	950	EALEHRHYDGVDVIRNIAKKNGMNKKAVMPIVFTSVLSENPDDSFDSLVDFDNIHFFSTR	1009
à	43		42
q	1010	TSQVYIDNQVYEINGGLYITWDYVEQIFEHEVIESMFDQYIAVIQKAVSGEDVSTIQMNE	1069
ò	43		42
QQ	1070	KSRQMI SAYNDTDQSFDAKPLHELFTGQVKHGPDRMALKHHDEVMTYQELDEKSNQVARF	1129
ò	43	-DP	44
g	1130	LIGKGVEKGDYIGVIGKRSLGTIVNLLAVLKTGAAYIPLDPDYPEERKAYIQSKSNCKFF	1189
ò	45		44
g	1190	ISHDVYDKEHIERFSKAPVDRKVDLDDMAYVIFTSGSTGKPKGVQITHVPQRNTILDINE	1249
ò	45	SLGAOFRV	52
g	1250	KFNVTEQDNIMGISSLCFDLSVYDVFGALSSGASLVIIDDQRDVFSLKETAEKERITIWN	1309
ò	53		. 09
g	1310	SVPAIMGMTADVYPDNELNHHLRLILLSGDWIPLQLPATIKKTFKNAEVISLGGATEGSI	1369
ò	61		09
20	1370	WSIYYPIQKVEEDWKSIPYGKPLANQKIYVLNQNKQLCPVGVEGELYIGGAGVASGYIHD	1429
ò	61		09
a	1430	QEKTEHSF1QHQELGY1YKTGDYGVLKEDGYVEFLGRKDSQVK1RGYRVEMGE1ENTLVS	1489
ò	61	TEPECAPNITA	71
윱	1490	HQEITKASVIDYTSPDGIKNLYAFVVAENAISQLDVKEFLQKTLPDYMIPAKFVQIEEIP	1549
ò	72		71
g	1550	LTVNGKVDKRTLHDLAEQHTADEGQRGGRMLPENETQAMLLEIWKDIFGLDSINLDVSYY	1609
ò	72		

Q	1610 EIGGDSLKAISII7	SIITEINKRMNVEMPISEIFKNDTIIALDHYLKNREESDMEHPIQKAREK 1	1669
ò	72	2	1,1
g	1670 EYYPTSPAQQRMYN	EYYPTSPAQQRMYMLSMLENERGAYHIPMALLVEGRINAMQLENALKTFLORHEILRTGF 1	1729
ò	72	7	75
qq	1730 EIQNNELIQKIYE	QKIYENVDFRLEYECLDASITDQHALMEITSRYCKESIKPFDLSRPPLMRAK 1	1789
ò	94	2	75
엄	1790 LIKIDDIRHILVINFHHII	SDGVSQGILMNEILELYSNVPLPEVNVQYKDYVEWNHTFNQ	1849
ò	92	£	75
q	1850 SAAMKKQEAYWLDVYRDI	PSKLDFPYDYKRHHIDTFEGSSVFLEMERELSDHIRKLAKHN	1909
ò	94	£	75
qq	1910 GTTLYTVMLSAYY	GTTLYTVMLSAYYVLLNKYTNQTDIVVGTAAAGRLHPDLQDVFGVFGVFTALRNEVDTSY 1	1969
ò	92		75
qq	1970 SFKEFLQQTKERT	SFKEFLQQTKERTIAAFDNSEYPFDDLIRKLNGVRESNRNPLFDTMFVLEDARMFTKQKG 2	2029
ò	92	7	75
q	2030 DVKLSPIIFELDN	DVKLSPIIFELDNAKFDMIFNVLDFEQKIVLNIEYSTSLFKDETIQKIAEDYFRILEEVS 2	2089
ò	92	2	75
q	2090 ENLDVALHQIDMI	ENLDVALHQIDMISRQEKRTLLESFNHTKTAYPKGKAIHQLFEEQAKRIPDHTAVVFEDQ 2	2149
ò	94		75
q	2150 KLTYRQLNEKANO	KLTYRQLNEKANQVARLLREKGVKPDTLVGIMMERSSDMIAAILGVLKAGGAYLPIDPEY 2	2209
ò	92		75
셤	2210 PPERMRYMAFDSE	PPERMRYMAFDSEVKVIISDVPLAEELTAESIELIHMDDERIAGODRSDIDNVNOSGDLA 2	2269
ò	92		85
q	2270 YVIYTSGSTGKPK	YVIYTSGSTGKPKGVMIEHQSLINLCSWHQSCFEVGQNDNSSIYASISFDAFVWELFPYI 2	2329
ò	86	8	85
g	2330 TAGATVHVLNQETI	TAGATVHVLNOETRLDVEKLNRYFHDHHITISFLPTPVCEQFTALDNHSLRTLLTGGDKL 2	2389
ò	98		85
qq	2390 NVFKEKSYQIVNN	NVFKEKSYQIVNNYGPTENTVVATSFPIDKSHQNIPIGKPIDNVKYYILNKDLQLCPLGA 2	2449
ò	98		82
QQ	2450 SGELCIAGEGLAR	SGELCIAGEGLARGYUNRPELTREKFIGNPFVPGERMYRTGDLAKMLPDGNIQFLGRVDQ 2	2509
ò	98	8	85
g	2510 QVKIRGYRIEPGE	QVKIRGYRIEPGEIENRLLKYEKIEEAAVIAREDGDHDPYLCAYVTVKKEVEPEKIRAFL 2	2569
ò	98	9TIN	91
q	2570 KKSLPDYMIPQYF	FVQLDGLPLTVNGKVDKKSLPVPERSVTMDRRYEAPRÖMEEKLVSIW 2	2629
ò	92		91
ద	2630 EEALGINKIGINS	EEALGINKIGINSHFFEAGGHSLKAAALVSTIHKELNVKLPLRQIFETPTIKGLRDISVR 2	2689
ò	95	6	91
qq	2690 RRKCFYIDRKTEE	RRKCFYIDRKTEEKPYYRLSSAQKRLYILSQTGSHVAYNMPFAMTLEGDFDIRRFENTLK 2	2749

		ò	125	
ò		q	3830 FDSQEEKVF	124
qq	) 2750 NMVKRHESFRTSFVMIDGEVMQQIEKEIDFQVAYSDIGKESAEEKIKSFIRPFHLEKAPL 2809	ò	125	•
ò	, 92	qq	3890 FETLYLOAL	
g	2810 LRAEVVKLNEREHLLMFDMHHIISDGVSTDIFIQELGALYEGKSLKPFHIQYKDYAEWEN 2869	6		
ò	92 91	; £	3950 KLERDTFE	
q	) 2870 SHARSEELKRQEEYWLKTYKGDIPVLDLPIDHKRPLTKSSEGDTVTAAIESETFRKLQHM 2929	ł è		
ò		i	4010 MMEGHGRET	
g	2930 AKENGUTMYMLLLAGYTALLSKYTGQEDIIVGTPAAGRNHEDIQHLIGMFUNTLAIRNHP 2989	3 8		
ò	7 92 91	;	4070 GVI.KYMTEF	1
đ	2990 EGKKTFRDYLQEVKENTLQAYENQDYPFEELVEKVNIKRDMARNPLFDTMLVYHNTDVKP 3049	} &		
ò	, 92 91	3 AB	4130 AISLNGELT	
쉱	3050 FEAECLRSRLVEIKRGISKFDITVTASEAADGLRLEVEYSTTLFNKERMERLSEHLISLL 3109	ò	132	
ò	/ 92 91	2 2	4190 GLEELELIP	
g	3 3110 EQAADHPDIAINQIDVLTKGERHRVLYDFNRTDGVFCKEMTIPELFEKQAEKTPDHPAVA 3169	ò	132	•
ò	92	qq	4250 EESFHEIVE	124
g	3170 FGDETISYRELNERANSLAFTLRQKGVGPDVIAGILTERSIEMIVGIMGILKAGGAYLPI 3229	ò	132	
ò	92	QO	4310 EDQEKGFDI	
요	3230 DPAYPQERISYIVKDSDVSVLCAAGÖVÖPGEAYTGDIIRIDQTGQNDHVENLKHDIKPQH 3289	ò		•
ò	96 66 /	3 6	4370 ESRRIKEP	-
d d	3290 LAYVIYTSGSTGKPKGVMIEHHSVNNLVHGLNERIYQHLDAHLNVALVAPYIFDASVKQI 3349	ìè		
ò	97 110	ý é	A430 VISESKEL	-
g	) 3350 FAALLEGHTLCIVPRETAWDAMSLIEYYSKNNINVSDWTPAHLNMLAYVDKTELEFDVKE 3409	3 6	135	•
ò	/ 111 110	i 8	4490 EEMVGLFI	•
QQ	o 3410 LIVGGDALTPDVIGGLEHKFPNLSCNITNVYGPTECCVDAASHQIESGKVPQTPSIPIGR 3469	2		
ò	111 110	5 6		-
a	o 3470 PLLNTSIYIVDKELRPLPVGIAGELCIAGEGVARGYVNRPELTAEKFVDHPFEFGKKMYK 3529	}		
ò	/ 111LPDG 114	ें दे	Wallendy Orde	
q	   3530 TGDLAMWLPDGQIEFLGRADHQVKIRGYRIELGEVEQQLLTHEKIKEAAVIAGKDQNGNS 3589	8 8	145	
ò	γ 115 114	, E	4670 FLFEEDAM	
đ	D 3590 YLCAYIASDKELPAADVRQFLEREMPDYMIPSYFVKLDRLPRTPSGKVDRSALPEADGNV 3649		146	
ò	y 115 114	<u> </u>	4730 11G11G11	_
පු	D 3650 NVMEGTGYDPPRNEIERKLVQVWREILGAEDIGISHHFFAAGGDSIKALQIVSRLAKWNL 3709	}	145	
ò	y 115 124	7		-
qq	:	ga 	4/90 HLLSEENL	•
ò	y 125 124	RE	SULT 5	
Q	b 3770 FMLFRKDGYDENIVRTAFNKILEQHDALRMIYEEKDGDIIQYNRGYRENLFDLDVYDVRG 3829		ID HTS1 COCCA AC Q01886;	
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ò	125 -	124
g	3830 F	FDSQEEKVFELATGIQKKSSIRKGKLVHLGIFRADEGDHLLIAIHHLVVDGVSWRILFED 3889
ò	125 -	124
q	3890 F	FETLYLQALKGEPLDIGYKTDSYQEFARQLKKYAQSRRLLKEREYWQKALBADVPFIPAE 3949
ò	125 -	124
gg	3950 }	KLERDTFEHSATLSIRIGPDVTAKLLRNAFKAYNTEINDI <i>LLTA</i> LIAAVRDITGENKLKV 4009
ò	125 -	124
q	4010 N	MMEGHGREDILDGVDITRTIGWFTTVYPVFIDLGEEKEISQNIKWVKEALRKIPNKGIGY 4069
ò	125	124
qq	4070	GVLKYMTEELQKIQTQAPLSFNYFGEMNNDMNRKVFSQSPFSPGESIGGKIVRHCAIEMN 4129
ò	125 -	131   : :
qq	4130 7	AISLNGELTIYTTFNQDQYQTSTIEQLNQSFKENLEKIVDHCVDKEGSDMTPSDYGDVSL 4189
ò	132 .	131
g	4190	GLEELELIKDKYSAFQIEKIYPLANMQKGMLFHNAMDQTSGAYFQQIVIKLKGRVHPDIL 4249
ò	132	131
qq	4250 E	EESFHEIVKRHEILRASFEYEITAEPRQIIARDRKTPFTSIDLTGENRTROHRFIETYLK 4309
ò	132	133
Q	4310 1	EDQEKGFDLSSEALMRVCLIKMSDESYRLIWSHHILLDGWCLGIVLSELFSLYGKIMKG 4369
ò	134	134
q	4370	ESRRLKEPKPYGDYIKWLEKQDQEEAVAYWKDYLKGYESRSELPAFNRGATSEEYCGKEK 4429
ò	135	134
qq	4430	VISFSKELTTKITRIAKQHHVTINTVLQGIWGMILAKYKNTDEVVFGTVVSGREAPVDGI 4489
à	135	137 137
g	4490	EEMVGLFIHTIPTRISFEGARSFKEVLKKTQAESIESNRYSYMNLSEIQVLSEMKRELÍT 4549
ò	138 1	E
g	4550 }	HVMAFQNYAFDEELFRSQSGETGFELEGVHGKERTNYNFNLTGVLEDEQLKLKLTFNENV 4609
ò	145	144
g	4610	YDNTIIETLEKHIITVAEQVAEDETQTLRDINLVSKEEQHRILHTFNDTXTGYPKDKPLH 4669
ò	145	144
g	4670 1	ELFEEQAMKTPDHTALVFGAQRMTYRELNEKANQTARLLREKGIGRGSIAAIIADRSFEM 4729
ò	145	144
g	4730	IIGIIGILKAGGTYLPIDPETPRDRIDYMLKNSGAALLVTTDSLLKPFDIKTVDLCSDEL 4789
ò	145	
g	4790 1	HLLSEENLPRVNRSSDTAYIVYTSGSTGTPKGVVI 4824

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                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 275:4906-4911(2000).

-1- FUNCTION: Non-ribosomal peptide synthetase, able to activate proline and AEO (2-amino-9,10-epoxi-8-oxodecanoic acid), and epimerize L-Pro. Catalyzes the production of HC-toxin: a cyclic tetrapeptide: Activates and thioesterifies L-Pro, and epimerizes it to D-Pro; also uses D-Ala as a substrate but this is epimerized from L-Ala by TOXG.

-1- COFACTOR: CONTAINS 4 COVALENTLY BOUND PHOSPHOPANTETHEINES.
-1- PATHWAY: NON-RIBOSOWAL BIOSYNTHESIS OF HC-TOXIN.
                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 90105 / SB111;
MEDLINE=931001328; PubMed=1281482;
SCOCKT-Craig J.S., Panaccione D.G., Pocard J.-A., Walton J.D.;
"The cyclic peptide synthetage catalyzing HC-toxin production in the filamentous fungus Cochliobofus catalyzing HC-toxin production in the 15.7-kilobase open reading frame.";
J. Biol. Chem. 267:26044-26049(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 4 ACYL CARRIER DOMAINS.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                        Cheng Y. Q., Walton J.D.; "A eukaryotic alanine racemase gene involved in cyclic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphopantetheine; Repeat
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PHOSPHOPANTETHEINE (BY SIMI)
PHOSPHOPANTETHEINE (BY SIMI)
PHOSPHOPANTETHEINE (BY SIMI)
W, 033109CS400163A5 CRC64;
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ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FUN-2002 (Rel. 41, Last annotation update)
HC-toxin synthetase (EC 6.3.2..) (HTS).
                                                               Cochliobolus carbonum (Bipolaris zeicola).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0154; AMPBINDING.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 4.
PROSITE; PS00455; AMP BINDING; 3.
PROSITE; PS50075; ACP DOMAIN; 1.
Ligase; Multifunctional enzyme; Phosphops
REPEAT 249 642 DOMAIN 1.
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DOMAIN 2.
DOMAIN 3.
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InterPro; IPR01242; Condensatn.
InterPro; IPR01380; Ppantne_attach.
Pfam; PF00550; AMP-binding; 4.
                                                                                                                                                                                                                                                              STRAIN=ATCC 90305 / SB111;
MEDLINE=20138231; PubMed=10671527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00668; Condensation; 5.
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HSSP; P14687; 1AMU.
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                                                            36; Indels 4702;
   DB 1; Length 5217;
                               Pred. No. 19;
20; Mismatches
   Score 222;
                                                            20;
Query Match 28.7%;
Best Local Similarity 1.8%;
Matches 87; Conservative :
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g	1309	3
à	18	
g	1369	RVATSLQNSQPAVDIGCLVEAWKDTVALHAALRTVILESSLPATGILHQVVLRSHDPDIV 1428
ò	26	11
g	1429	ILDVRDVTAAITILDSYPPPTEEGIALIKRPPHRLLICTTIEGSVLIKFQVNHLVFDGMS 1488
ò	28	30
q	1489	TDKIIQDLSKAYTCRHSNKLPDHŞESKLHDGTYGNRPTKPPLAEFIRYIRDPQRKQDSIN 1548
ò	31	11
QQ	1549	YWKNALRGATTCSFPPLFDQITSEKAMPRQSWASVPIPLCVDSKELSKTLANLGITMSTM 1608
ò	38	37
දු	1609	FQTVWAIVLRIYSQNGQSVFGYLTSGRDAPVDGIDSAVGNFIAMLVCFFDFDDDGVHTVA 1668
ò	38	37
g	1669	DMARKIHNASANSISHQACSLAEIQDALGLSTSTPLFNTAFTYLPKRPTNVKAGEPEHHL 1728
ò	38	
g	1729	CFEELSMSDPTEFDLTLFVEPTQESNEVSAHLDFKLSYISQAYATSIASTVAHILSELVH 1788
ò	43	DP
g	1789	   DPYRALNTLPIVSEHDTAIIRSWNDHLFPPATECIHETFSRKVVEHPQREAICSWDGSLT 1848
ò	45	SLGAQFRVHLVKM57
q	1849	YAELSDLSQRLSIHLVSLGIKVGTKIPICFEKSMMTIVTILAVVQAGGVFVLLEPGHPES 1908
ò	58	64
8	1909	RLSGIIKQVQAELLLCSPATSRMGALQNISTQMGTEFKIVELEPEFIRSLPLPPKPNHQP 1968
ò	65	67
q	1969	MVGLNDDLYVVFTSGSTGVPKGAVATHQAYATGIYEHAVACGMTSLGAPPRSLQFASYSF 2028
ò	68	73
g	2029	DASIGDIFTTLAVGGCLCIPREEDRNPAGITTFINRYGVTWAGİTPSLALHLDPDAVPTL 2088
ò	74	73
g	2089	KALCVAGEPLSMSVVTVWSKRLNLINMYGPTEATVACIANQVTCTTTTVSDIGRGYRATT 2148
ò	74	73
g	2149	WVVQPDNHNSLVPIGAVGELIIEGSILCRGYLNDPERTAEVFIRSPSWLHDLRPNSTLYK 2208
ò	74	73
QQ	2209	TGDLVRYSADGKIIFIGRKDTQVKMNGQRFELGEVEHALQLQLDPSDGPIIVDLLKRTQS 2268
ò	74	73
g	2269	GEPDLLIAFLFVGRANTGTGNSDEIFIATSTSSLSEFSTVIKKLQDAQRAMEVLPLFMVP 2328
ò	74	79 11   1
g	2329	QAYIPIEGGIPLTAAGKIDRRMLRKLCEPFNRNDLISFTSKALSTSVKDAETTDTVEDRL 2388
ò	80	79

q	D 2389 ARIWEKVLGVKGVGRESDFFSSGGNSMAAIALRAEAQRSGFTLFVAD	FVADIFTNPRLADMAKL 2448
ò	80 х	64 19
qq	b 2449 FSHGQSVSPSSSTLRTKVPISSLQKRSSGLQTAAPVSNGSPVRRCQKENI	RCQKENIIDCPVAFEYE 2508
ò	80	82
Q	2509 EGPSDTQLKEASRICGISSRSIEDVFPCTPMQEALVALSLI	PGAQASYALHAAFELRPGL 2568
ò	у 83	83
qq	b 2569 DRNRFRSAWESTVKAQPILRSRIISGSNGSSVVVTSATDSIPQLDVSGLDT	provsciotfieogiova 2628
ò	y 83	98
Q	2629	VLALYTNGELPPPGPSF 2688
ò		85
Q	D 2689 KHFARNLNLVQSKLDSEDFWRKLLVKPDQESFRFPDVPVGHKPATRCTTNFHFPFSMQSK	PATRCITNFHFPFSMQSK 2748
ò	y 86y	88
g	2749 IGTTANTCINAAWAITLAQY	SHMTGPTIVTVPROVNVI 2808
ò	68 Ki	88
g	30 PESSVAEFLQDLQKSLAVVLPHQHLGLHRIQALGPIARQACDF	FSTLLVVNHGSSISWSEL 2868
ò	68 Ki	888
q	D 2869 EAADIVPVPLRSSDLYAYPMVVEVENASSDTLDIRVHSDPDCI	IEVQLLERLMEOFGHNLQ 2928
ò	68 K	88
qq	2929 TLCRAASFDPGKRIAELMDDTATTHLRTLFSWNSR	VKDSPDVAAIAVHKLLEETAQSQPA 2988
ò	68 K	88
QC	2989 ESAIVAHDGQLSYMQMDRCADVLARQIRKTNMISAQSPFV	CIHLLRSATAVVSMLAVLKA 3048
ò		16 91
qq	3049 GGAFMPVDISQPRSRLQNLIEESGAKLVLTLPESANALATLSGLTKVI	SLTKVIPVSLSELVOQIT 3108
ò	92DTDP	56
б	3109 DNTTKKDEYCKSGDTDPSSPAYLLYTSGT	SGKPKGVVMEHRAWSLGFTCHARYMGFNSCT 3168
ò	96 λζ	56
qq	3169 RILQFSSLMFDLSILEIWAVLYAGGCLFIPSDKERVNNLQDFT	TRINDINTVFLTPSIGKL 3228
ò	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	96
q	3229 LNPKDLPNISFAGFIGEPMTRSLIDAWTLPGRRLVNSYG	PTEACVLVTAREISPTAPHDK 3288
ò	96	86
QQ	3289 PSSNIGHALGANIWVVEPQRTALVPIGAVGELCIEAPSLAR	CYLANPERTEYSFPSTVLD 3348
ò	66	105
dg	DD 3349 NWQTKKGTRVYRTGDLVRYASDGTLDFLGRKDGOIKLRGORI	ELGEIEHHIRRLMSDDPR 3408
ò	ογ 106ον	105
q	Db 3409 FHEASVQLYNPATDPDRDATVDVQMREPYLAGLLVLDLVSLMRSWDSMHVLNIANT	RSWDSMHVLNIANTSENL 3468
ò	Ογ 106	105

qq	3469 QTLVTE	QTLVTELKKSLRGVLPHYMVPLHFVAVSRLPTGSSGKLDHAFVRACLRELTAPLDGNFPK 3528	è	129
ò	106	105	ò á	200 0000
g	3529 VEQVLT	VEQVLTINESVLRQWWGTVLAMDPHSIQRGDDFFSLGGSSISAMRLVGLARSSGHKLQHE 3588	3 6	
ò	106	RPDL109	∂ —	
; a		:    DIFMCPRLADMAGQISFVQEASVSPTTSPTIKFDLLDDCEVDEVIDHILPQLDMNKELIE 3648	ය (	4669 KLLR(
Š	110	109	λ 	132
à		8055 OLGET CHARACTER TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE	qq	4729 EAMS
9 (			ò	132
ò			qa	4789 EYQQ
g	3709 PSQQAI	PSQQALQVVVKHEELSWESFPSIQSFKDHFYRSLGYGKPLARLAVITQALDTKQPISHGT 3768	ò	132
ò	110		do do	4849 LLHD
අ	3769 REARTH	REARTKNSQDTVMVVVGAHHSIYDAHVLSMIWRRLYREFIGSQADGILEAETSRSEGVVP 3828	ò	135
ò	110		- අධ	4909 NHAA
g	3829 FKSYVE	FKSYVEKLLRGKONDESLLFWKEKLRGVSSSQFPPASWPRVLEHQPSATQTLITKVSLPT 3888	ò	141
ò	114 GNROVRGVT	RGVT122		AGEG DARL
qq	: : 3889 SSRKKI	:	3 2	
ò	123	122	<b>3</b>	1 0
q	3949 VPLRII	VPLRIIIDFQTVVSDFLSTLQKDIVRAAYFGQMMGLNSIAHIDNDCRDACGFKSIIVVQV 4008	<u> </u>	
ò	123	122	ò	
£ 5		PDECENHUCEBANDEOMSLESIGHEPAPLVVEVEOSESTDVLIRMAYDPVLVPEKLAHFI 4068	අ <u>ග</u>	5089 GLSA
è		122	RES	RESULT 6
3 8		SDTFTTTMSNLSAANPKAKVESIPALSEAHLAELDVTCPEWILGKAKDEKIRTESHOCLO 4128	HE	RE_HUMAN_BIRE_HUMA
è		125	PAC	09NR09; Q
8 8		RPEAPVCLLFEKSKWA	면	16-OCT-20 15-JUN-20
ò	126	125	388	BIR-domain
g	4189 UVAMIC	VVAMIGIIKAGGCFVPLDPSYPHERLEHIISETGSSVIVTSAAYSKLCLSLSVRGIVCDG 4248	S 8 6	
ò	126	125		Mammalia,
đ	4249 SVFSS1	SVFSSTKKPLPSTADSPSFSVRPNQAAYILFTSGSTGKPKGVVMEHHSVCSALIALGKR 4308	N C	
ò	126	GAC128	R R R	TISSUE=Br
qq	4309 MGLGP(	MGLGPOSRVLQFNSYWFDVMLLDIFGTLVYGGCLCIPKEEQRMSNLSGWVQKFKVNTMLL 4368		
ò	129	128	RT	
g	4369 STSVSI	STSVSRLMQPADTPSLETLCLTGEAVLQSDVDRWAPKLHLIAGYGPTETCIMSVSGELTP 4428	Z Z G	
ò	129	128	28.2	TISSUE=Br
g	4429 SSPANI	SSPANLIGKPVSCQAWVINPLKETELAPYGATGELYIQGPTVARGYLHDDVLTSKAFIVD 4488	8.8	
ò	129	128	RT	
đ	4489 PQWLT	PQWLTGYKTNENQWSRRAYKTGDLVFWGPQSNLYYVRRKDSSQVKIRGQRVELAEIEEVI 4548	RT	for
ò	129		88	++
g	4549 RQHIP	RQHIPPDVTVCVDLLSSDDQNTRIILGAVLGIGDRALGGPEDLEVIGYMDDLKSHIIPAL 4608	-	+

ò	129131
qq	4609 EASLPHHMIPEAYVPFVQLPTLGSGKLDRKTVRRVAGPLAFSLPQASARHPNQPTVTHTQ 4668
ò	132 131
QQ	4669 KLLRQLWCKILPQLDESAVNKQDNFLGIGGDSIAAIKLVALLRQHGISLAVAEIFTRPTL 4728
ò	132 131
qq	4729 EAMSSLIDEHNFVVSHAGILSDVTRNTSGVMRQTTNLIAGRHSMAVEKSRECDNSTLPCT 4788
ò	132 131
d D	4789 EYQQMFLAGTEAFTGAHSAQFIFRLPEKIDLDRLQAAFDHCADWYPNLRTQIHKDADTGR 4848
ò	132 134
d d	4849 LLHDISPIGVKVPWSCHYSDDLNTVLSHDKKFPPGLDGPLHRVTIMRHRDPTESMLVWTL 4908
ò	135 140
qq	4909 NHAAYDAWSLRMMLEHITEAYANPDYEPSYSLGWTAFVLHTENTKEASRSFWSSYLSDVK 4968
ò	141 140
д	4969 PARLMENYNLVSNPRQDRLYEARINIPKRVLSQATAATVLLAGLTLLVARVCDTRDVILA 5028
ò	141 140
đ	5029 HLLTGRTLPLAGIENCPGPTITKVPLRIPLMDQDLVTLELDSVAKKITAELMRVMPHEHS 5088
ò	141GFDL 144
qq	5089 GLSAIREFIPQAEGTTTSSGKFHAGSVLGRLPLDLVIHPKGGLDL 5133
RES	9 170
BIE	IMAN RE HUMAN
A C	NR09; Q9ULD1;
ន់ដន់	-OCT-2001 (Rel. 40,
3 8 8	peat-containing protein 6
S E	RC6 OR KIAA1289.
ဗ ဝ	omo sapiens (Human). Ikaryota; Metazoa; Chordata; Craniata; Vertebrata;
88	mmalia, Eutheria, Primates; Catarrhini, Hominidae; PRI TaxID=9606:
N C	OTENCE BROWN
2	SSUE-Brain;
X	iDLINE=ZVUIZ/59; FubMed=1044019; hen Z., Naito M., Hori S., Mashima T., Yamori T., Tsuruo T.;
ጸተ	i human IAP-family gene, apollon, expressed in numan brain ells.":
7 Z Z	Biochem. Biophys. Res. Commun. 264:847-854(1999).
2 2 C	SEQUENCE OF 3238-4829 FROM N.A.
7 X 3	MEDLINE=20039619; PubMed=10574462;
<b>\$ \$</b>	Nagase I., Isnikawa NI., Nikullo N., Nilosawa II., Komula II., Ohara O.;
RT	"Predict
R	for large proteins in vitro.";
58	-1- FUNCTION: MAY PROTECT CELLS FR
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	ò	25
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/	q	621 MNNIMSKSLHDD
Send an email to license@isb-sib.ch).	ò	30
IL; AF26555; AAF75772.1; IL; AB033115; BAA86603.1;	q	681 VFPKPGTLVQCL
~	ò	34 LN
605638; Pro; BIR.	q	741 LNKLNSALCNRR
	ò	36
nm; PF00653; BIR; 1. >Dom; PD000461; UBQ_conjugat; 1.	QC	801 KMNYATRIVTLE
.RT; SM00238; BIR; 1. .RT; SM00212; UBCc; 1.	ò	36
OSITE; PS01282; BIR_REPEAT_1; FALSE_NEG. OSITE; PS50143; BIR_REPEAT_2; 1.	QQ	861 FEREKTSDISTI
OSITE; PS00183; UBIQUITIN_CONJUGAT_1; FALSE_NEG. OSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1	ò	36
optosis; Thiol protease inhibitor; Ubl conjugation pathway; Ligase. PEAT 256 330	QQ	921 TDRLCACTKGGE
4548 4676 4597 4597	ò	48
2 8 POLY-ALA. 1632 1640 POLY-ALA.	qa	981 VDLLVDQPFTLE
4829 AA; 527604 MW; C67126A672CD3653 CRC6	ò	48
27.9%; Score 216; DB 1; Length 4829; Similarity 2.0%; Pred. No. 29;	q	1041 DAAQHTRTWKLC
85; Conservative 29; Mismatches 33; Indels 4105; Gaps	ò	57
AAGGILH	qq	1101 APGLGKVNALNI
AAGVSEWLVLRDGCMHCDADGLHSLSYHPALNAILAVTSRGTIKVIDGTSGATLQASALS	ò	57
	ą	1161 ASGLDLSGHAGN
AKPGGQVKCQY1SAVDKV1FVDDYAVGCRKDLNG1LLLDTALQTPVSKQDDVVQLELPVT	ò	64
	q	1221 LKHQSNKGYSL
EAQQLLSACLEKVDISSTEGYDLFITQLKDGLKNTSHETAANHKVAKWATVTFHLPHHVL	ò	64
	QQ	1281 TSISKERVQRC
KSIASAIVNELKKINQNVAALPVASSVMDRLSYLLPSARPELGVGPGRSVDRSLMYSEAN	ò	64
	QQ	1341 SSKEGNENLLS
	ò	64
20	qq	1401 LKALLDNMSFL
21 ERHSPNCPFVKGEHTQNVPLSVTLATSPAQFPCTDGTDRISCFGSGSCPHFLAAATKRGK 380	ò	64
20	qq	1461 EALLOTRYGUY
81 ICIWDVSKLMKVHLKFEINAYDPAIVQQLILSGDPSSGVDSRRPTLAWLEDSSSCSDIPK 440	ò	64 EG
20	qq	 1521 AAEGSFTSLTG
41 LEGDSDDLLEDSDSEEHSRSDSVTGHTSQKEAMEVSLDITALSILQQPEKLQWEIVANVL 500	ò	99
20 24 :	q	1581 LSSAAQVALQS
	Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Cont	### ### ### ### ### ### ### ### ### ##

q	501 EDTVKDLEELGANPCLTNSKSEKTKEKHQEQHNIPPPCLLAGGLLTYKSPATSPISSNSH	095 н
ò	., 25	24
qq	561 RSLDGLSRTQGESISEQGSTDNESCTNSELNSPLVRRTLPVLLLYSIKESDEKAGKIFSO	30 620
ò	25	29
g	621 MNNIMSKSLHDDGFTVPQIIEMELDSQEQLLLQDPPVTYIQQFADAAANLTSPDSEKWNS	VS 680
ò	30	VLTN 33
q	691 VFPKPGTLVQCLRLPKFABEENLCIDSITPCADGIHLLVGLRTCPVESLSAINQVEALNN	NN 740
ò	) 34 LN	35
q	141 LNKLNSALCNRRKGELESNLAVVNGANISVIQHESPADVQTPLIIQPEQRNVSGGYLVLY	LY 800
ò		35
g	3 801 KANYATRIVTLEEEPIKIQHIKDPQDTITSLILLPPDILDNREDDCEEPIEDMQLTSKNG	VG 860
ò		35
QQ	) 861 FEREKTSDISTLGHLVITTQGGYVKILDLSNFEILAKVEPPKKEGTEEQDTFVSVIYCSG	SG 920
ò	36AELLRDPSLG	47
q	o 921 TDRLCACTKGGELHFLQİĞGTCDDIDEADILVDGSLSKGIEPSSEGSKPLSNPSSPGISG	SG 980
ò		47
q	> 981 VDLLVDQPFTLEILTSLVELTRFETLTPRFSATVPPCWVEVQQEQQQRRHPQHLHQQHHG	HG 1040
ò	48	56
q	1041 DAAQHTRTWKLQTDSNSWDEHVFELVLPKACMVGHVDFKFVLNSNITNIPQIQVTLLKNK	NK 1100
ò	57	95
g	o 1101 APGLGKVNALNIEVEQNGKPSLVDLNEEMQHMDVEESQCLRLCPFLEDHKEDILCGPVML	WL 1160
ò	57	63
q	5 1161 ASGLDLSGHAGMLTLTSPKLVKGMAGGKYRSFLIHVKAVNERGTEEICNGGMRPVVRLP	PS 1220
ò	٨ و4	63
q	b 1221 LKHQSNKGYSLASLLAKVAAGKEKSSNVKNENTSGTRKSENLRGCDLLQEVSVTIRRFKK	
ò	64	63
g	b 1281 TSISKERVQRCAMLQFSEFHEKLLNTLCRKTDDGQITEHAQSLVLDTLCWLAGVHSNGPG	PG 1340
ò	λ 64	63
<del>Q</del>	b 1341 SSKEGNENLLSKTRKFLSDIVRVCFFEAGRSIAHKCARFLALCISNGKCDPCOPAFGPVL	VL 1400
ò	λ	63
g	D 1401 LKALLDNMSFLPAATTGGSVYWYFVLLNYVKDEDLAGCSTACASLLTAVSRQLQDRLTPM	PM 1460
ò	γ 64	63
q	b 1461 EALLQTRYGLYSSPFDPVLFDLEMSGSSCKKVYNSSIGVQSDEIDLSDVLSGNGKVSSCT	CT 1520
ò	у 64 БС	65
qq	b 1521 AAEGSFTSLTGLLEVEPLHFTCVSTSDGTRIERDDAMSSFGVTPAVGGLSSGTVGEASTA	TA 1580
ò	λ	65
q	b 1581 LSSAAQVALQSLSHAMASAEQQLQVLQEKQQQLLKLQQQKAKLEAKLHQTTAAAAAASA	ISA 1640

ò	99		65
qq	1641	VGPVHNSVPSNPVAAPGFFIHPSDVIPPTPKTTPLFMTPPLTPPNEAVSVVINAELAQLF	1700
ò	99	APNITAN	72
qq	1701	PGSVIDPPAVNLAAHNKNSNKSRMNPLGSGLALAISHASHFLQPPPHQSIIIERMHSGAR	1760
ò	73		82
g	1761	RFVTLDFGRPILLTDVLIPTCGDLASLSIDIWTLGEEVDGRRLVVATDISTHSLILHDLI	1820
ò	83	3.	83
q	1821	PPPVCRFWKITVIGRYGSTNARAKIPLGFYYGHTYILPWESELKLMHDPLKGEGESANQP	1880
ઠે	84		83
8	1881	EIDQHLAMMVALQEDIQCRYNLACHRLETLLQSIDLPPLNSANNAQYFLRKPDKAVEEDS	1940
ò	84	SQTINPED	91
8	1941	RVFSAYQDCIQLQLQLALAHNAVQRLKVALGASRKMLSETSNPEDLIQTSSTEQLRTIIR	2000
ò	92		91
d G	2001	YLLDTLLSLLHASNGHSVPAVLQSTFHAQACEELFKHLCISGTPKIRLHTGLLLVQLCGG	2060
ò	92		91
g G	2061	ERWWGOFLSNVLQELYNSEQLLIFPQDRVFMLLSCIGQRSLSNSGVLESLLNLLDNLLSP	2120
ò	92		91
g	2121	LQPQLPMHRRTEGVLDIPMISWVWLVSRLLDYVATVEDEAAAAKKPLNGNQWSFINNNL	2180
ò	93		91
qq	2181	HTQSLNRSSKGSSSLDRLYSRKIRKQLVHHKQQLNLLKAKQKALVEQMEKEKIQSNKGSS	2240
ò	95	OTO	94
a	2241	YKLLVEQAKLKQATSKHFKDLIRLRRTAEWSRSNLDTEVTTAKESPEIEPLPFTLAHERC	2300
ò	95	PGHADLVLYITR	106
පු	2301	ISVVQKLVLFLLSMDFTCHADLLLFVCKVLARIANATRPTIHLCEIVNEPQLERLLLLLV	2360
ò	107		106
g	2361	GTDFNRGDISWGGAWAQYSLTCMLQDILAGELLAPVAAEAMEEGTVGDDVGATAGDSDDS	2420
ò	107		106
g	2421	LQQSSVQLLETIDEPLTHDITGAPPLSSLEKDKEIDLELLQDLMEVDIDPLDIDLEKDPL	2480
ò	107		106
සු	2481	AAKVFKPISSTWYDYWGADYGTYNYNPYIGGLGIPVAKPPANTEKNGSQTVSVSVSQALD	2540
ò	107		106
g	2541	arlevgleqqaelmlkmmstleadsilqaltntsptlsqsptgtddsllgglqaanqtsq	2600
ò	107		106
g	2601	LIIQLSSVPMLNVCFNKLFSMLQVHHVQLESLLQLWLTLSLNSSSSGNKENGADIFLYNA	2660
ò	107		106
g	2661	NRI PVISLNQASITSFLTVLAWYPNTLLRTWCLVLHSLTLMTNMQLNSGSSSAIGTQEST	2720

ò	107	106
QQ	2721	AHLLVSDPNLIHVLVKFLSGTSPHGTNQHSPQVGPTATQAMQEFLTRLQVHLSSTCPQIF 278
ò	107	106
g	2781	SEFLLKLIHILSTERGAFOTGQGPLDAQVKLLEFTLEQNFEVVSVSTISAVIESVTFLVH 284(
ò	107	109
QQ	2841	HYITCSDKVMSRSGSDSSVGARACFGGLFANLIRPGDAKAVCGEMTRDQLMFDLLKLVNI 2900
ò	110	5LP
Ωp	2901	LVQLPLSGNREYSARVSVTTNTTDSVSDEEKVSGGKÖGNGSSTSVQGSPAYVADLVLANQ 2960
ò	116	115
q	2961	QIMSQILSALGLCNSSAMAMIIGASGLHLTKHENFHGGLDAISVGDGLFTILTTLSKKAS 3020
ò	116	115
qq	3021	TVHMMLQPILTYMACGYMGRQGSLATCQLSEPLLWFILRVLDTSDALKAFHDMGGVQLIC 3080
ò	116	115
QQ	3081	NNMVTSTRAIVNTARSMVSTIMKFLDSGPNKAVDSTLKTRILASEPDNAEGIHNFAPLGT 3140
ò	116	119
QQ	3141	ITSSSPTAQPAEVLLQATPPHRRARSAAWSYIFLPEEAWCDLTIHLPAAVLLKEIHIQPH 3200
ò	120	119
QQ	3201	LASLATCPSSVSVEVSADGVNMLPLSTPVVTSGLTYIKIQLVKAEVASAVCLRLHRPRDA 3260
ò	120	119
qq	3261	STLGLSQIKLLGLTAFGTTSSATVNNPFLPSEDQVSKTSIGWLRLLHHCLTHISDLEGMM 332C
ò	120	119
q	3321	ASAAAPTANLLQTCAALLMSPYCGMHSPNIEVVLVKIGLQSTRIGLKLIDILLRNCAASG 338C
ò	120	123
q	3381	SDPTDLNSPLLFGRLNGLSSDSTIDILYQLGTTQDPGTKDRIQALLKWVSDSARVAAMKR 3440
ò	124	123
qq	3441	SGRMNYMCPNSSTVEYGLLMPSPSHLHCVAAILWHSYELLVEYDLPALLDQELFELLFNW 3500
ò	124	123
qq	3501	SMSLPCNMVLKKAVDSLLCSMCHVHPNYFSLLMGWMGITPPPVQCHHRLSMTDDSKKQDL 3560
ò	124	123
g	3561	SSSLTDDSKNAQAPLALTESHLATLASSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHIS 3620
ò	124	L. C. C. C. C. C. C. C. C. C. C. C. C. C.
Q	3621	SSESIAQSIDISQDKLRRHHVPQQCNKMPITADLVAPILRFLTEVGNSHIMKDWLGGSEV 3680
ò	129	SPTWSCL135
Q C	3681	NPLMTALLFLLCHSGSTSGSHNLGAQQTSARSASLSSAATTGLTTQORTAIENATVAFFL 3740
ò	136	135
g	3741	QCISCHPNNQKLMAQVLCELFQTSPQRGNLPTSGNISGFIRRLFLQLMLEDEKVTMFLQS 3800
ò	136	135

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MIM, 604269; EMT2.

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InterPro; IPR00126; Cadharin.

InterPro; IPR00126; Cadharin.

InterPro; IPR001791; Laminin G.

Pfam; PF00028; Cadharin; 33.

Pfam; PF00028; CADHERIN.

SMART; SM00112; CA, 32.

SMART; SM00181; EGF; 2.

PROSITE; PS00223; CADHERIN.

PROSITE; PS00223; CADHERIN 1; 14.

PROSITE; PS00225; Laminin 1, 14.

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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                       3801 PCPLYKGRINATSHVIQHPMYGAGHKFRTLHLPVSTTLSDVLDRVSDTPSITAKLISEQK 3860
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MEDLINE=99360089; PubMed=9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
Tidentification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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09NYO8; 075091; 09NSR7;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin Fat 2 precursor (hFat2) (Multiple epidermal growth factor-like domains 1).
FAT2 OR MEGF1 OR CDHF8.
Homo sapiens (Human)
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Wu Q., Maniatis T.;
"Large exons encoding multiple ectodomains are a characteristic feature of protocoalherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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q	612 LNHFSGVIS	SLKRPFINLTAGQPTSYSLKITASDGKNYASPTTLNITVVKDPHFEVPVTCD 671
ò	19	FQAH22
qq	672 KTGVLTQFT	OFTKTILHFIGLONGESSDEEFTSLSTYQINHYTPQFEDHFPOSIDVLESVPIN 731
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qq	732 TPLARLAATI	PLARLAATDPDAGFNGKLVYVIADGNEEGCFDIELETGLLTVAAPLDYEATNFYILNVT 791
ò	23	27
q	792 VYDLGTPQK	VYDLGTPQKSSWKLLTVNVKDWNDNAPRFPPGGYQLTISEDTEVGTTIAELTTKDADSED 851
ò	28	27
q	852 NGRVRYTLL	NGRVRYTLLSPTEKFSLHPLTGELVVTGHLDRESEPRYILKVEARDOPSKGHQLFSVTDL 911
ò	28	31
임	912 IITLEDVNDNSPQCI	NSPQCITEHNRLKVPEDLPPGTVLTFLDASDPDLGPAGEVRYVLMDGAHGT 971
ò	32	31
g G	972 FRVDLMTGALI	LILERELDFERRAGYNLSLWASDGGRPLARRTLCHVEVIVLDVNENLHPPH 1031
ò	32	31
<b>අ</b>	1032 FASFVHQGQ	VHQGQVQENSPSGTQVIVVAAQDDDSGLDGELQYFLRAGTGLAAFSINQDTGMIQT 1091
ò	32	31
đ	1092 LAPLDREFA	SYYWLTVLAVDRGSVPLSSVTEVYIEVTDANDNPPQMSQAVFYPSIQEDAP 1151
ò	32	31
đ	1152 VGTSVLQLD	QLDAWDPDSSSKGKLTFNITSGNYMGFFMIHPVTGLLSTAQQLDRENKDEHILE 1211
ò	32	31
g	1212 VTVLDNGEP	SEKSTSRVVVGILDVNDNPPIFSHKLFNVRLPERLSPVSPGPVYRLVASDL 1271
ò	32	31
g	1272 DEGLNGRVT	YSIEDSYEEAFSIDLVTGVVSSNSTFTAGEYNILTIKATDSGQPPLSASVR 1331
ò	32	31
ପ୍ଧ	1332 LHIEWIPWP	RPSSIPLAFDETYYSFTVMETDPVNHMVGVISVEGRPGLFWFNISGGDKDM 1391
ò	32	3636
q	1392 DFDIEKTTG	:   :  SIVIARPLDTRRRSNYNLTVEVTDGSRTIATQVHIFMIANINHHRPQFLET 1451
ò	37	GAELLR
q	1452 RYEVRVPQDT	  TVPGVELLRVQAIDQDKGKSLIYTIHGSQDPGSASLFQLDPSSGVLVTVGK 1511
ò	43	42
q	1512 LDLGSGPSQ	LDLGSGPSQHTLTVMVRDQEIPIKRNFVMVTIHVEDGNLHPPRFTQLHYEASVPDTIAPG 1571
Š	43	42

qq	1572 TEL	TELLQVRAMDADRGVNAEVHYSLLKGNSEGFFNINALLGIITLAQKLDQANHAPHTLTVK 1631
ò	43	42
g	1632 AED(	AEDQGSPQWHDLATVIIHVYPSDRSAPIFSKSEYFVEIPESIPVGSPILLVSAMSPSEVT 1691
ò	43	42
g	1692 YEL	YELREGNKDGVFSMNSYSGLISTQKKLDHEKISSYQLKIRGSNNAGAFTDVMVVVDIIDE 1751
ò	43	42
g	1752 NDN	NDNAPMFLKSTFVGQISEAAPLYSMIMDKNNNPFVIHASDSDKEANSLLVYKILEPEALK 1811
ò	43	-DPSLG
qq	1812 FFK	FFKIDPSMGTLTIVSEMDYESMPSFQFCVYVHDQGSPVLFAPRPAQVIIHVRDVNDSPPR 1871
ò	54	53
a	1872 FSE	FSEQIYEVAIVGPIHPGMELLMVRASDEDSEVNYSIKTGNADEAVTIHPVTGSISVLNPA 1931
ò	54	09 -JIN
g	1932 FLG	FLGLSRKLTIRASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILG 1991
ò	61	09
QQ	1992 AQG	AQGNHLNDTLSYFLLNGTDMFHMVQSAGVLQTRGVAFDREQQDTHELAVEVRDNRTPQRV 2051
ò	61	TEP
qq	2052 AQG	AQGLVRVSIEDVNDNPPKFKHLPYYTIIQDGTEPGDVLFQVSATDEDLGTNGAVTYEFAE 2111
ò	64	63
g	2112 DYT	DYTYFRIDPYLGDISLKKPFDYQALNKYHLKVIARDGGTPSLQSEEEVLVTVRNKSNPLF 2171
ò	64	63
g	2172 OSP	QSPYYKVRVPENITLYTPILHTQARSPEGLRLIYNIVEEEPLMLFTTDFKTGVLTVTGPL 2231
ò	64	67
g	2232 DYE	DYESKTKHVFTVRATDTALGSFSEATVEVLVEDVNDNPPTFSQLVYTTSISEGLPAQTPV 2291
ò	89	
qq	2292 IQL	IQLLASDQDSGRNRDVSYQIVEDGSDVSKFFQINGSTGEMSTVQELDYEAQQHFHVKVRA 2351
ò	89	
q	2352 MDK	:
ò	84	83
Q	2410 DTS	DTSRLEYLILSGNQDRHFFINSSGIISMFNLCKKHLDSSYNLRVGASDGVFRATVPVYI 2469
ò	84	83
g	2470 NTT	NTTNANKYSPEFQQHLYEAELAENAMVGTKVIDLLAIDKDSGPYGTIDYTIINKLASEKF 2529
ò	94	83
QQ	2530 SIN	SINPNGQIATLQKLDRENSTERVIAIKVMARDGGGRVAFCTVKIILTDENDNPPQFKASE 2589
ò	84	SQTINPED91
g	2590 YTV	YTVSIQSNVSKDSPVIQVLAYDADEGQNADVTYSVNPEDLVKDVIEINPVTGVVKVKDSL 2649
ò	92	

2710 IGIVKAVAAQDPVIYSLVRGTTPESNKDGVFSLDPDTGVIKVRKPMDHESTKLYQIDVWA 2769 2770 HCLQNTDVVSLVSVNIQVGDVNDNRPVFEADPYKAVLTENMPVGTSVIQVTAIDKDTGRD 2829 2830 GQVSYRLSADPGSNVHELFAIDSESGWITTLQELDCETCQTYHFHVVAYDHGQTIQLSSQ 2889 2890 ALVQVSITDENDNAPRFASEEYRGSVVENSEPGELVATLKTLDADISEQNRQVTCYITEG 2949 2950 DPLGQFGISQVGDEWRISSRKTLDREHTAKYLLRVTASDGKFQASVTVEIFVLDVNDNSP 3009 3010 QCSQLLYTGKVHEDVFPGHFILKVSATDLDTDTNAQITYSLHGPGAHEFKLDPHTGELTT 3069 3070 LTALDRERKDVFNLVAKATDGGGRSCQADITLHVEDVNDNAPRFFPSHCAVAVFDNTTVK 3129 3130 TPVAVVFARDPDGGANAQVVYSLPDSAEGHFSIDATTGVIRLEKPLQVRPQAPLELTVRA 3189 3190 SDLGTPIPLSTLGTVTVSVVGLEDYLPVFLNTEHSVQVÞEDAPPGTEVLQLATLTRPGAE 3249 3250 KTGYRVVSGNEQGRFRLDARTGILYVNASLDFETSPKYFLSIECSRKSSSSLSDVTTVMV 3309 3310 NITDVNEHRPQFPQDPYSTRVLENALVGDVILTVSATDEDGPLNSDITYSLIGGNQLGHF 3369 3370 TIHPKKGELQVAKALDREQASSYSLKLRATDSGQPPLHEDTDIAIQVADVNDNPRRFFQL 3429 3430 NYSTTVQENSPIGSKVLQLILSDPDSPENGPPYSFRITKGNNGSAFRVTPDGWLVTAEGL 3489 3490 SRRAQEWYQLQIQASDSGIPPLSSLTSVRVHVTEQSHYAPSALPLEIFITVGEDEFQGGM 3549 3550 VGKIHATDRDPQDTLTYSLAEEETLGRHFSVGAPDGKIIAAQGLPRGHYSFNVTVSDGTF 3609 3610 TTTAGVHVYVWHVGQEALQQAMWMGFYQLTPEELVSDHWRNLQRFLSHKLDIKRANIHLA 3669 3670 SLQPAEAVAGVDVLLVFEGHSGTFYEFQELASIITHSAKEMEHSVGVOMRSAMPMVPCQG 3729 3730 PTCQGQICHNTVHLDPKVGPTYSTARLSILTPRHHLQRSCSCNGTATRFSGQSYVRYRAP 3789 2650 VGLENOTLDFFIKAQDGGPPHWNSLVPVRLQVVPKKVSLPKFSEPLYTFSAPEDLPEGSE 2709 114 -----GNRQVR------ 119 120 ------119 120 ------119 92 -----92 ------DTDPGH------DTDPGH-------92 105 120 -----92 -----105 120 5 8 5 2 8 ရ 6 6 6 ရ g S 8 2 8 දු ද 2 8 2 8 2 8 2 ò à 8

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                           3790 AARNWHIHFYLKTLQPQAILLFTNETASVSLKLASGVPQLEYHCLGGFYGNLSSQRHVND 3849
                                                                  3850 HEWHSILVEEMDASIRLMVDSMGNTSLVVPENCRGLRPERHLLLGGLILLHSSSNVSQGF 3909
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                                                                                                                                                                                                                                                                                                                                                  4268 LNEYTAISYYHSQFRQGGGGPCLADGGYKGVGMRLSRAGPSYAVCEVEGAPLAGQGQPRV 4327
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor) (RyRl)
(RYR-1) (Skeletal muscle calcium release channel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Norwegian Landrace; TISSUE=Skeletal muscle;
MEDLINE=93036501; PubMed=1329581;
Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.;
"DNA sequence of the skeletal muscle calcium release channel cDNA and
verification of the Arg615-->Cy8615 mutation, associated with porcine
malignant hyperthermia, in Norwegian landrace pigs.";
Anim. Genet. 23:395-402(1992).
                                                                                     ------ 133
                                                                                                         3910 EGCLDAVVVNEEALDLLAPGKTVAGLLETQALTQCCLHSDYCSQNTCLNGGKCS--WTHG
                                                                                                                                                                                                                                                                     4148 LPPAAVPSHSDNEPVIKRTWSSEEMVYPGGAMVWPPTYSRNERWEYPHSEVTQGPLPPSA
                                                                                                                                              3968 AGYVCKCPPQFSGKHCEQGRENCTFAPCLEGGTCILSPKGASCNCPHPYTGDRCEMEARG
                                                                                                                                                                    134 -----CLIT------
                                                                                                                                                                                      4028 CSEGHCLVTPEIQRGDWGQQELLIITVAVAFIIISTVGLLFYCRRCKSHKPVAMEDPDLL
                                                                                                                                                                                                          138
                                                                                                                                                                                                                              1088 ARSVGVDTQAMPAIELNPLSASSCNNLNQPEPSKASVPNELVTFGPNSKQRPVVCSVPPR
                                                                                                                                                                                                                                                                                                                               EDTGF------
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brenig B.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          5035 AA
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STRAIN=German Landrace; TISSUE=Liver;
MEDLINE=94117003; PubMed=8288238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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ID RYR1_PIG
AC P16960;
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DEPOLARIZATION OF T-TUBULES.

--- SUBBUNT: HOWOTETRAMER (POTENTIAL).

--- MISCELLANEOUS: The calcium release channel is modulated by calcium ions, magnesium ions, ATP and calmodulin.

--- MISCELLANEOUS: The calcium release channel activity resides in the C-terminal region while the remaining part of the protein constitutes the 'foot' structure againing the junctional gap between the SR and the T-tubule. It is possible that the foot structure interacts with the cytoplasmic region of the dihydropyridine receptor.

--- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Calminatory and interional SR and modulates its activity.

--- SIMILARITY: CONTAINS 3 SPRY DOWAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       SEQUENCE OF 4785-5015 FROM N.A.
MEDLINE=91065640; PubMed=2174405;
Harbitz I., Chowdhary B., Thomeen P.D., Davies W., Kaufman U.,
Kran S., Gatsvisson I., Christensen K., Hauge J.G.;
"Assignment of the porcine calcium release channel gene, a candidate
for the malignant hyperthermia locus, to the 6p11-->q21 segment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Transmembrane; Ionic channel; Calcium channel; Repeat; Phosphorylation; Glycoprotein.
Leeb T., Schmolzl S., Brem G., Brenig B.; "Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) gene coding region 4624 to 7929."; Genomics 18:349-354(1993).
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M. (POTENTIAL).

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EMBL; X68247; CAA46318.1; --
EMBL; X68465; CAA46325.1; --
EMBL; M32501; AA431022.1; --
PIN, A37105; A37105.
InterPro; IPR000699; Ca-rel_channel.
InterPro; IPR001682; Ca-rel_channel.
InterPro; IPR001682; Ca-rel_channel.
InterPro; IPR001682; Ca-rel_channel.
InterPro; IPR0018215; Ryanodn_receptor.
InterPro; IPR001312; Ryanodn_receptor.
InterPro; IPR001312; Ryanodn_receptor.
InterPro; IPR001313; Ryanodn_receptor.
InterPro; IPR001313; Ryanodn_receptor.
Pfam; PF001625; SPRY; 3.
Pfam; PF001625; RYDR_ITPR; 2.
Pfam; PF001625; RYDR_ITPR; 2.
Pfam; PF02815; MIR; 4.
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SMART; SM00449; SPRY; 3
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82	7	77	ò
1995	6 VKLQMCNLLEYFCDQELQHRVESLAAFAERYVDKLQANQRDRYGILMKAFTMTAAETARR	1936	đ
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1935	6 EBEBEBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB	1876	qq
92		77	ò
1875	6 LGEAVRDGGQHARDPVGGSVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEE	1816	q
92		77	ò
1815	:   :   6 NGPRRHGLPGVGTTSLRPPHHFSAPCFVAALPAVGAAEAPARLSPSIPLEALRDKALRM	1756	đ
91	3LTSS	73	ò
1755	6 HALEDAHLPGPLRAGYYDLLISIHLESACRSRRSMLSEYIVPLTPETRAITLFPPGKRTE	1696	q
72		73	ò
1695	S MMALHIPEENRCMDILELSERLDLQQFHSHTLRLYRAVCALGNNRVAHALCSHVDQAQLL	1636	đ
72		.73	ò
1635	S SAAMFLSERKNPAPQCPPRLEMQMLMPVSWSRMPNHFLRVETRRAGERLGWAVQCOEPLT	1576	a
72		73	ò
1575		1516	쉱
72	0	70	ò
1515	5 DYHQHDMNFDLTKVRAVTVTMGDEQGNIHSSLKCSNCYMVWGGDFVSPGQQGRISHTDLV	1456	qq
69		70	ò
1455	AAM	1396	g
69	/ WVILTEPEGAPNI	57	ò
1395	RRSAGRWGEAEGGKEGTAKEGAPGGTAQAGVEAQPPRAENEKDATTEKNKKRGFLFKAKK	1336	සු
95	XA	55	ò
1335	; TWGSQNSLVEMLFLRLSLPVQFHQHFRCTAGATPLAPPGLQPPAEDEARAAEFDPDYENL	1276	a
54	SSLGAQFRVHL	45	ò
1275	: ICGLQEGFEPFAINMQRPVTTWFSKSLPQFEAVPLEHPHYEVSRVDGTVDTPPCLRLTHR	1216	Q
4 4		45	ò
1215	; TENTIIFTLNGEVLMSDSGSETAFRDIEVGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFA	1156	a a

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Q	2236	FLCYFCRISRQNQRSMFDHLSYLLENSGIGLGMQGSTPLDVAAASVIDNNELALALQEQD	2295
ò	94		93
요	2296	LEKVVSYLAGCGLQSCPMLLAKGYPDIGWNPCGGERYLDFLRFAVFVNGESVEENANVVV	2355
ò	94	- dQ-	95
g	2356	RLLIRKPECFGPALRGEGGSGLLATIEEAIRISEDPARDGPGVRRDRRREHFGEEPPEEN	2415
ò	96	GHA	101
g	2416	RVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKGEALRIRAILRSLVPLDDLVGIISLPL	2475
ò	102		101
a	2476	QI PTLGKDGALVQPKMSASFVPDHKASMVLFLDRVYGIENQDFLLHVLDVGFLPDMRAAA	2535
ò	102		101
a	2536	SLDTATFSTTEMALALNRYLCLAVLPL1TKCAPLFAGTEHRAIMVDSMLHTVYRLSRGRS	2595
ઠે	102		101
윱	2596	LTKAQRDVIEECLMALCRYIRPSMLQHLLRRLVFDVPILNEFAKMPLKLLTNHYERCWKY	2655
ò	102	DYTTRPDLELPDLEL	113
g G	2656	YCLPTGWANFGVTSEEELHLTRKLFWGIFDSLAHKKYDPELYRMAMPCLCAIAGALPPDY	2715
ò	114		115
සු	2716	VDASYSSKAEKKATVDAEGNFDPRPVETLNVIIPEKLDSFINKFAEYTHEKWAFDKIQNN	2775
ò	116		
g G	2776	WSYGENIDEELKTHPMLRPYKTFSEKDKEIYRWPIKESLKAMIAWEWTIEKAREGEEEKT	
ò	116		115
g	2836	EKKKTRKISQSAQTYDAREGYNPQPPDLSGVTLSRELQAMAEQLAENYHNTWGRKKKQEL	2895
ò	116		115
g	2896	EAKGGGTHPLLVPYDTLTAKEKARDREKAQELLKFLQMNGYAVTRGLKDMELDTSSIEKR	2955
ò	116		115
qq	2956	FAFGFLQQLLRWMDISQEFIAHLEAVVSSGRVEKSPHEQEIKFFAKILLPLINQYFTNHC	3015
ò	116		115
q	3016	LYFLSTPAKVLGSGGHASNKEKEMITSLFCKLAALVRHRVSLFGTDAPAVVNCLHILARS	3075
ò	116		123
g	3076	LDARTVMKSGPEIVKAGLRSFFESASEDIEKMVENLRLGKVSQARTÖVKGVGÖNLTYTTV	3135
ò	124		123
g	3136	ALLPVLTTLFQHIAQHQFGDDVILDDVQVSCYRTLCSIYSLGTTRNPYVEKLRPALGECL	3195
ò	124		125
g	3196	ARLAAAMPVAFLEPQLNEYNACSVYTTKSPRERAILGLPNSVEEMCPDIPVLERLMADIG	3255
ò	126	9	126
g	3256	i GLAESGARYTEMPHVIEITLPMLCSYLPRWWERGPEAPPPALPAGAPPPCTAVTSDHLNS	3315
ò	127		126
g	3316	LLGNILRIIVNNLGIDEASWMKRLAVFAQPIVSRARPELLHSHFIPTIGRLRKRAGKVVA	3375

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                                                                                                                                                                                                                                                                                 3496 GDRYSVQTSLIVATLKKMLPIGLNMCAPTDQELITLAKTRYALKDTDEEVREFLQNNLHL 3555
                                                                                                                                                                                                                                                                                                                                                                                                   3556 QGKVEGSPSLRWQMALYRGLPGREEDADDPEKIVRRVQEVSAVLYHLEQMEHPYKSKKAV 3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3676 AGEQEEEEEEVEEKKPDPLHQLVLHFSRTALTEKSKLDEDYLYMAYADIMAKSCHLEEGG 3735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3736 ENGEAQEEVEVSFEEKEMEKQRLLYQQARLHNRGAAEMVLQMISACKGETGAMVSSTLKÜ 3795
                                                 3376 EEEQLRLEAKAEAEEGGELLVRDEFSVLCRDLYALYPLLIRYVDNNRAHWLTEPNPSAEEL 3435
                                                                                                                                                                  3436 FRAVGEIFIYWSKSHNFKREEQNFVVQNEINNMSFLTADNKSKMAKSGGSDQERTKKKRL 3495
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadharin Fat 2 precursor (Multiple epidermal growth factor-like domains 1).
FAT2 OR MEGF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=98360089; PubMed=963030;
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InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
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HSSP; P08709; 1BF9.
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GOATTIVIIDIVDCNNHAPVFNRSSYEGTLDENIPPGTSVLTVTATDQDHGDNGHITYSI 497
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                                                                                                                                                                                                                                                                                                                                                                        558 NDNQPMFEEVNCTVSLRQDVPVGKSIMAVSAIDMDELQNLKYEIVSGNEQDYFHLNHFSG 617
                                                                                                                                                                   AAGVFKTEEHVVGNFCFLRIRTKSSNTALLNREVRDSYTLIVQASDKSLEFEALTQVVVH 137
                                                                                                                                                                                            138 ILDQNDLKPLFSPPSYRVTISEDRPLKSPICKVTATDADLGQNAEFYYAFNARSEVFAIH 197
                                                                                                                                                                                                                     198 PTSGVVTVAGKLNVTRRGKYELQVLAVDRMRKISEGNGFGNLASLVIRVEPVHRKPPAIN 257
                                                                                                                                                                                                                                             258 LVVLNPPEGDEGDIYAIVTVDTNGSGAEVDSLEVVGGDPGKYFKVLRSYAQGNEFNLVAV 317
                                                                                                                                                                                                                                                                     RDINWAEHPHGFNISLQTHSWSRFPPHSIIRAFHLPSWKLANLRFEKAVYRVKLSEFSPP 377
                                                                                                                                                                                                                                                                                              378 GSRVALVKVTTALPNLRYSLKPSSRNTAFKLNARTGLITTTKLVDFHEQNQYQLHVKTSL 437
                                                                                                                                                                                                                                                          618 VISLKRSFMNLTAVRPTIYSLKITASDGKNYASPTTLKVTVVKDPHSEVPVQCDKTĠVĹT
                                                                                                                                                                                                                                                                                                                                                                                                                         678 HITKTILQSAGLQSQELGEBEFTSLSNYQINHHSPQFEDHFPQSIDILEQVPINTPLARL
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35; Mismatches 35; Indels 4077;
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Gaps

à	7 -		9
ą	798 P	PPKSSWKLLTVTVKDWNDNPPRFPPGGYQLTISEDTEVGTTIAELKTEDADSEDNRRVRY	857
à	- 1		9
ą	858 T	TLLTPTEKFSLHPFTGELVVTGHLDRESESQYILKAARARDQPTKGHQLFSVTDLIVTLED	917
à			9
ą	918 I	INDNPPQCITEHRRLKVPEDMPLGTVLTFLDASDPDLGPAGEVKYILVEDAHGTFQVHPM	716
ጵ	7 -	NTITH.	12
ą	978 T	TGALSLEKELDFERRAGYNLSFWASDSGKPLSRRTLCHVEVLVMDVNENLHSPHFSSFVY	1037
à	13 -	AVGPDVFQAHQE	24
ą	1038 Q	QGQVQENSPAGTPVMVVTAQDDDSGLDGELQYFLRAGTGLETFSINQDTGMLETLAPLDR	1097
ል	25 -		24
g	1098 E	EFTPYYWLTVLAVDRGSVPLSAVTEVYI EVTDINDNI PSMSRPVFYPSVLEDAPLGTSVL	1157
ጵ	25 -		24
ရ	1158 Q	<b>QLEAMDPDSSSSQCKLTFNLTSGNHLGHFIVHPFTGLLTTAKQLDRENKDEYVLEVTVQDN</b>	1217
ጵ	25 -		24
ą	1218 G	GDPSLRSTSRVVVCILDVNDNPPMFSHKLFNVRLSERLSPLSPEPVYRLVASDPDEGLNG	1277
à	25 -		24
ą	1278 S	SVTYSIEESDEESFRIDPVTGVVSSSSTFAAGEYNILTIKATDSGQPALSTSVRLHIEWI	1337
ጵ	25 -		24
a	1338 P	PQPRPSSIPLSFDESYYSFTVMETDPVNHMVGVISVEGRPGLFWFHISDGDKDMDFDIEK	1397
ጵ	25 -	YVLTNLN	35
g	1398 T	TTGSIVIARPLDTRRKSSYNLTVEVTDGPHTIATQVHIFMIANINHHRPQFLQDHYEIRV	1457
à	36 -	IGABLILR	42
ą	1458 P	 PQDTLPGVELLRVQATDQDHGKGLIYTILSSQDPGSANLFQLDPSSGVLVTVGTLELHSG	1517
ጵ	43 -		42
ą	1518 P	PSQHILTVMVRDQEMPIKRNFVWVTIHVEDGNLHSPHFTQLRYEANVPDTTAPGTELLQV	1577
à	43 -		42
g	1578 R	RAVDADRGANAEIHYSFLKGNSDGFFNIDSLLGIITVAORLYHVHLTRHALTVKAEDOGS	1637
à	43 -		42
g	1638 P	PRRHDLALVVIHVHPSDSSAPVFSKDEYFIEIPESVPIGSPILLLSAGSSSEVTYELREG	
à	43 -		42
g	1698 N	NKDSVFSMNSYSGLISTQKRLDHEKVPSYRLRIRGSNMAGVFTEVVALVYIIDENDNPPA	1757
à	43 -		44
q	1758 F	FGKPTFLGHISEAAPLHSLILGEDNSPLVVRASDSDREANSLLVYKILEPEALKFFKIDP	1817
ò	45 8	SLGAQFRV	52
g	1818 \$	 SMGTLTTTSELDFEDTPLFQFNIYVHDQGTPILFAPRSAKVIIHVRDVNDSPPRFSEQIY	. 1877
ò	53 -		52

68	06	σ̈́	ò
2957	  8 ITDENDNPPRFASEDYRGSVVENNEPGELVATLKTLDADVSDQNRQVTCYITEGDPLGQF	289	Q
68		æ	ò
2897	.8 LSVEPGSNIHELFAVDSESGWITTLQELDCETQQTYRFYVVAFDHGQTIQLSSQALVEVS	283	q
87	1SQTI	α	ò
2837	8 DLVSLVSVSIQVEDVNDNRPVFEADPYKAFLTENMPGGTTVIQVTANDQDTGSDGGVSYR	277	đ
80		80	ò
2777	8 AAQDPIIYSLVQGTTPESNSDDVFSLDQDTGVLKVRKAMDHESTKWYQIDLMAHCPHEDT	271	g
90	11	81	ò
2717	8 VDFNIKAQDGGPPHWDSLVPVRLQVVPNEIPLPKFSEPLYTFSAPEDLPEGSEIGSVKAV	2658	qq
80	1	81	ò
2657	8 VSRDSPIIQVLAYDADEGRNADVTYSVDSTEDLAEEIIEVNPTTGVVKVKGSLVGLENRA	2598	g
80	1	æ	ò
2597	8 TTLQKLDRENSTERVIAIKVMARDGGGKVAFCTVKIILTDENDNAPQFKASGYTVSIPSN	253	qq
80	1	81	ò
2537	8 SPEFQQNVYEAELAENAKVGTKVIELLAIDKDSGPYGTVDYTIINKLAGERFFINPRGQI	2478	QQ
80	1	80	ò
2477	8 ILSGNQDRHFSINSTSGIISMFNLCKKQLDSSYNLRVGASDGVFRATVPVYINTTNANKY	241	qq
80	TIN 8	9	ò
2417	8 PLTGETLVVVNVSDINDNPPKFREPQYEANVSELATCGHLVLKVQALDPDIGDTSRLEYL	2358	qq
67	8	99	ò
2357	8 DQDSGQNQDVSYQIVEDGSDVSKFFRINGSTGEIFTIQELDYETHQHFRVKVRAMDKGDP	2298	Ω
67		89.	ò
2297	8 KHVFTVRATDTALGSFSEATVEVLVEDINDNPPTFSQLVYTTSVSEGSPAQTPVIQLLAS	223	Q
67		ý	ò
2237	8 VKVPENITLYTPILHTQARSPEGLRLIYNIVEEEPLMLFTTDFKTGVLTVTGPLDYESKN	2178	q
63	,	Ÿ	ò
2177	8 IDPYVGDISLKKPFDYQALNKYHLRVIARDSGIPPLQTEVEVHVTVRNKSNPLFQSPYYK	211	g
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2117	8 VSVEDVNDNIPEFQHLPYYTVIQDGTEPGDVLFQVSATDKDLGANGSVTYGFAEDYAYFR	2058	තු
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2057	8 NDTLSYFLLNGTDLFHMIESAGVLQTRGGTFDREQQDTHEVAVEVRDNRVPQRVAQALVR	1998	đ
09	1	61	ò
1997	:       8 KFSIRASDGLYHDTAVVKISLTQVLDKSLQFDQDVYRARVTENTPHRKALVILGVHGNHL	193	g
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1937	8 EVAVVEPIHPGMGLLTVQAEDNDSRVTYSIKTSNADEAVTIHPTTGQISVVNPATLRLFQ	187	g G

å	2958 SISQVGDEWRISSRKTLDREHIAKYLLRVTASDGKFQASVPVEVFVVDINDNSPQCSQLL 3017	,	
ò	90EDDTDPGH97	ò	131
<u>8</u>	:           XTGKVREDVTPGHEILKVSAIDVDMDTNAOITYSIHGPGAOFFKLDPHTGELTTITVILDR	đ	4098 QASPAIELDPLNTSSCNNLNQPEPSKTSVPN
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3 8		ò	136 ITEDIGF
S 8	ADL	q	4218 MPDPTGLYGGFPFPLELENKRAPLPPRYSNO
2	3138 FAKDPDÇKANAQVVYSLIDSADGQFSIDATSGVIRLEKPLQVRASSAVELTVRASDLGTP 3197	ò	145GVTI 148
ò	101	· £	4278 YXHSOFBOGGGBCI.AEGGYKGVSW
q	3198 IPLSTLGTVTVSVVGLEDYLPIFLNAEHSTQVPEDAPIDMEVLHLATLTRPGSEKTGYHI 3257	2	
ò	101 104	RESU	RESULT 10
QQ	3258 TGGNEQGKFRLDAHTGILYVNGSLDFETNPKYFLSIECSRKSSSSLSDVTTIVINVTDVN 3317	ID	RYR1 HUMAN STANDARD; PRT;
ò	105 104	P E	PZ1817; Q16368; Q16314; Q9NPKL; Q9PI 01-MAY-1991 (Rel. 18, Created)
q	3318 EHHPRFTHDLYTVRVLENAVVGDVILTVSASDDGPVNSAITYSLVGGNQLGHFTINPKK 3377	T C	16-OCT-2001 (Rel. 40, Last sequence 15-JUN-2002 (Rel. 41, Last annotatio
ò	105 104	B B C	Ryanodine receptor 1 (Skeletal muscl (RYR-1) (Skeletal muscle calcium rel
qq	3378 GKLQVAKALDWEQTPSYSLRLRATDSGQPPLHEDTEVAVEVVDVNDNPPRFFQLNYSTSV 3437	S O	KYKI OK KYDK. Homo sapiens (Human).
ò	105	88	Eukaryota, Metazoa, Chordata, Crania Mammalia, Eutheria, Primates, Catarr
qq	3438 QENSPIGIKVLQLILDDPDSPQNGPPYFFRITEGNTGSVFRVTPDGWLVTAASLSKKARE 3497	N N	D=9606;
ò	105	8 8 C D	SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE=Skeletal muscle;
g	3498 WYQLHIEVSDSGLPPLSSSTLVRVQVTEQSRYPPSTLPLEISITKGEEEFQGGMIGKIHA 3557	RX RA	MEDLINE=90130482; PubMed=2298749; Zorzato F., Fujii J., Oteu K., Phill
ò	105	RA RT	Meissner G., Maclennan D.H.; Molecular cloning of cDNA encoding
g	3558 TDRDPQDTLTYSLEQEGGLDRYFTVGASDGKIIASQGLPHGRYSFNVTVSDGTFTTTTGV 3617	RT	Ca2+ release channel (ryanodine rece sarcoplasmic reticulum.";
ò	105	R L N	J. Biol. Chem. 265:2244-2256(1990). [2]
g	3618 HVHVWHMEPEVPQQAVWLGFHQLTPEELVSDHWRNLQRFLSNLLDVKRANIHLASLQPAE 3677	አ ማ ማ	REVISIONS TO 2324; 2840 AND 3380, VA. CYS-471; LEU-1787 AND CYS-2060.
ò	105	S X	TISSUE=Muscle; MEDLINE=92372020; PubMed=1354642;
셤	3678 VTAGVDVLLVFERHSGTSYDLQELASAIAHSVREIEHSVGIRMRSALPVVPCQGĠSCQDQ 3737	R R	Gillard E.F., Otsu K., Fujii J., Duf Britt B.A., Worton R.G., McLennan D.
ò	111 110	RRT	"Polymorphisms and deduced amino acti sequence of the ryanodine receptor (
QQ	3738 TCQETVSLEPRVGPSYSTARLSILTPRHHLGRNCSCNGTTLRFSGQSYVQYRPLEAQNWQ 3797	RE	malignant hyperthermia."; Genomics 13:1247-1254(1992).
ò	141	X X 1	EVISIONS TO 1365-1368, VARIANT CCD
q	3798 IHFYLKTLQPWALLMFTNETASISLKLANGFSHLEYHCPGGFYGNLSSRYPVNDGQWHSM 3857	X X ;	3C1e; 1035117; PubMed=8220422;
ò	111 124	<b>a</b> a :	Zhang Y., Chen H.S., Khanna V.K., de Schappert K., Britt B.A., Brownell A
Q	3858 LEERRDTSVHLLVDITDNASLVIPPECQCLRTERQLLLGGLVPSNPSSNVSLGFEGCLDA 3917	RRI	station in the human ryanodine ral core disease.";
ò	125 130		Nat. Genet. 5:46-50(1993). [4]
g	3918 VVVNGERLELLGREKKMEGRLETWALSQCCWPGTACSQSPCLNGGSCSPALGSGYLCRCP 3977	ማ አ ማ አ የ	SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=96299657; Pubmed=8661021;
ò	131		Philips M.S., Fujii J., Khanna V.K. de Jong P.J., McLennan D.H.;
g	3978 PPFSGRNCELGRENCTSAPCQEGGTCVSSPEGTSCNCPHPYTGDRCEMEARGCSGGHCLI 4037		"The structural organization of the receptor (RYR1) gene.";
ò	131		Genomics 34:Z4-41(1996).
QQ	4038 TPEIKRGDWGQQEFLVITVALPLVIIATVGLLLYCRRRKSHKPVTMEDPDLLARSIGVDT 4097	ğκ Υ	SEQUENCE OF 598-/22 FROM N.A. TISSUE=Skeletal muscle;

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RKKHWEYPHPETMQGTLPPSPRRHVGPAV 4217
                           IELVTFGPSSKQRPMVCSVPPRLPPAAVSS 4157
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d substitutions in whe coding
RYR1) gene in individuals with
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hini; Hominidae; Homo.
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Sun J., Xin C., Eu J.P., Stamler J.S., Meissner G.;
"Cysteine-3635 is responsible for skeletal muscle ryanodine receptor
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MEDILIRE-9215959; PubMed=1774074;
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MEDLINE=94282042; PubMed=8012359;
Quanne K.A., Keating K.E., Manning B.M., Healy J.M.S., Monsieurs K.,
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Quane K.A., Healy J.M.S., Keating K.E., Manning B.M., Couch F.J.,
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"Mutations in the ryanodine receptor gene in central core disease malignant hyperthermia.";
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"Partial cloning and differential expression of ryanodine
"receptor/Calcium-release channel genes in human tissues including
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mutation in a pedigree with
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4696-4974 FROM N.A.
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Censier K., Urwyler A., Klauenitzer M., Muller C.R., Heffron J.J.A.,
McCarthy T.V.;
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Manning B.M., Quane K.A., Ording H., Urwyler A., Tegazzin V.,
Lehane M., O'Hallornan J., Hartung E., Giblin L.M., Lynch P.J.,
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Monsteurs K., Fagerlund T.H., Wolz W., Heffron J.J.A., Mueller C.R.,
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MEDLINE=98111378; PubMed=9450902;
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Db 615 S	PGRELLLQTNLINYVTSIRPNIFVGRAEGTTQYSKWYFEVMVDEVTPFL	73
Oy 30 - Db 675 T	VLTNLNIG	. 17
Oy 38 -	75	Qy 77
Db 735 H	HLLAPEDVISCCLDLSVPSISFRINGCPVQGVFESFNLDGLFFPVVSFSAGVKVRFLLGG 794	77
	37	Db 1875 BEEEDBEEEGBEEDBEEKEEDBEETAQEKEDEBKEBEEBAAEGEKBEGLEEGLLQMKLPES
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855	VDTVQIVLPPHLERIREKLAENIHELWALTRIEQGWTYGPVRDDNKRLHPCLVDFHSLPE 914	1935 VKLOMCHLLEYFCDQELQHRVESLAAFAERYVDKLQANQRSR
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Db 915 F	PERNYNLQMSGETLKTLLALGCHVGMADEKAEDNLKKTKLPKTYMMSNGYKPAPLDLSHV 974	1975 183
		DD 2055 EETTLGSRLMSLLEKVRLVKKKEEKPEEERSAEESKPRSLOELVSHWVVRWAQEDFVQSP
	975 RLTPAQTTLVDRLAENGHNVWARDRVGQGWSYSAVQDIPARRNPRLVPYRLLDEATKRSN 1034	Oy 86
		Db 2115 ELVRAMFSLLHRQYDGLGELLRALPRAYTISPSSVEDTMSLLECLGGIRSLLIVQMGPQE
Db 1035 F	1035 RDSLCQAVRTLLGYGYNIEPPDQEPSQVENQSRCDRVRIFRAEKSYTVQSGRWYFEFEAV 1094	Qy 94
1095	ELAYVFNGHRGQRWHLGSEPFGRPWQPGDVVGCMIDL	21
Oy 49 -	48	
Db 1155 1	TENTIIFTLNGEVLMSDSGSETAFREIEIGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFA 1214	2235
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Db 1215 1	ICGLQEGFEPFAINMQRPVTTWFSKGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLRLTHR 1274	DD ZZYS DEKNYOTLAGCCOLGSCFFTLOANGFFTTGWARCCGGBRTLDFFTTGAGGGGGFTGAGGGGGGGGGGGGGGGGGGGGGGGG
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		Oy 102
1455	DYHQHDMSFDLSKVRVVTVTMGDEQGNVHSSEKCSNCYMVWGGDFVSPGQQGRISHTDLV 1514	N
	TAN7	102
	1515 IGCLVDLATGLMTFTANGKESNTFFQVEPNTKLFPAVFVLPTHONVIQFELGKOKNIMPL 1574	Db 2595 LTKAQRDVIEDCLMSLCRYIRPSMLQHLLRRLVFDVPILNBFAKMPLKLLTNHYERCWKY

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	2715 VDASYSSKAEKKATVDAEGNFDPRPVETLNVIIPEKLDSFINKFAEYTHEKWAFDKIQNN 27	2774
	116 115	15
	2775 WSYGENIDEELKTHPMLRPYKTFSEKDKEIYRWPIKESLKAMIAWEWTIEKAREGEEEKT 28	2834
	116 115	15
	2835 EKKKTRKISQSAQTYDPREGYNPOPPDLSAVTLSRELQAMAEQLAENYHNTWGRKKKQEL 28	2894
	116 115	15
	2895 EAKGGGTHPLLVPYDTLTAKEKARDREKAQELLKFLQMNGYAVTRGLKDMELDSSSIEKR 29	2954
	116 115	51
	2955 FAFGFLQOLLRWMDISQEFIAHLEAVVSSGRVEKSPHEQEIKFFAKILLPLINQYFTNHC 30	3014
	116 115	15
	3015 LYFLSTPAKVLGSGGHASNKEKEMITSLFCKLAALVRHRVSLFGTDAPAVVNCLHILARS 30	3074
	116RQVRGVTQ 123	23
	3075 LDARTVMKSGPEIVKAGLRSFFESASEDIEKMVENLRLGKVSQARTQVKGVGQNLTYTTV 313	134
	124 123	,
	3135 ALLPVLTTLFQHIAQHQFGDDVILDDVQVSCYRTLCSIYSLGTTKNTYVEKLRPALGECL 319	194
	124LG 125	25
	3195 ARLAAAMPVAFLEPQLNEYNACSVYTTKSPRERAILGLPNSVEEMCPDIPVLERLMADIG 325.	254
	126 G	56
	3255 GLAESGARYTEMPHVIEITLPMLCSYLPRWWERGPEAPPSALPAGAPPPCTAVTSDHLNS 331	314
	127 126	. 93
	3315 LLGNILRIIVNNLGIDEASWMKRLAVFAQPIVSRARPELLQSHFIPTIGRLRKRAGKVVS 337	374
	127 126	56
	3375 EEEQLRLEAKAEAQEGELLVRDEFSVLCRDLYALYPLLIRYVDNNRAQWLTEPNPSAEEL 343	134
	127 126	92
	3435 FRMVGEIFIYMSKSHNFKREEQNFVVQNEINNMSFLTADNKSKMAKAGDIQSGGSDQERT 349	194
	127 131	31
	3495 KKKRRGDRYSVQTSLIVATLKKMLPIGLNMCAPTDQDLITLAKTRYALKDTDEEVREFLH 355	554
	132 131	31
	3555 NNLHLQGKVEGSPSLRWQMALYRGVPGREEDADDPEKIVRRVQEVSAVLYYLDQTEHPYK 361	514
	132WLITEDTGFD 143	13
	3615 SKKAVWHKLLSKORRRAVVACFRMTPLYNLPTHRACNMFLESYKAAWILTEDHSFEDRMI 367	574
	144 143	13
	3675 DDLSKAGEQEEEEEVEEKKPDPLHQLVLHFSRTALTEKSKLDEDYLYMAYADIMAKSCH 373	734
	144 143	13

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3735 LEEGGENGEAEEEVEVSFEEKQMEKQRLLYQQARLHTRGAAFMVLQMISACKGETGAMVS 3794
                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrocidine synthetaes III Includes: ATP-dependent asparagine
adenylase (AsnA) (Asparagine activase); ATP-dependent tyrosine
adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase
(Vall) (Valine activase); ATP-dependent ornithine adenylase (OrnA)
(Ornithine activase); ATP-dependent leucine adenylase (Leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OPTIONAL)

-INSCELLANEOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLLC
DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSITIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.
-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- COFACTOR: CONTAINS 6 COVALENTLY BOUND PHOSPHOPANTETHEINES (BY SIMILARITY)
-:- PATHWAY: CYCLIA peptide antibiotic tyrocidine biosynthesis
-:- SUBUNIT: LARGE MULTIENZYME COMPLEX OF TYCA, TYCB AND TYCC.
-:- DOWAIN: CONSISTS OF SIX MODULES, AND HARBORS A PUTATIVE
--- THIOESTERASE DOMAIN AT ITS C-TERMINAL END. BACH MODULE
INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE
ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITATION MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION (OPTIONAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 8185;
MEDLINE=98012987;
MEDLINE=98012987;
MEDLINE=98012987;
MOOTZ H.D., Marahiel M.A.;
"The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleocide sequence and biochemical characterization of functional internal adenylation domains "; J. Bacteriol. 179:6843-6850(1997).
-!- FUNCTION: INCORPORATES SIX AMINO ACIDS (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Bacillales, Paenibacillaceae, Brevibacillus.
VCBI_TaxID=1393;
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InterPro; IPR001242; Condensatn.
InterPro; IPR001880; Ppantna_attach.
InterPro; IPR001891; Par eatrs site.
InterPro; IPR001031; Thioesterase.
                                                                                                                                                                                          PRT;
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                                                                                                                                                                                        STANDARD;
                                                                                 3795 STLKLGISI 3803
                                           144 ----LGVTI 148
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992 DFFDLGGHSLKAMTVVFQVSKALEVELPVKALFEHPTVAELARFLSRSEKTEYTAIQPVA 1051
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                                      TETVVGCMIYLYDPQTTTQESVPIGVPADNVQLYLLDASMQPVPVGSLGEMYIAGDGVAK 811
                                                                                                                                     IETRLIQHEAVKEAVVIVEKDESGQNVLYAYLVSERELTVAELREFLGRILPSYMIPSFF 931
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|ASGSIVSIMAEHSLELIVAIMAVLRSGAAYLPIDPEYPQDRIQYLLDDSQTTLLLTQSHL
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                                                                                                                                                              (VALINE-ACTIVATING).
                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 1; Length 6486;
Pred. No. 1.3e+02;
32; Mismatches 33; Indels 604
                                                                                                                                       (GLUTAMINE-ACTIVATING)
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                                                  PROSITE; PS00012; PHOSPHOPANTETHEINE; 6.
PROSITE; PS00455; AMP BINDING; 6.
PROSITE; PS50075; ACP_DOMAIN; 6.
Ligase; Antibiotic biosynthesis; Phosphopantetheine; Multifunctional enzyme; Repeat.
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           PF00550; pp-binding; 6.
PF00668; Condensation; 6.
PF00975; Thioesterase; 1.
PF00501; AMP-binding; 6.
                                                PRINTS; PR00154; AMPBINDING PROSITE; PS00012; PHOSPHOPAL
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ò	ος λο	64 48
ପ୍ଧ	Db 2972 SALAAYFTADEQLDVTKLWSHLSKRLPSYMIPAHFVQLDQLPLTPNGKVDKKALPRPEGK	GKVDKKALPKPEGK 3031
ò	ος λο	49
qq	Db 3032 PVTEAQYVAPTNAVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQV	AMAVAAQVHREYOV 3091
à	ογ δο	64 ************
d	3092 ELPLKVLFAQPTIKALAQYVATSGKETYVPIEPAPLQEYY	PVSSAQKRMYVLRQFADTGT 3151
ò	ογ δο	49
අු	Db 3152 VYNMPSALYIEGDLDRKRFEAAIHGLVERHESLRTSFHTVNGEPVQRVHEHVELNVQYAE	RVHEHVELNVQYAE 3211
ò	δγ 50	64 48
qq	Db 3212 VTEAQVEPTVESFVQAFDLTKAPLLRVGLFKLAAKRHLFLLDMHHIISDGVSAGIIMEEF	ISDGVSAGIIMEEF 3271
ò	ος λο	64 46
g	Db 3272 SKLYRGEELPALSVHYKDFAVWQSELFQSDVYTEHENYWLNAFSGDI	IPVLNLPADFSRPL 3331
ò	ογ δο	49
q	Db 3332 TQSFEGDCVSFQADKALLDDLHKLAQESQSTLFMVLLAAYNVLLAKYSGQEDIVVGTPIA	YSGQEDIVVGTPIA 3391
ò	Oy 50	49
q	Db 3392 GRSHADIENVLGMFVNTLALRNYPVETKHFQAFLEEVKONTLOAYAHODYPFEA	HODYPFEALVEKLD 3451
ò	Oy 50	49
g	Db 3452 IQRDLSRNPLFDTMFILQNLDQKAYELDGLKLEAYPAQAGNAKFDLTLEAHEDETGIHFA	TLEAHEDETGIHFA 3511
ò	Ογ 50	49
qq	Db 3512 LVYSTKLFQRESIERMAGHFLQVLRQVVADQATALREISLLSEEERRIVTVDFNNTFAAY	RIVTVDFNNTFAAY 3571
ò	ζὸ 50	64 48
q	Db 3572 PRDLTIQELFEQQAAKTPEHAAVVMDGQMLTYRELNEKANQLAHVLRQNGVGKE	RUNGVGKESIVGLL 3631
ò	ζς ξο	49
qq	Db 3632 ADRSLEMITGIMGILKAGGAYLGLDPEHPSERLAYMLEDGGVKVVLVQKH <b>LJ</b> PLVGEGLM	VOKHLIPLVGEGLM 3691
ò	λς δο	64 48
qq	Db 3692 PIVLEEESLRPEDCGNPAIVNGASDLAYVMYTSGSTGKPKGVMVEHRNVTRLVMHTNYVQ	RNVTRLVMHTNYVQ 3751
ò	2y 50	64 48
QQ	Ob 3752 VRESDRMIQTGAIGFDAMTFEIFGALLHGASLYLVSKDVLLDAEKLGDFLRTNQITTMWL	SDFLRTNQITTMWL 3811
ò	λα 20	64 48
d	Db 3812 TSPLFNQLSQDNPAMFDSLRALIVGGEALSPKHINRVKSALPDLEIWNGYGPTENTTFST	ANGYGPTENTTFST 3871
ò	2y 50	64 48
q	3672 CYLIEQHPEEQIPIGKPIANSTAYIVDGNNQPQPIGVPGELCVGGDGVARGYVNKPELTA	SVARGYVNKPELTA 3931
ò	2y 50	64 48
qq	3932 EKFVPNPFAPGETMYRTGDLARWLPDGTIEYLGRIDQQVKIRGYRIELGEIETVLSQQAQ	ELGEIETVLSOOAQ 1991
ò	λς 50	64 48

g G	3992	VKEAVVAVI EEANGQKALCAYFVPEQAVDAAELREAMSKQLPGYMVPAYYVQMEKLPLTA	4051
ò	20	,	49
g	4052	NGKVDRRALPQPSGERTTGSAFVAAQNDTEAKLQQIWQEVLGIPAIGIHDNFFEIGGHSL	4111
ò	20		49
g	4112	KAMNVITQVHKTFQVELPLKALFATPTIHELAAHIAESAFEQFETIQPVEPAAFYPVSFA	4171
ò	20		49
유	4172	QKRMYILHQFEGSGISYNVPSVLVLEGKLDYDRFAAAIQSLVKRHESLRTSFHSVNGEPL	4231
ò	20	FRUHLUK	56
8	4232	QRVHPDVELPVRLLEATEDQSESLIQELIQPFDLEIAPLFRVNLIKLGAERHLFFMDMHH	4291
ò	57		56
g	4292	IISDGVSLAVIVEEIASLYAGKQLSDLRIQYKDFAVWQTKLAQSDRFQKQEDFWTRTFAG	4351
ò	57	WVLLT (	61
QQ	4352	BIPLENLPHDYPRPSVQSFDGDTVALGTGHHLLEQLRKLAAETGTTLFWVLLAAYHVLLS	4411
ò	62		61
g	4412	KYAGQEEI VVGTPI AGRSHADVER I VGMFVNTLALKNTAAGSLSFRAFLEDVKQNALHAF	4471
ò	62		61
g	4472	EHQDYPFEHLVEKLQVRRDLSRNPLFDTMFSLGLAESAEGEVADLKVSPYPVNGHIAKFD	4531
ò	62		61
g	4532	LSLDAMEKQDGLLVQFSYCTKLFAKETVDRLAAHYVQLLQTITADPDIELARISVLSKAE	4591
ò	62		61
g	4592	TEHMLHSFLATKTAYPTDKTFQKLFEEQVEKTPNEIAVLFGNEQLTYQELNAKANQLARV	4651
ò	62		61
අ	4652	LRRKGVKPESTVGILVDRSLYMVIGMLAVLKAGGTFVPIDPDYPLERQAFMLEDSEAKLL	4711
ò	62		99
임	4712	LTLOKMNSOVAFPYETFYLDTETVDQEETGNLEHVAQPENVAYIIYTSGTTGKPKGVVIE	4771
ò	67		99
g	4772	HRSYANVAFAWKDEYHLDSFPVRLLQMASFAFDVSTGDFARALLTGGQLVIÇPNGVKMDP	4831
ò	67		99
임	4832	<b>ASLYETIRRHEITIFEATPALİMPLMHYVYENELDMSQMKLLILGADSCPAEDFKTLLAR</b>	4891
ò	63	LING	7.0
g	4892	;     PGQKMRIINSYGVTEACIDTSYYEETDVTAIRSGTVPIGKPLPNMTMYVVDAHLNLQPVG	4951
ò	71		7.0
a a	4952	VVGELCIGGAGVARGYLNRPELTEEKFVPNPFAPGERLYRTGDLAKWRADGNVEFLGRND	5011
ò	11	AN	72
QQ	5012	HQVKIRGVRIELGEIETQLRKLDGITEAVVVAREDRGQEKELCAYVVADHKLDTAELRAN	5071
ò	73		82
QQ	5072	I LLKELPQAMIPAYFVTLDALPLTANGKVDRRSLPAPDVTMLRTTEYVAPRSVWEARLAQV	5131

ò	83	WSCTIVNITOSW
q	5132	:  WEQVLNVPQVGALDDFFALGGHSLRAMRVLSSMHNEYQVDIPLRILFEKPTIQELAAFIE 5191
ò	89	88
Q	5192	ETAKGNVFSIEPVQKQAYYPVSSAQKRMYILDQFEGVGISYNMPSTMLIEGKLERTRVEA 5251
ò	89	88
QQ	5252	AFQRLIARHESLRTSFAVVNGEPVQNIHEDVPFALAYSEVTEQEARELVSSLVQPFDLEV 5311
ò	89	88
g	5312	APLIRVSLLKIGEDRYVLFTDMHHSISDGVSSGILLAEWVQLYQGDVLPELRIQYKDFAV 5371
ò	89	95 95DTDP 95
qq	5372	WQQEFSQSAAFHKQEAYWLQTFADDIPVLNLPTDFTRPSTQSFAGDQCTIGAGKALTEGL 5431
ò	96	100 GHADL 100
QQ	5432	HOLAQATGTTLYMVLLAAYNVLLAKYAGQEDIIVGTPITGRSHADLEPIVGMFVNTLAMR 5491
ò	101	100
QQ	5492	NKPQREKTFSEFLQEVKQNALDAYGHQDYPFEELVEKLAIARDLSRNPLFDTVFTFQNST 5551
ò	101	107RF 107
q	5552	EEVMTLPECTLAPFMTDETGQHAKFDLTFSATEEREEMTIGVEYSTSLFTRETMERFSRH 5611
ò	108	117
gg	5612	FLTIAASIVQNPHIRLGEIDMLLPEEKQQILAGFNDTAVSYALDKTLHQLFEEQVDKTPD 5671
ģ	118	126 126
g	5672	QAALLFSEQSLTYSELNERANRLARVLRAKGVGPDRLVAIMAERSPEMVIGILGILKAGG 5731
ò	127	A
QQ	5732	AYVPVDPGYPQERIQYLLEDSNAALLLSQAHLLPLLAQVSSELPECLDLNAELDAGLSGS 5791
ò	128	127
QQ	5792	NLPAVNQPTDLAYVIYTSGTTGKPKGVMIPHQGIVNCLQMRRDBYGFGPSDKALQVFSFA 5851
ò	128	-CS- 129
QQ	5852	FDGFVASLFAPLLGGATCVLPQEAAAKDPVALKKLMAATEVTHYYGVPSLFQAILDCSTT 5911
ò	130	137
qq	5912	TDFNQLRCVTLGGEKLPVQLVQKTKEKHPAIEINNEYGPTENSVVTTISRSIEAGQAITI 5971
ò	138	137
QC	5972	GRPLANVQVYIVDEQHHLQPIGVVGELCIGGAGLARGYLNKPELTAEKFVANPFRPGERM 6031
ò	138	137
qq	6032	YKTGDLVKWRTDGTIEYIGRADEQVKVRGYRIEIGEIESAVLAYQGIDQAVVVARDDDAT 6091
ò	138	137
QQ	6092	AGSYLCAYFVAATAVSVSGLRSHLAKELPAYMIPSYFVELDQLPLSANGKVDRKALPKPQ 6151
ò	138	137
q	6152	QSDATTREYVAPRNATEQQLAAIWQEVLGVEPIGITDQFFELGGHSLKATLLIAKVYEYM 6211

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                                                                                                                                                                                                                                                                                                                                                                                6212 QIELPLNLIFQYPTIEKVADFITHKRFESRYGTAILLNQETARNVFCFTPIGAQSVYYQK 6271
                                                      6272 LAAEIQGVSLYSFDFIQDDNRMEQYIAAITAIDPSGPYTLMGYSSGGNLAFEVAKELĖER 6331
                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteria (class); Actinobacteridae,
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERMEDIATES.
COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTETHEINES.
PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND
                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase
EC 6...--) (ACV synthetase) (ACVS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS.
                                                                                                                                                                               . PRT; 3649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001842; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001380; Ppantine_attach.
InterPro; IPR001031; Thioesterase.
Pfam; PF00550; AMP-binding; 3.
Pfam; PF00568; Condensation; 3.
Pfam; PF00675; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROO154; AMPBINDING.
PROSITE; PSO0012; PHOSPHOPANTETHEINE;
PROSITE; PSO0455; AMP_BINDING; 1.
PROSITE; PSS0075; ACP_DOWAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X57310; CAA40561.1; -. PIR; S18268.
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                         Nocardia lactamdurans
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                         GY--GVT 6336
                                                                                 141 GFDLGVT 147
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                 Amycolatopsis.
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NOCLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840 VEDVFALRTLDALAGHLESQGHAEPEVVAEEVTTGSEPVRVLANGLQOGLLYHHLKTAGG 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 DDAYVVQSVHRYHAPIRPELMKDAWQAARQTYPALRLRFDWAEEPVQIVDNDDKPFDWRF 959
                                                                                                                                                                                                                                                            180 AAGCLHWRIAYAGEFFEDKIIAGVLDVAREVLGOFIGRPEQLVADIDLVSAEQELQLHQW 239
                                                                                                                                                                                                                                                                                                              240 NGTDGEFDEDKRLNELFEDVVRRAPDREAVVCGDVRLTYREVNERANGFAHWLIQGPVRV 299
                                                                                                                                                                                                                                                                                                                                                                   30 RPGALIGLYLDKSDLGVVATFGIWKSGAAYVPIDPAYPAERIRFLVGDTGLSGIVTNRRH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 VPKYHYSVVNSITDLSERYDMRRPGTERVALFASYVFEPHLRQTLIALINEQTLVIVPDD 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 VRLDPDLFPEYIERHGVTYLNATGSVLQHFDLRRCASLKRLLLVGEELTASGLRQLREKF 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 LYIGGCGVAPGYLNRDDLTAERFTANPFQTEEEKARGRNGRLYRTGDLARVLLNGEVEFM 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
                                                                                                                                                                                                                                    1 AAG------61L-----GIL------61
                     DOMAIN 1 (ADIPATE-ACTIVATING).
DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 2.
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
THIOESTERASE (BY SIMILARITY).
THIOESTERASE (BY SIMILARITY).
79 MW; 6FD095704F858E6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 AGRVVNEYAFTEAAFVTAVKEFGPGVTERRDRSIGRPLRNVKWYVLSQGLKQLPİGAIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 GRADFQLKLNGVRVEPGEIEAQATEFPGVKKCVVVAKENATGDRHLVGYYLVEDGAEVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780 GSNAPLLAITEQLRAIWSEVLGVPQNRIGERDDFFRLGGQSISCILLIARVRQRLSLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                      360 AERLREVLGDEHASVHVIEVEAVVAGPHPEOARENPGLALSSRDRAYVTYTSGTTGVPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----IGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 .....VFQAHQEDT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GAQFRVHLVKM
                                                                                                                                                                               , Score 209; DB 1; Length 3649;
Pred. No. 27;
23; Mismatches 43; Indels 2965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthesis; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                               8 LELL--------VAVGPD----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.0%;
                                                                                                                                                         404079
                                                                                                                                                                                               2.6%;
                                                                                                                                                                                                                                                                                       Conservative
                                       1937
2985
857
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2981
820
1896
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3502
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1896 189
2944 294
3502 350
 Antibiotic
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                     BINDING
BINDING
BINDING
ACT SITE
SEQUENCE
              Repeat;
REPEAT
                                                                 DOMAIN
DOMAIN
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                                       REPEAT
                                                   REPEAT
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1020 GWSLPVLH	GWSLPVLHDEVHRNYLALRAGQPIESDVDNAYVAAQRYWEAHRNDHAAYWVEQLGRIDER 1079
58	57
1080 GDFAGLLN	GDFAGLLNEKSRYRVSLGDYDHVQRHRTRKLYLGADLTGALKAGCAADQVTLHSVLQFVW 1139
58	57
1140 HKVLHAIG	HKVLHAIGGGNTTVVGTIVSGRNLPVDGIENSAGLFINTLPLIVDHDQQAGQNVAEAVRD 1199
58	57
1200 IQAAVNTM	IQAAVNTMNSKSIVELGRLQSGËMKRRLFDTLLVLENYPRLLDEEEELAHQEALRFEKAY 1259
58	25
1260 DADKVDYF	DADKVDYPIAVVAREEGDELTVTLWYAGELFDEDTIDTLLDVARTLFRQVTEDIARPVRE 1319
58	57
1320 LDLISPSM	LDLISPSMRARFDSWNETAEEFPADKTLHAVFEEMAERWPDEIAVVYRENRLTYRELNER 1379
85	57
1380 ANRLAHYL	ANRLAHYLRSVVELRPDDLVALVLDKSELMITAIIAAWKTGAAYVPIDSGYPDDRISFML 1439
58	. 57
1440 SDTAARVV	SDTAARVVVTNEIHSDRLRSLAETGTPVLEIELLHLDDQPAVNPVTETTSTDLAYAIYTS 1499
58	VILTEPEGAPNITANL73
1500 GTTCKPKA	GTTGKPKAVLVEHRGVVNLQVSLAKLFGLDKAHRDEALLSFSNYIFDHFVEQMTDALLNG 1559
74	79
1560 QKLVVLDE	QKLVVLDDSMRTDPGRLCRYMNDEQVTYLSGTPSVLSLYDYSSATSLTRIDAIGEDFTEP 1619
80	62
1620 VFAKIRGT	VPAKIRGTFPGLIINGYGPTEISITSHKRPYPPDVHRVNKSIGFPVANTKCHVLNKAMKP 1679
80	62
1680 VPVGGIGE	VPVGGIGELYIGGIGVTRGYLNREDLTADRFVENPFQTAEERRLGENGRLYKTGDLVRWL 1739
80	42
1740 PNGEVEYI	PNGEVEYLGRIDLQVKIRGQRVELGEVEAALSSYPGVVRSLVVAREHAVGQKYLVGFYVG 1799
80	62
1800 EQEFDEQU	EQEFDEQDLKQWMRKKLPESVVPARVLRITDIPVTPSGKLDARRLPETDFGAGEGAEYVA 1859
80	98 88
1860 PVSEFELF	
89	88
1920 LOHTTLA	LOHTTLAAQAEHIQAAALEHTAWTPPPTAVEHPPVSLAQERLLFIDDFEGGTAAYNIPFV 1979
68	92
1980 LRLPAHTE	LRLPAHTRAALPGALGTLVRRHPALRTLLKTDDQGVRRQYPIPADDVRLEVPSTTVDSRA 2039
93	86 35
**************************************	

ò	93	92
qq	2100	DGVPEADLGALRGTYGEFAVWORQYLTGKRLAALTEFWTGALGGFETIALPLDHPRPPRF 2159
ò	93	92
q	2160	DYRGRELEFELDERTTEALRELARTARVSLYSVLLGAWCLMLNMYTGQHDLVVGTPSANR 2219
ò	93	104
QQ	2220	GRPEFDRAVGFFANLLALRVRVDPA-ÅTLPAÝVRSVGEAVVAAQVHGELPFEQLVKELKV 2278
ò	105	110
С	2279	EKDPSRHPILQLNFTLQNVSDHTSALTGYQPDSGGWTTTKFDLSATMTETATGLAGNLTY 2338
ò	111	116
q	2339	AASLEDDTSASGFIATFKHVLAEFASAAAQTPIAQLTALDEPGQAALPDATRRARRPGGP 2398
ò	117	116
qq	2399	GRCTRLFEEVAATWPDRVAVVHGDVRLTYRELNERANRLAHHLRSVAEPRADELIALVLD 2458
ò	117	123
qq	2459	KSELTLVAILAVWKAGAAYMPIDPSYPDDRIAFMLSDTGAKLVLAGEAHGSRVRGLTSGD 2518
ò	124	
QQ	2519	VLDLEQLDLTGEPAENPVTETTSTELAYAIYTSGTTGKPKAVLVSHGSVDSFRAQLSGRY 2578
ò	124	126
qq	2579	FGSPDESAEAVLFLANYVFDFSVEQLALSVLGGHKLLVPPPSAADDPAFYELANREGLSY 2638
ò	127	126
qq	2639	LSGTPTQVERFDLARLSHLRCVLVAGEAFQPQHFEKWRGEFAGPILNAYGTTETTVYNTV 2698
ò	127	126
QQ	2699	HRFEPGDAYRNTLGAPLGNTRLYVLGDGMKLLPTGAVGELYLAGDCVTEGYLHRPELTRE 2758
ò	127	127
q	2759	RFLPNPFAAESGRFPMIYRTGDVVRRGPDGELQYLGRNDAQVKINGLRIEPGEVEAALAG 2818
ò	128	CSPTWSCLI136
q	2819	:   CSGVRQCAVVAGADPQAPERKRLVGYYLPEPGAAVDEADLFAALRAQLMPSMVPSLLVRL 2878
ò	137	136
q	2879	DRPLPMTITGKLDVDALPSADFSPKRAAYAAPRDRVEARLCHLWSAQLPGGTVGIDDDFF 2938
ò	137	136
qq	2939	RCGGDSISALHLASQVQREIERKVSVKYLFDHPTVRSFVDNVLSGLAESSGDDEPEQGRL 2998
ò	137	136
đ	2999	TGECPMLPIQEWFFAKPLADRHRWNHNFAIRTPPLDPGELRTALDRLVEHHDAFRLRFPE 3058
ò	137	136
qq	3059	SGGEVYAEDAAPITLHELDVRGLADADLRQRLVDWQRTFDLANGPTACAAYLHGFDDGTA 3118
ò	137	136
qq	3119	RVWFALHHLVVDTVSWHILAQDLEILYNGGDLGAKTGSYRQWAQAVRDYTPAEGEREFWA 3178
ò	137	TEDTGF 142

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SUCUENCE TROUGH NO. 6.

RA Adama M.D. (Celliker S.E. I. 19 PW. Hoskins R.A., Galle R.F.,
Adama M.D. (Celliker S.E. I. 19 PW. Hoskins R.A., Galle R.F.,
Adama M.D. (Celliker S.E. I. 19 PW. Hoskins R.A., Galle R.F.,
RA Adama M.D. (Celliker S.E. I. 19 PW. Hoskins R.A., Galle R.F.,
RA George R.A., Island S.E., Yandell M.D., Zhang G., Chen Lix,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Bandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Bens A., Bankendale J., Bayrakersoglu L., Beaslay E.M.,
RA Ballew R.M., Gange P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadteu E., Cener A., Chandra I.,
RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ra Beson K.Y., Bens P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Buttis K.C., Busam D.A., Deng Z., Mays A.D., Dew II., Dietz S.M.,
Ra Belos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,
RA Grerry J.M., Cawley S., Dalike C., Davenson M. Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Alalali M., Kalush F., Karpen G.H., Wei Z., Gunn P., Harris M.,
Alalali M., Kalush F., Karpen G.H., Wei M., Neison D.L.,
RA Harris N.L., Martel B.E., Kodira C.D., Kraff C., Kraff C., Kraff C., Kraff C., Scheler F., Shen H.,
RA Merkulov G., Milshina N.V., Mobaryy C., Moriso J., Monster D.,
RA Merkulov G., Milshina N.V., Mobaryy C., Morris J., Monster D.,
RA Reinert K., Remington K.A., Nobaryy C., Morris J., Wang X.,
Ra Reinert K., Remington K., Sunders E., Spredling A.C., Stepleton M., Stups M., Wang X.,
Ranger E., Spredling A.C., Stepleton M., Stups M., Wang X.,
Ranger E., Spredling A.C., Stepleton M., Stups M., Wang X.,
Ranger S., Wender E., Strong R.M., Worley K.C., Wu D., Yang S., Zhon X.,
Ranger S., Wenger E., Strong F.N., Zhong M., Zhong X., Zhon X., Smith H.C.,
Rheng R.M., Whyer E.M., Rheimer E.M., Rheng R.M., Rheime S.M., Worley B.C., Steplet
3179 ETTRDMESAELLAQTEGTTRRREEFALTAPDTRTLLAESPWAYDTEVNDLLLTATGFALR 3238
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Panorustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92069752; PubMed=1959133;
Mahoney P.A., Weber U., Onofrechuk P., Biessmann H., Bryant P.J.,
Goodman C.S.,
"The fat tumor suppressor gene in Drosophila encodes a novel member
of the cadherin gene superfamily.";
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P33456; Q9VQXS;
D1-FBE-1994 (Rel. 28, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin-related tumor suppressor precursor (Fat protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERMIT PROVOCAS; CACHETIN; 34.

PERMIT PROVOCAS; CACHETIN; 34.

PRINTS; PRO0205; CADHERIN.

PRINTS; PRO0205; CADHERIN.

PROSTES; PSO0232; CADHERIN.

PROSTES; PSO0022; EGF 1.

PROSTE; PSO0022; EGF 1.

PROSTE; PSO0022; EGF 1.

PROSTE; PSO0025; LAMG DOWAIN, 2.

PROSTE; PSO0025; LAMG DOWAIN, 2.

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REQUIRED FOR CORRECT MORPHOGENESIS
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CYTOPLASNIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                         -i- SIMILARITY: CONTAINS 34 CADHERIN DOMAINS.
-i- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
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FlyBase, FBgn0001075, ft.
InterPro, IPR002126, Cadherin.
InterPro, IPR000561, EGF-like.
InterPro, IPR000742, EGF 2.
InterPro, IPR001791, Laminin_G.
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EMBL; AE003577; AAF51036.1;
PIR; A41087; IJFFTM.
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QQ	2418	LNSQVRYFLKEGDSDLFRINASSGDIALLKPLDREQOSEYTLTLVAMDTGSPPLTGTGIV 2477
ò	33	NINIGAELL 51
g	2478	RVEVQDINDNDPVFELQSYHATVRENLPSGTHVLTPRATDKDEGLNAKLKFNLLGEHMHR 2537
ò	52	57
තු	2538	FHIDSETGEISTATTLDREETSVYHLTLMAQDSSITEPRASSVNLTISVSDVNDNIPKFD 2597
ò	58	
g	2598	STTYNVAVPERISKGEFVFGARALDLDDGENAVVHYTISGRDQHYFDINTKTGVVSTKLE 2657
ò	28	64
g	2658	LKTKTKSHDDLTYTIVISAMDQGEQSLSSKAELTVILRPPELFPTFAYMANSHFAMSEDV 2717
ò	65	99 94
g	2718	RPGKMITKVSATSPKKGLVGKIRYAIAGGIMGDSLRVDPNSGLLSVGQDGLDYELTHLYE 2777
ò	65	99 94
g	2778	IWIEAADGDTPSLRSVTLITLNVTDANDNAPVMEQLIYNAEVLEEESPPQLIAVVKASDR 2837
ò	65	67GAP 67
g	2838	DSGDNGNVIYRLQNDFDGTFEITESGEIYTRMRLDREEIGDYAFVVEAVDQĞVPHMTGTA 2897
ò	68	76
g	2898	SVLLHLLDKNDNPPKFTRLFSLNVTENAEIGSFVIRVTSSDLDLGANANASYSFSENPGE 2957
ò	77	92
q	2958	KFRIEPQSGNITVAGHLDREQQDEYILKVVASDGAMRAETPITITIQDQNDNAPEFEHSF 3017
ò	77	94
q	3018	YSFSPPELQOSIALVGQIIATDRDKQGPNSVISYSLQOPSPMFSIDPATGEVFSKKAVRF 3077
ò	77	18 81
g	3078	KHSQYVRSPENMYALTVLATDNGKPPLYSECLVNINIVDAHNNPPKFEQAEYLAPLPQDA 3137
ò	82	89 GMSQTINP 89
qq	3138	VRGQRIVRVHANDKQDLGTNEMDYSLMTFNLSSIFSVGRHDGWITLVKPIQVPPNTRYEL 3197
ò	90	EDD 92
q	3198	VVRATDRGVPPQSDETRVVIVVTGENMDTPRFSVNSYQVIVPENEPVGSTILTVGATDDD 3257
ò	93	TDPG96
g	3258	 TGPNGMLRYSISGGNERQDFSVDERTGGIVIQQQLDYDLIQEYHLNITVQDLGYHPLSSV 3317
ઠે	97	96
qq	3318	AMLTIILTDVNDNPPVFNHKEYHCYIPENKPVGTFVFQAHAADKDSPKNAIIHYAFLPSG 3377
ò	97	96
g	3378	PDRHFFIMNQSNGTISSAVSFDYEERRIYTLQIKAKNPDSSMESYANLYVHVLGVNEFYP 3437
ò	97	HADLVLY 103
g	3438	QFLQPVFHFDVSETSAVGTRVGAVQATDKDSGEDGRVYYLLVGSSNDKGFRIDTNTGLIY 3497
ò	104	1TR
QQ	3498	:   VARHLDRETONRVVLTVMAKNYGSIRGNDTDEAQVIISIQDGNDPPEFIKHYYTSTISEA 3557

137	4	DY 13/	75.	12.4 SDIDIVYHYKGYREAAGLRKYKASVPPVSAYTHHKHONSGSOOOOOHRHTAPFVTRNOG	137	4	Qy 137 136	Db 4878 GKDVHSNSERSLNSPVMSQLSGQSSSASRQKPGVPQQQAQQTSMGLTAEEIERLNGRPRT 4937	137	DB 4938 CSLISTLDAVSSUSEAFRYSSSALHMSLGGDVDAHSUSISTDBSGRUGSTICUSELEIDUNGL 1997	4	Oy 144	:   NASDDDIANHLSGIYRKANGAASPSATTLGWEYLLNWGPSYENLMGV 5105				01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34,	15-JUN-2002 (Rel. 41, Last annotatic	protein 1).	Homo sapiens (Human). Eukarvota: Metazoa; Chordata; Craniata; Vertebrata;	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NELTAXID=9606;	RN L1. RP SEQUENCE FROM N.A. PX MPDI.IND=95724638: PubMed=7736581:	Gluecksmann-Kuis M.A., Tayber O., Woolf E.A., Bov Deng N., Alperin G.D., Iris F., Hawkins F., Munro	Duyk G., Schneider M.C., Geng L., Zhang F., Zhao Z., Iorobian Reeders S.T., Bork P., Pohlschmidt M., Loehning C., Kraus B.,	KA NOWICKS U., Leung A.L.S., Filachaul A.T., K RT "Polycystic kidney disease: the complete structure of the PKD1 gene DT and its notesin".	Cell		Ward C.J., Peral B., Hugh			den Ouweland A.M.W., Eussen B.,		RT Polycystic Kidney Disease Consortium."; RL Cell 77:881-894(1994).
00 107	Db 3558 APVGTKVTTVKAIDKDVRTQNNQFSYSIINGNLKQSFKIDVQTGEISTASRLDREETSTY 3617	Qy 107 106	Db 3618 NLVIGAIDTGLPPQTGSATVHIELEDVNDNGPTFTPEGLNGYISENEPAGTSIMTLIASD 3677	Oy 107 111	Db 3678 PDLPRNGGPFTYQLIGGKHKSWLSVDRNSGVVRSTTSFDREMTPILEAIIEVEDSGKPKQ 3737	0y 112 111	3738 KSQHLLTITVLDQNDNPSTTRSLHTAVSLFNGDLPSNVKLADVRPNDIDIVGDYRCRLQK	112		Db 3858 SVSIMVRNMTAXHFLANHYRPILEMIKSRMSNEDEVILYSLLEGGSGNSTNLQLLMAVRL 3917	Qy 112 111	Db 3918 AKTSYQQPKYLIERLREKRSAFSELLQKEVIVGYEPCSEPDVCENGGVCSATWRLLDAHS 3977	gy 112 111	Db 3978 FVIQDSPALVLSGPRVVHDYSCQCTSGFSGEQCSRRQDPCLPNPCHSQVQCRRLGSDFQC 4037	Oy 112 114	Db 4038 MCPANRDGKHCEKERSDVCYSKPCRNGGSCQRSPDGSSYFCLCRPGFRGNQCESVSDSCR 4097	Qy 115 114	Db 4098 PNPCLHGGLCVSLKPGYKCNCTPGRYGRHCERFSYGFQPLSYMTFPALDVTTNDISIVFA 4157	Oy 115 114	Db 4158 TTKPNSLLLYNYGMQSGGRSDFLAIELVHGRAYFSSGGARTAISTVIAGRNLADGGWHKV 4217	115NRQVRGVT	DD 4218 TATRNGRVMSLSVAKCADSGDVCTECEFGDSSCrADEVGFVGFLNFNRQFLMTGGLSSAD 42//	PILERPGQVHSDDLVGCLHSVHIGGRALNLSLPLQQKGILAGCNRQACQPALAAERCGGF	Qy 132	Db 4338 AGQCIDRWSSSLCQCGGHLQSPDCSDSLEPITLGEGAFVEFRISEIYRRMQLLDNLYNSK 4397	Qy 134 133	Db 4398 SAWLDNQQMRERRAVSNFSTASQIYEAPKMLSMLFRTYKDQGQILYAATNQMFTSLSLRE 4457	Qy 134 133	Db 4458 GRLVYYSKQHLTINMTVQETSTLNDGKWHNVSLFSESRSLRLIVDGRQVGDELDIAGVHD 4517	Qy 134	Db 4518 FLDPYLTILNVGGEAFVGCLANVTVNNELQPLNGSGSIFPEVRYHGKIESGCRGDIGQDA 4577	Qy 137 136	Db 4578 AQVADPLSIGFTLVIVFFVILVVAILGSYVIYRFRGKQEKIGSLSCGVPGFKIKHPGGPV 4637

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STRUCTURE BY NMR OF 275-354
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q	803 GNGVSRHNLSCSFDVVSP	VAGLRVIYPAPRDGRLYVPTNGSALVLQVDSGANATATARWP 8	862
ò	. 45SLGAQFR	S SHIDVKMV S	28
qq	863 GGSLSARFENVCPALVAT	FVPACPWETNDTLFSVVALPWLSEGEHVVDVVVENSASRANL 9	922
ò		5	58
qq	923 SLRVTAEEPICGLRATPSP	EARVLOGVLVRYSPVVEAGSDMVFRWTINDKQSLTFQNVVF 9	982
ò			28
g	983 NVIYQSAAVFKLSLTA	SNHVSNVTVNYNVTVERMNRMQGLQVSTVPAVLSPNATLALTAG 1	1042
ò	65	5	28
g	1043 VLVDSAVEVAFLWTFGDGE	QALHQFQPPYNESFPVPDPSVAQVLVEHNVTHTYAAPGEYL 1	1102
ò		5	28
පු	1103 LTVLASNAFENLTQQVPVSVRASL	PSVAVGVSDGVLVAGRPVTFYPHPLPSPGGVLYTWD	1162
ò	65		28
g	1163 FGDGSPVLTQSQPAANHTY	ASRGTYHVRLEVNNTVSGAAAQADVRVFEELRGLSVDMSLA 1	1222
ò	65		64
qq	1223 VEQGAPVVVSAAVQTGDNI	TWTFDMGDGTVLSGPEATVEHVYLRAQNCTVTVGAGSPAGH 1	1282
ò		9 45-	99
Q	1283 LARSLHVLVFVLEVLRVEP	AACIPTQPDARLTAYVTGNPAHYLFDWTFGDGSSNTTVRGC 1	1342
ò	67 PNITANLTSS	8LLSVC	81
g	:        1343 PTVTHNFTRSGTFPLALVL	:    SSRVNRAHYFTSICVEPEVGNVTLQPERQFVQLGDEAWLVA	1402
ò	82		81
QQ	1403 CAWPPFPYRYTWDFGTEEAA	PTRARGPEVTF1YRDPGSYLVTVTASNN1SAANDSALVEV	1462
ò	82		81
q	1463 QEPVLVTSIKVNGSLGLELQQPYL	FSAVGRGRPASYLWDLGDGGWLEGPEVTHAYNSTGD	1522
ò	82GW	8	87
qq	1523 FTVRVAGWNEVSR	SEAWLNVTVKRRVRGLVVNASRTVVPLNGSVSFSTSLEAGSDVRYSW 1	1582
ò	88		87
qq	1583 VLCDRCTPIPGGPTISYTFR	SVGTFNIIVTAENEVGSAQDSIFVYVLQLIEGLQVVGGGR 1	1642
ò	88	8	87
g	1643	YFPTNHTVQLQAVVRDGTNVSYSWTAWRDRGPALAGSGKGFSLTVLEAGTYHVQLRATNM 1	1702
ò	88	6	87
q	1703	LGSAWADCTMDFVEPVGWLMVAASPNPAAVNTSVTLSAELAGGSGVVYTWSLEEGLSWET 1	1762
ò	88		87
QQ	1763 SEPFTTHSFPTPGLHLVTMTAGN	PLGSANATVEVDVQVPVSGLSIRASEPGGSFVAAGSS	1822
ò	88	00	87
q	1823	VPFWGQLATGTNVSWCWAVPGGSSKRGPHVTMVFPDAGTFSIRLNASNAVSWVSATYNLT 1	1882
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q	 1883 AEEPIVGLVLWASSKVVAPGQLVHFQILLAAGSAVTFRLQVGGANPEVLPGPRFSHSFPR 1942	<u>ස</u>	2963 IRPESLQGADHRPYTFFIS
ò	91 91	ò	134
g	1943 VGDHVVSVRGKNHVSWAQAQVRIVVLEAVSGLQVPNCCEPGIATGTERNFTARVQRGSRV 2002	අධ	3023 MVWRTEGLLPLEETSPRQAV
ò	91 90	ò 1	
g	2003 AYAWYFSLQKVQGDSLVILSGRDVTYTPVAAGLLEIQVRAFNALGSENRTLVLEVQDAVQ 2062	<b>α</b> Ω	3083 VCLVTYMVMAAILHKLDQLI
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дg	2243 QSIQANVTVAPERLVPIIEGGSYRVWSDTRDLVLDGSESYDPNLEDGDGTPLSFHWACVA 2302	3 (	
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q	2483 AVHALTTKVHFECTGWHDAEDAGAPLVYALLLRRCRQGHCEEFCVYKGSLSSYGAVLPPG 2542	3 8	מביים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים שניים
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a	2543 FRPHFEVGLAVVVQDQLGAAVVALNRSLAITLPEPNGSATGLTVWLHGLTASVLPGLLRQ 2602	g ;	3623 hPDEDDIEVESFAVIFVSAN
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g	2663 QIAAALAQCMGPSRELVCRSCLKQTLHKLEAMMLILQAETTAGTVTPTAIGDSILNITGD 2722	යි .	3743 ELGPPRLRQVRLQEALYPDF
ò	132 131	ò	
임	2723 LIHLASSDVRAPQPSELGAESPSRMVASQAYNLTSALMRILMRSRVLNEEPLTLAGEEIV 2782	යි .	3803 LGAWSWGSCAVYDSGGYVQE
ò	132 131	ò :	
g	2783 AQGKRSDPRSLLCYGGAPGPGCHFSIPEAFSGALANLSDVVQLIFLVDSNPFPFGYISNY 2842	8	3863 LHAAVTLRLEFPAAGRALAA
ò	132 131	δ :	
g	2843 TVSTKVASMAFQTQAGAQIPIERLASERAITVKVPNNSDWAARGHRSSANSANSVVVQPQ 2902	a a	3923 HREGRWRVLRLGAWARWLLN
ò	132 131	S 8	44111111111111111111111111111111111111
g G	2903 ASVGAVVTLDSSNPAAGLHLQLNYTLLDGHYLSEEPEPYLAVYLHSEPRPNEHNCSASRR 2962	3	
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AVCLTRHLTAFGASLFVPPSHVRFVFPEPTADVNYIVMLTCA 3082 HRNSLDIFRIATPHSLGSVWKIRVWHDNKGLSPAWFLQHVIV 3202 ATCCVLLICLFLGANAVWYGAVGDSAYSTGHVSRLSPLSVDT 3322 DPPGPRVHTCSAAGGFSTSDYDVGWESPHNGSGTWAYSAPDL 3802 LDASRGRAIPFCGQRGRFKYEILVKTGWGRGSGTTAHVGIML 3142 VETEANGGLVEKEVLAASDAALLRFRRLLVAELQRGFFDKHI 3262 LFLFRMSRSKVAGSPSPTPAGQQVLDIDSCLDSSVLDSSFLT 3382 FLDDSKSLVCWPSGEGTLSWPDLLSDPSIVGSNLRQLARGQA 3442 PAKSFSASDEDLIQQVLAEGVSSPAPTQDTHMETDLLSSLSS 3502 PPSPGLNWEQPQAARLSRTGLVEGLRKRLLPAWCASLAHGLS 3562 PPGVSVAWILSSSASFLASFLGWEPLKVLLEALYFSLVAKRL 3622 JOSAIKQELHSRAFLAITRSEELWPWMAHVLLPYVHGNQSSP 3742 DELGLSLEESRDRLRFLOLHNWLDNRSRAVFLELTRYSPAVG 3862 AALSVRPFALRRLSAGLSLPLLTSVCLLLFAVHFAVAEARTW 3922 JVALTAATALVRLAQLGAADRQWTRFVRGRPRRFTSFDQVAH 3982 ARVPRVRPPHGFALFLAKEEARKVKRLHGMLRSLLVYMLFLL 3682 SPGSRDPAGSYHLNLSSHFRWSALQVSVGLYTSLCQYFSEED 3022 137 KAAQHVRFVRQMSVFGKTLCRALPELLGVTL 4031

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                                                                                                                                                                                                    TISSUE-Lymphocyces;

MEDLINE-96163873; PubMed=856420;

MEDLINE-96163873; PubMed=856420;

A Da S. M., Zhao Q. Beverley P.C.L., Owen M.J.;

T "Molecular cloning and tissue expression of FAT, the human homologue of the Drosophila fat gene that is located on chromosome 4q34-q35 and tencodes a putative adhesion molecule.";

T encodes a putative adhesion molecule.";

T encodes a putative adhesion procession PROTEIN.

- PUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.

- I SUBCELLULAR LOCATION: Type I membrane procein (By similarity).

- TISSUE SPECIFICITY: EXPRESSED IN MANY EPITHELIAL AND SOME

ENDOTHELIAL AND SMOOTH MUSCLE CELLS.

- SIMILARITY: CONTAINS 5 GG-LIKE DOMAINS.

- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR Genew; #GNGC:3595; FAT.

DR Genew; #GNC:3595; FAT.

DR InterPro; IPR00152; Asx hydroxyl.

DR InterPro; IPR001246; Gadherin.

DR InterPro; IPR001246; Gadherin.

DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR001791; Laminin_G.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF00008; EGF-1ike.

DR Pfam; PF000126; Cadherin.

DR SWART; SM00119; EGF-CA;

DR SWART; SM00119; EGF-CA;

DR SWART; SM0011; EGF-CA;

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DR SWART; SM00116; EGF-CA;

DR SWART; SM00116; EGF-CA;

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DR SWART; SM001186; E
                                                                                                                  Homo sapiens (Human).
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin-related tumor suppressor homolog precursor (Fat protein
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CADHERIN-RELATED TUMOR SUPPRESSOR
HOMOLOG.
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CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
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HSSP; P01132; 1EGF.
STANDARD;
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2.1%; Pred. No. 67;
ive 23; Mismatches 36; Indels 4137;
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qq	476 VPIGTTIMSLSAVDPDEGENGYVTYSIANLNHVPFAIDHFTGAVSTSENLDYELMPRVYT 535	ò	43
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අ	536 LRIRASDWGLPYRREVEVLATITLNNLNDNTPLFEKINCEGTIPRDLGVGEQITTVSAID 595	ò	49
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අ	596 ADELQLVQYQIEAGNELDLFSLNPNSGVLSLKRSLMDGLGAKVSFHSLRITATDGENFAT 655	2 3	0 0
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3 8	בחור של הייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני בייני ביינ	ò	16
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8	.CYVEVEVVDVNENLHPPVFSSFVEKGTVKEDAPVGSLVMTVSAHDEDAGRDGEIRYSIRD	ò	16
ò	TERYVLT32	q	2156
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qq	1496 8	SRDPLSLKKFRLDPATGSLYTSEKLDHEAVSPAHLTVMVRÖQDVPVKRNFARIVVNVSDT 1555
ò	35	NIGABLLR 42
q	1556 1	NDHAPWFTASSYKGRVYESAAVGSVVLQVTALDKDKGKNAEVLYSIESGNIGNIGNSFWI 1615
ò	43	DPSLGA
q	1616	: DPVLGSIKTAKELDRSNQAEYDLMVKATDKGSPPMSEITSVRIFVTIADNASPKFTSKEY 1675
ò	49	48
q	1676	SVELSETVSIGSFVGMVTAHSQSSVVYEIKDGNTGDAFDINPHSGTIITQKALDFETLPI 1735
ò	4.9	
g	1736 1	YTLIIQGTNMAGLSTNTTVLVHLQDENDNAPVFMQAEYTGLISESASINSVVLTDRNVPL 1795
ò	. 62	EP
qq	1796 1	VIRAADADKDSNALLVYHIVEPSVHTYFAIDSSTGAIHTVLSLDYEETSIFHFTVQVHDM 1855
ò	. 49	BGAPNIT 70
q	1856 (	GTPRLFAEYAANVTVHVIDINDCPPVFAKPLYEASLLLPTYKGVKVITVNATDADSSAFS 1915
ò	71	75 ANLTS 75
g	1916 (	QLIYSITEGNIGEKFSMDYKTGALTVQNTTQLRSRYELTVRASDGRFAGLTSVKINVKES 1975
ò	- 94	75
QQ	1976	KESHLKFTQDVYSAVVKENSTEAETLAVITAIGSPINEPLFYHILNPDRRFKISRTSGVL 2035
ò	. 94	
g	2036	STTGTPFDREQQEAFDVVVEVIEEHKPSAVAHVVVKVIVEDQNDNAPVFVNLPYYAVVKV 2095
ò	- 94	75
qq	2096	DTEVGHVIRYVTAVDRDSGRNGEVHYYLKEHHEHPQIGPLGEISLKKQFELDTLNKEYLV 2155
ò	- 9/	75
g	2156 1	TVVAKDGGNPAFSAEVIVPITVMNKAMPVFEKPFYSAEIAESIQVHSPVVHVQANSPEGL 2215
ò	- 92	15
q	2216	KVFYSITDGDPFSQFTINFNTGVINVIAPLDFEAHPAYKLSIRATDSLTGAHAEVFVDII 2275
ò	. 94	15
q	2276 \	VDDINDNPPVFAQQSYAVTLSEASVIGTSVVQVRATDSDSEPNRGISYQMFGNHSKSHDH 2335
ò	. 94	15
. 염	2336	FHVDSSTGLISLLRTLDYEQSRQHTIFVRAVDGGMPTLSSDVIVTVDVTDLNGNPPLFEQ 2395
ò	. 94	75
qq	2396 (	QIYEARISEHAPHGHFVTCVKAYDADSSDIDKLQYSILSGNDHKHFVIDSATGIITLSNL 2455
ò	. 94	15
OD	2456 1	HRHALKPPYSLNLSVSDGVPRSSTQVHVTVIGGNLHSPAPLQNBYEVELAENAPLHTLVM 2515
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q	2516 E	EVKTTDGDSGIYGHVTYHIVNDFAKDRFYINERGQIFTLEKLDRETPAEKVISVRLMAKD 2575
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۵	2576	AGGKVAFCTVNVILTDDNDNAPQFRATKYEVNIGSSAAKGTSVVKSASDADEGSNADITY	2635
_	16		75
	2636	AI EADSESVKENLEINKLSGVITTKESLIGLENEFFTFVRAVDNGSPSKESVVLVYVKI	2695
٠ _	76		75
0	2696	LPPEMQLPKFSEPFYTFTVSEDVPVGTEIDLIRAEHSGTVLYSLVKGNTPESNRDESFVI	2755
_	16	STTSNC	81
0	2756	DRQSGRLKLEKSLDHETTKWYQFS1LARCTQDDHEMVASVDVS1QVKDANDNSPVFESSP	2815
_	83	MD -	83
0	2816	YEAFIVENLPGGSRVIQIRASDADSGTNGQVMYSLDQSQSVEVIESFAINMETGMITTLK	2875
_	84		83
0	2876	ELDHEKRDNYQIKVVASDHGEKIQLSSTAIVDVTVTDVNDSPPRFTAEIYKGTVSEDDPQ	2935
`	84	SOTIN	. 88
0	2936	GGVIAILSTTDADSEEINRQVTYFITGGDPLGQFAVETIQNEWKVYVKKPLDREKRDNYL	2995
>-	89	CERT	91
Ω	2996	LTITATDGTFSSKAIVEVKVLDANDNSPVCEKTLYSDTIPEDVLPGKLIMQISATDADIR	3055
>-	92		91
۵	3056	SNAEITYTLLGSGAEKFKLNPDTGELKTSTPLDREEQAVYHLLVRATDGGGRFCQASIVV	3115
>-	92	DTDPG	96
Ω	3116	TLEDVNDNAPEFSADPYAITVFE	3175
>-	97		96
۵	3176	INELSGIIQLEKPLDRELQAVYTLSLKAVDQGLPRRLTATGTVIVSVLDINDNPPVFEYR	3235
>-	97		96
Ω	3236	EYGATVSEDILVGTEVLQVYAASRDIEANAEITYSIISGNEHGKFSIDSKTGAVFIIENL	3295
>	97		96
Ω	3296	DYESSHEYYLTVEATDGGTPSLSDVATVNVNVTDINDNTPVFSQDTYTTVISEDAVLEOS	3355
>	97		96
Д	3356	VITVMADDADGPSNSHIHYSIIDGNQGSSFTIDPVRGEVKVTKLLDRETISGYTLTVQAS	3415
>-	97		96
Д	3416	DNGSPPRVNTTTVNIDVSDVNDNAPVFSRGNYSVIIQENKPVGFSVLQLVVTDEDSSHNG	3475
>-	97		96
Q	3476	PPFFFTIVTGNDEKAFEVNPQGVLLTSSAIKRKEKDHYLLQVKVADNGKPQLSSLTYIDI	3535
>	97		96
Д	3536	RVIEESIYPPAILPLEIFITSSGEEYSGGVIGKIHATDQDVYDTLTYSLDPQMDNLFSVS	3595
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ā	3596	STGGKLIAHKKLDIGQYLLNVSVTDGKFTTVADITVHIRQVTQEMLNHTIAIRFANLTPE	3655
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4496 YPLDMSEPQTKGTGENSTCREPHAPYPPGYQRHFEAPAVESMPMSVYASTASCSDVSACC 4555
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                                                                                     3716 KINSSVIDIEEIIGVRILNVFQKLCAGLDCPWKFCDEKVSVDESVMSTHSTARLSFVTPR 3775
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3656 EFVGDYWRNFQRALRNILGVRRNDIQIVSLQSSEPHPHLDVLLFVEKPGSAQISTKQLLH 3715
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COMPUTER: TOWN COMPUTER: COMPUTER: COMPUTER: STEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 201 503 8474

TELEFAN: 201 503 8807

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15-281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 264; DB 2; 0.8%; Pred. No. 0.013;
APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Kurt
APPLICANT: Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827706artis Corporation
STREET: 59 Route 10
CITY: Bast Hanover
STRIE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                              US-09-413-814-80
US-08-896-449A-2
US-09-132-652-2
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ATCC 34921
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Patent No. 5827706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     44655
44655
46655
33665
337112
8998
8988
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                                                                                                                                                                                                                                             4472
3072
3079
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Best Local Similarity
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2, Appli
                                                                                                                         March 20, 2003, 12:36:42; Search time 15 Seconds (without alignments) 290.306 Million cell updates/sec
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                                                                                                                                                                                                       SEQID_1_1SFUSED
773
1 AAGGILHLELLVAVGPDVFO......SPTWSCLITEDTGFDLGVTI 148
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Sequence 8,
Sequence 6,
Sequence 13,
Sequence 13,
Sequence 315s
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-36-364A-7
US-09-105-537-6
US-09-315-917-6
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US-09-310-918-9-5
US-09-568-412-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Match I
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Perfect score:
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Matches 1 2098	102; Conservative 24; Mismatches 21; Indels 12475; G AGGIL
	TOTAL THE MESCAGUES I TOLEFOUSANOFUNKAAQTFPQLEGKAQVHVGT 2157
2158 AMDT(	AMDTGRLSALSPDLIVINSVAQYFPSREYLAEVVEALVRIPGVRRIFFGDMRTYATHKDF 2217
2218 LVAR# 12	
	KVNNELSSYRYGAVLHIRNHNONOSRSIHKINAFGWIDFAGGOMMOTATATATATATATATATATATATATATATATATATA
12	13.7
2338 SIAV	
:	
2398 QLAEI	OLAEDAGFRVEVSWARQRSONGALDVFFHHFQPTENESRALVDFPTDYKGQQARSLTNRP 2457
	11
2458 LORV	LORVESRRIEAQVREOLGVLLPAYMIPARIVVLQNMPLNTSGKVDRKELTLRAKVTAART 2517
-	
PSSE	PSSELVAPRDSIEAIICKEFKDVLGVEVGITDNFFNVGGHSLLATKLAARLSRQLNAQIA 2577
:	
2578 VKDI	VKDIFDRPVIADLAATIQQDTTEHNPILPTSYTGPVEQSFAQGRLWFLDQLNVGATWYLM 2637
-	11
PFAV	PFAVRLRGPLVVSALAAALLALEERHETLRTTFIEQEGIGMQVIHPFAPKELRVIDVSGE 2697
i	11
EEST	EESTIQKILEKEQTTPFNLASEPGFRLALLKTGEDEHILSTVMHHAISDGWSVDIFQQEI 2757
GQFYS	GQFYSAILRGHDPLAQIAPLSIQYRDFATWQRQIFQVAEHRRQLAYWTKQLADNKPAELL 2817
	11
TDFK	TDFKRPPMLSGRAGEIPVVVDGLIYEKLQDFCRIRQVTAFTVLLAAFRAAHYRMTGTEDA 2877
:	
rigr	TIGTPIANRNRPELEGLIGFFVNTQCMRITVDVEDSFETLVHQVRETTLAAHANQDVPFE 2937
:	
JIVS	QIVSNILPGSSDTSRNPLVQLMFALHSQQNLGKVRLEGIEEEIISIAETTRFDIEFHLYO 2997
:	
SAERL	EAERLNGSIVYAADLFVPETIQSVITIFQGILQKGLGEPDMPVASMALDGGLESLRSTG: 3057
:	
оди	DESTRLSYADLDRKSDQVACWLSRRGIA
:	
ETFV!	PETFVAILAPRSCETIVAILGVLKANLAYLPLDVNVPASRLEAILSEVSGSMLVLVGAET 3177

ò	19	
g	3178	PIPEGMAEAETIRITEILADAKTDDINGLAASOPTAASLAYVIFTSGSTGRPKGVMVEHR 3237
ò	19	
ద	3238	GIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLLESTAL 3297
ò	19	18
셤	3298	EKVFFDQRVNVALLPPALLKQCLDNSPALVKTLSVLYIGGDRLDASDAAKARGLVQTQAF 3357
ò	19	18
g	3358	NAYGPTENTVMSTIYPIAEDPFINGVPIGHAVSNSGAFVMDQNQQITPPGAMGELIVTGD 3417
ò	19	
g	3418	GLARGYTTSSLNTGRFINVDIDGEQVRAYRTGDRVRYRPKDLQIEFFGRIDHQVKIRGHR 3477
ò	19	18
셤	3478	IEPAEVEYALLSHDLVTDAAVVTHSQENQDLEMVGFVAARVADVREDESSNOVGEWQTHF 3537
ò	19	18
g	3538	DSIAYADITTIDQQSLGRDFMSWTSMYDGSLIKKSQMQEWLDDTWRSLLDSQPPGHVLEV 3597
δ	19	18
g	3598 (	GTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGLEDRIRVEVGTATDIDRL 3657
ò	13	18
q	3658 (	GDDLHAGLVVVNSVAQYFPSQDYLAQLVRDLTKVPGVERIFFGDMRSHAINRDFLVARAV 3717
ò	19	18
a a	3718	HALGDKATKAEIQREVVRMEESEDELLVDPAFFTSLTTQVENIKHVEILPKRMRATNELS 3777
ò	19	18
a a	3778 \$	SYRYAAVLHVNDLAKPAHKVSPGAWVDFAATKMDRDALIRLLRGTKISDHIAIANIPNSK 3837
ò	19 -	18
g	3838 T	TIVERTICESVYDLGGDAKDSNDRVSWLSAARSNAVKVASLSAIDLVDIAQEAGFRVEIS 3897
ò	19 -	18
g	3898 0	CARQWSQNGALDAVFHHLGPSPQSSHVLIDFLTDHQGRPEEALTNHPLHRAQSRRVERQI 3957
ò	19 -	18
g	3958 R	RERLOTLLPAYMIPAQIMVLDKLPLNANGKVDRKQLTQRAQTVPKAKQVSAPVAPRTEIE 4017
ò	19 -	18
QQ	4018 R	RVLCQEFSDVLGVDIGIMENFFDLGGHSLMATKLAARISRRLETHVSVKEIFDHPRVCDL 4077
ò	19 -	18
g	4078 V	VLIVQQGSAPHDPIVSTKYTGPVPQSFAQGRLWFLDQLNFGATWYLMPLAVRLRGAMNVH 4137
ò	19	18
e G	4138 AI	ALTAALLALERRHELLRTTFYEQNGVGMQKVNPVVTETLRIIDLSNGDGDYLPTLKKEQT 4197
ò	19 -	18
d G	4198 AF	APFHLETEPGWRVALLRLGPGDYILSVVMHHIISDGWSVDVLFQELGQFYSTAVKGHDPL 4257

ò	19	18	
Q	4258	SQTTPLPIHYRDFALWQKKPTQESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGQAG 4317	
ò	19	18	
Q	4318	EMSVTIEGALYKNLEEFCRVHRVTSFVVLLAALRAAHYRLTGSEDATIGTPIANRNRPEL 4377	
ò	19	18	
Q	4378	EQIIGFFVNTQCIRITVNEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDAS 4437	
ò	19	18	
g	4438	RNPLVQLMFAVHSQKNLGELKLENAHSEVVPTEITTRFDLEFHLFQQDDKLEGSILYSTD 4497	
ò	19	18	
g	4498	LFEAVSVQSLLSVFQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSV 4557	
ò	19		
g G	4558	VDVFHEQVSINPDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCE 4617	
ò	19	18	
Q	4618	TIIAFLGILKANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVP 4677	
ò	19	18	
g	4678	IRDTFTTLTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMVQHRNIVRLVKNSNVV 4737	
ò	19	23	
g	4738 7	: AKOPAAARIAHISNLAFDASSWEIYAPLLNGGAIVCADYFTTIDPQALQETFQEHERGA 4797	
ò	24	23	
g	4798 N	MLPPSLLKQCLVQAPDMISRLDILFAAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILS 4857	
ò	24 -		
g G	4858 T	TIYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDGLARGYMDPKL 4917	
δ	24 -	23	
g	4918 D	DADRFIQLTVNGSEQVRAYRTGDRVRYRPKDFQIEFFGRMDQQIKIRGHRIEPAEVEQAF 4977	
ò	24 -	23	
q	4978 L	LNDGFVEDVAIVIRTPENQEPEMVAFVTAKGDNSAREEEATTQIEGWEAHFEGGAYANIE 5037	
ò	24 -		
g	5038 E	EIESEALGYDFMGWTSMYDGTEIDKDEMREWLNDTWRSLLDGKPAGRVLEVGTGTGMIMF 5097	
ò	27 -	ERYV 30	
Op Op	N 8605	NLGRSQGLERYIGLEPAPSAAEFVNNAAKSFPGLAGRAEVHVGTAADVGTLQGLTSDMAV 5157	
ò	31 -	30	
g	5158 I	INSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAMNRDFAAARAAYSLADNASKD 5217	
ò	31 .	30	
В	5218 R	RVRQKMMELEEKEEELLLVDPAFFTALASQLQDRIQHVEILPKRMKATNELSSYRYAAVLH 5277	
ò	31 -	30	
οg	5278 I	ISDEPLPIYKIDPEAWINFEGSRLTREALAQVLKENENAESVAISNIPYSKTVVERHIVR 5337	
ò	31		

d D	5338	SLDQEDANAPEESMDGSDWISAVRTRAQQCHTLSASDLFDIAEDAGFRVEVSWARQHSQH	539
ò	31	NLT	33
С	5398	  GALDAVFHHLKPATEDSRVLIKFPTDHQGRPLKSLTNQPLLPAQSRRAELLIREGLQTLL	545
ò	34		33
qq	5458	PPYMIPSQITLIDRMPLNANGKVDRRELARRAKITQKSKPVEDIVPPRNSVEATVCKGFT	5517
ò	34		33
q	5518	DVLGVEVGITDNFFNLGGHSLMATKLAARLGROLNTRISVRDVFDQPVVADLAAVIORNS	5577
ò	34		38
QQ	5578	   APHEPIKPADYTGPVPQSFAQGRLWFLDQLNVGATWYLMPLGIRLHGSLRVDALATAISA	5637
ò	39		38
. <b>Q</b>	5638	LEQRHEPLRTTFHEEDGVGVQVVQDHRPKDLRIIDLSTQPKDAYLAVLKHEQTTLFDLAT	5697
ò	39		38
q	5698	EPGWRVALIRLGEEEHILSIVWHHIISDGWSVEVLFDEMHRFYSSALRQQDPWEQILPLP	5757
ò	39		38
ф	5758	IQYRDFAAWQKTEEQVAEHQRQLDYWTEHLADSTPAELLTDLPRPSILSGRANELPLTIE	5817
ò	39		38
qq	5818	GRLHDKLRAFCRVHQATPFVILLAALRAAHYRLTGAEDATLGTPIANRNRPELENMIGFF	5877
ò	39		38
qq	5878	VNTQCMRIALEENDNFESLVRRVRSTATSAFANQDVPFESIVSSLLPGSRDASRNPLVQV	5937
ò	39		38
đ	5938	ILAVHSQQDLGKLTLEGLRDEAVDSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLRTI	5997
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g	5998	ESVVSVFLETLRRALDQPLTPLAVLPLTDGVGEIASKGLLDVPRTDYPRDANIVEVFQQH	6057
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g	6058 \	VRATPDAIAVKDATSILTYAQLDQQSDRLAIWLSRRHMMPETLVGVLAPR <b>S</b> ÇETIIAMFG	6117
ò	39		38
qq	6118 1	IMKANLAYLPLDINSPAARLRSILSAVDGNKLVLLGSGVTAPEQENPEVEAVGIQEILAG	6177
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QQ	6238 A	AHLANIAFDASIWEIATTLLNGATLVCLDYHTVLDCRTLKEVPERESITVVTLMPALLKO (	6297
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Q Q	6298 C	CVAEIPETLAHLDLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTVISTIYEVDADE 6	6357
ò	39 -		38
q	6358 M	MFVŅGVPIGKTVSNSGAYVMDRNQQLVPSGVVGELVVTGDGLARGYTDPSLNKNRFIYIT 6	417
ò	39 -	8	8

ò	62	19
qq	7558	CPDSIAVKDSSSQLTYAQLDEQSDRVAAWLHERHMPAESLVGVLSPRSCETIIAYFGIMK
ò	62	9
a	7618	ANLAYLPLDVYAPDARLAAILDTVEGERLLLLGAGVPQPGIQIPRLSTAYIAEALSHATT
ò	. 62	
g	7678	-   -   -   -   -   -   -   -   -   -
ò	99	
ద	7738	FSNLAWDAATWEIYTAVLNGGTVVCIDRDTMLDIAALNSTFRKENVRAAFFTPAFLKQCL 7797
ò	99	73
q	7798	AETPELVANLEILHTAGDRLDPGDANLAGKTAKGGIFNVLGHTENTAYSTFYPVVGEETF 7857
ò	74	73
g	7858	VNGVPVGRGISNSHAYIIDRHQKLVPAGVMGELILTGDGVARGYTDSALNKDRFVYIDIN 7917
ò	74	
g	7918	GKSTWSYRTGDKARYRPRDGQLEFFGRMDQMVKIRGVRIEPGEVELTLLDHKSVLAATVV 1977
ò	74	. 82
g	7978	VRRPPNGDPEMIAFITIDAEDDVQTHKAIYKHLQGILPAYMIPSHLVILDQMPVTDNGKV 8037
ò	74	
മ്	8038	DRKDLALRAQTVQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEVGITDGFFDLGGHSLLA 8097
ò	74	73
දු	8098	TKLAARLSROLNTRVSVKDVFDQPILADLADIIRRGSHRHDPIPATPYTGPVEQSFAQGR 8157
ઠે	74	73
g	8158 I	LWFLEQLNLGASWYLMPFAIRWRGPLQTKALAVALNALVHRHEALRTTFEDHDGVGVQVI 8217
ò	74	
q	8218	QPKSSQDLRIIDLSDAVDDTAYLAALKREQTTAFDLTSEPGWRVSLLRLGDDDYILSIVM 8277
ò	74 -	73
q	8278 H	HHIISDGWTVDVLRQELGQFYSAAIRGQEPLSQAKSLPIQYRDFAVWQRQENQIKEQAKQ 8337
ે	74 -	73
g	8338 L	LKYWSQQLADSTPCEFLTDLPRPSILSGEADAVPMVIDGTVYQLLTDFCRTHQVTSFSVL 8397
ò	74 -	
g G	8398 1	LAAFRTAHYRLTGTLDATVGTPIANRNRPELEGLIGFFVNTQCMRMAISETETFESLVQQ 8457
à	74 -	73
QQ	8458 V	VRLTTTEAFANQDVPFEQIVSTLLPGSRDTSRNPLVQVMFALQSQQDLGRIQLEGMTDEA 8517
ò	74 -	73
q	8518 L	LETPLSTRLDLEVHLFQEVGKLSGSLLYSTDLFEVETIRGIVDVFLEILRRGLEQPKQRL 8577
ò	74 -	73
යු	8578 M	MAMPITDGITKLRDGGLLTVAKPAYPRESSVIDLFRQQVAAAPDAIAVWDSSSTLTYADL 8637

73	EA 8	:		73								73					DGLQKYVGLDPAPSAAIFVNEAVKS 9177	78	VAQYFPTSEYLIKVVKAVVEVPSVK 9237													100				
· · · · · · · · · · · · · · · · · · ·	B DGQSNKLAHWLCQRNMAPETLVAVFAPRSCLTIVAFLGVLKANLAYLPLDVNAPAARI	4	8 ILSAVPGHKLVLVQAHGPELGLTMADTELVQIDEALASSSSGDHEQIHASGPTATSLAYV		8 MFTSGSTGKPKGVMIDHRSIIRLVKNSDVVATLPTPVRMANVSNLAFDISVQEIYTALLN	·	3 GGTLVCLDYLTLLDSKILYNVFVEAQVNAAMFTPVLLKQCLGNMPAIISRLSVLFNVGDR		LDAHDAVAASGLIQDAVYNAYGPTENGMQSTMYKVDVNEPFVNGVPIGRSITNSGAYVMD		GNOQLVSPGVMGEIVVTGDGLARGYTDSALDEDRFVHVTIDGEENIKAYRTGDRVRYRPK		DFEIBFFGRMDQQVKIRGHRIEPAEVEHALLGHDLVHDAAVVLRKPANQEPEMIAFITSQ		EDETI EQHESNKQVQGWGEHFDVSRYADIKDLDTSTFGHDFLGWTSMYDGVDI PVNEMKE		WLDETTASLLDNRPPGHILEIGAGTGMILSNLGKVDGLQKYVGLDPAPSAAIFVNEAVKS		LPSLAGKARVLVGTALDIGSLDKNEIQPELVVINSVAQYFPTSEYLIKVVKAVVEVPSVK		RVFFGDIRSQALNRDFLAARAVRALGDNASKEQIREKIAELEESEEELLVDPAFFVSLRS		OLPNIKHVEVLPKLMKATNELSSYRYAAVLHISHNEEEQLLIQDIDPTAWVDFAATOKDS		GGLRNLLQQGRDDVMIAVGNIPYSKTIVERHIMNSLDQDHVNSLDGTSWISDARSAAAIC		TSFDAPALTQLAKEEGFRVELSWARQRSQNGALDAVFHRLATDANCERSRVLVHFPTDHQ		GRQLRTLTNRPLQRAQSRRIESQVFEALQTALPAYMIPSRIIVLPQMPTNANGKVDRKQL		ARRAQVVAKRKAVSARVAPRNDTEIVLCEEYADILGTEVGITDNFFDMGGHSLMATKLAA		RLSRRLDTRVTVKEVFDKPVLADLAASIEQGSTPHLPIASSVYSGPVEQSYAQGRLWFLD		<b>QFNLNATWYHMSLAMRLLGPLNMDALDVALRALEQRHETLRTTFEAQKDIGVQVVHEAGM</b>	
7	8638	7	8698	7,	8758	7,	8818	74	8878	74	8938	74	8668	74	9028	74	9118	79	9178	79	9238	79	9298	79	9358	82	9418	82	9478	82	9538	82	9538	82	9658	83
ò	a	ò	g	ò	q	ò	q	ò	q	ò	g	ò	g	ò	q	ò	qo	ò	qq	ò	Ω	ò	අු	ò	g	ò	a	ò	q	ò	g	ò	qq	ò	g	ò

Q C	b 9718	KRLKVLDLSDKNEKEHMAVLENEQMRPFTLASEPGWKGHLARLGPTEYILSLVMHHMFSD 9	777
ô	у 82	GWS	4
원	b 9778	   GWSVDILRQELGQFYSAALRGRDPLSQVKPLPIQYRDFAAWQKEAAQVAEHERQLAYWEN 98	837
ô	у 85	84	4
g	9838	QLADSTPGELLTDFPRPQFLSGKAGVIPVTIEGPVYEKLLKFSKERQVTLFSVLLTAFRA 98	897
ò	y 85	8	4
đ	9898	THFRLTGAEDATIGTPIANRNRPELEHIIGFFVNTQCMRLLLDTGSTFESLVQHVRSVAT 99	957
ò	/ 85	8	4
යි	9958	DAYSNQDI PFERIVSALLPGSRDASRSPLIQLMFALHSQPDLGNITLEGLEHERLPTSVA	10017
ò	, 85	88NILO	
q	10018	TRFDMEFHLFQEPNKLSGSILFADELFQPETINSVVTVFQEILRRGLDQPQVSISTMPLT 100	7400
ò	89	88	_
qq	10078	DGLIDLEKLGLLEIESSNFPRDYSVVDVFRQQVAANPNAPAVVDSETSMSYTSLDQKSEQ 101	137
ò	68	06BB	_
d	10138	   IAAWLHAQGLRPESLICVMAPRSFETIVSLFGILKAGYAYLPLDVNSPAARIQPILSEVE 101	197
ò	91	06	_
q	10198	GKRLVLLGSGIDMPQSDRMDVETARIQDILTNTKVERSDPMSRPSATSLAYVIFTSGSTG 102	257
ò	91	06	
g	10258	RPKGVMIEHRNILRLVKQSNVTSQLPQDLRMAHISNLAFDASIWEIFTAILNGGALICID 103	317
ò	91	06	
a	10318	YFTLLDSQALRTTFEKARVNATLFAPALLKECLNHAPTLFEDLKVLYIGGDRLDATDAAK 1037	377
ò	91	06	
QQ	10378	IOALVKGTVYNAYGPTENTVMSTIYRLTDGESYANGVPIGNAVSSSGAYIMDOKQRLVPP 104	437
ò	91	06	
qq	10438	GVMGELVVSGDGLARGYTNSTLNADRFVDIVINDOKARAYRTGDRTRYRPKDGSIEFFGR 104	497
ò	91	06	
đ	10498 1	MDQQVKIRGHRVEPAEVEQAMLGNKAIHDAAVVVQAVDGQETEMIGFVSMASDRFSEGEE 105	557
ò	91	93	
Q	10558 1	 EITNQVQEWEDHFESTAYAGIEAIDQATLGRDFTSWTSMYNGNLIDKAEMEEWLDDTMQS 106;	517
ò	46	86	
g	10618 I	10	577
ò	94	66	
පු	10678	OILVGTAEDIKLVKDFHPDVVVINSVAQYFPSRSYLVQIASELIHMTSVKTIFFGDMRSW 1073	137
ò	94 -	56dqdg	
qq	10738 A	 ATINRDFLVSRALYTLGDKATKDQIRQEVARLEENEDELLVDPAFFTSLTSGWPGKVKHVE 10797	97
ò	- 96		

g	10798	3 ILPKRMRTSNELSSYRYAAVLHICRDGEGRNRYGRRVHSVEENAWIDFASSGMDRHALVQ	10857
ઠે	96		95
a	10858	MLDERRDAKTVAIGNIPHSNTINERHFTTSLDTEGEGIAQDSLDGSAWQSATKAMAARCP	10917
ò	96		95
8	10918	CLSVTELVEIGGAAGFRVEVSWARQRSQHGALDVVFHHLEDDRVGRVLINPPTDFERLPP	10977
ò	96		95
g	10978	STGLTSRPLQRIQNRRFESQIREQLQTLLPPYMVPSRIVVLERMPLNANSKVDRKELARK	11037
ò	96	HD	97
g	11038	ARTLQTIKPSATRVAPRNDIEAVLCDEFQAVLGVTVGVMDNFFELGGHSLMATKLAARLS	11097
ò	98	ADIV	101
g	11098	:    RRLDTRVSVKD1FNQP1LQDLADVVQTGSAPHEA1PSTPYSGPVEQSFSQGRLWFLDQLN	11157
à	102		101
g	11158	LNASWYHMPLASRLRGPLRIEALQSALATIEARHESLRTTFEEQDGVPVQIVRAARNKQL	11217
à	102		101
g	11218	RIIDVSGTEDAYLAALKQEQDAAFDLTAEPGWRVALLRLGPDDHVLSIVMHHIISDGWSV	11277
à	102	-1. Λ	103
g	11278		11337
à	104		103
අ	11338	LADFTRPKALSGDADVI PIEIDDQVYQNLRSFCRARHVTSFVALLAAFRAAHYRLTGAED	11397
ሯ	104		103
g	11398	ATIGSPIANRNRPELEGLIGCFVNTQCLRIPVKSEDTFDTLVKQARETATEAQDNQDVPF	11457
ጵ	104	ITHERDIETILLEBERTILLEBERTILLEBERT	111
ą	11458	: ERIVSSMVASSRDTSRNPLVQVMFAVHSQHDLGNIRLEGVEGKPVSMAASTRFDAEMHLF	11517
⋧	112		111
ą	11518	EDQGMLGGNVVFSKDLFESETIRSVVAVFQETLRRGLANPHANLATLPLTDGLPSLRSLC	11577
≿	112	DD	113
ą	11578	 LQVNQPDYPRDASVIDVFREQVASIPKSIAVIDASSQLTYTELDERSSQLATWLRRQVTV	11637
⋩	114	GNROV	118
ą	11638	PEELVGVLAPRSCETIIAFLGIIKANLAYLPLDVNAPAGRIETILSSLPGNRLILLGSDT	11697
⋩	119	α-	119
ð	11698	QAVKLHANSVRFTRISDALVESGSPPTEELSTRPTAQSLAYVMFTSGSTGVPKGVMVEHR	11757
<b>≿</b>	120	GVT	122
ð	11758	GITRLVKNSNVVAKQPAAAAIAHLSNIAFDASSWEIYAPLLNGGTVVCIDYYTTIDIKAL	11817
≿	123		122
ည	11818	EAVFKQHHIRGAMLPPALLKQCLVSAPTMISSLEILFAAGDRLSSQDAILARRAVGSGVY	11877
≿	123		122
ð	11878	NAYGPTENTVLSTIHNIGENEAFSNGVPIGNAVSNSGAFVMDQNQQLVSAGVIGELVVTG	11937

ò	123		122
අු	11938	DGLARGYTDSKLRVDRFIYITLDGNRVRAYRTGDRVRHRPKDGQIEFFGRMDQQIKIRGH	11997
ò	123		122
đ	11998	RIEPAEVEQALARDPAISDSAVITQLTDEEEPELVAFFSLKGNANGTNGVNGVSDQEKID	12057
ò	123		122
QQ	12058	. GDEQHALLMENKIRHNLQALLPTYMIPSRIIHVDQLPVNANGKIDRNELAVRAQATPRTS	12117
ò	123		122
qq	12118	SVSTYVAPRNDIETIICKEFADILSVRVGITDNFFDLGGHSLIATKLAARLSRRLDTRVS	12177
ò	123		122
qq	12178	VRDVFDTPVVGQLAASIQQGSTPHEAIPALSHSGPVQQSFAQGRLWFLDRFNLNAAWYIM	12237
ò	123		122
අ ර	12238	PFGVRLRGPLRVDALQTALRALEERHELLRTTFEEQDGVGMQIVHSPRMRDICVVDISGA	12297
ò	123		122
q	12298	NEDLAKLKEEQQAPFNLSTEVAWRVALFKAGENHHILSIVMHHIISDGWSVDIFQQELAQ	12357
ò	123		122
අ	12358	FYSVAVRGHDPLSQVKPLPIHYRDFAVWQRQDKQVAVHESQLQYWIEQLADSTPAEILSD	12417
ò	123		122
qq	12418	FNRPEVLSGEAGTVPIVIEDEVYEKLSLFCRNHQVTSFVVLLAAFRVAHYRLTGAEDATI	12477
ò	123		122
QQ	12478	GTPIANRNRPELEDLIGFFVNTQCMRIALEEHDNFLSVVRRVRSTAASAFENQDVPFERL	12537
ò	123		122
qq	12538	VSALLPGSRDASRNPLVQLMFVVHSQRNLGKLQLEGLEGEPTPYTATTRFDVEFHLFEQD	12597
ò	123		122
QQ	12598	KGLAGNVVFAADLFEAATIRSVVEVFHEILRRGLDQPDIAISTMPLVDGLAALNSRNLPA	12657
ò	123		122
QQ	12658	VEDIEPDFATEASVVDVFQTQVVANPDALAVTDTSTKLTYAELDQQSDHVAAWLSKQKLP ;	12717
ò	123		122
qq	12718	AESIVVVLAPRSSETIVACIGILKANLAYLPMDSNVPEARROAILSEIPGEKFVLLGAGV	12777
ò	123		1.2.2
g	12778	PIPDNKTADVRMVFISDIVASKTDKSYSPGTRPSASSLAYVIFTSGSTGRPKGVMVEHRG	12837
ò	123		122
q	12838	VISLVKQNASRIPQSLRMAHVSNLAPDASVWEIFTTLLNGGTLFCISYFTVLDSKALSAA	12897
ò	123		122
q	12898	FSDHRINITLLPPALLKQCLADAPSVLSSLBSLYIGGDRLDGADATKVKDLVKGKAYNAY 1	12957
ò	123		122
QQ	12958	GPTENSVMSTIVTIEHETEANGVPIGTSLABKSKAVIMDONOLVPAGNGELVVAGNGI. 1	13017

ò	123	
QQ	13018 ARGYTDPSLNTGRFIHITIDGKQVQAYRTGDRVRYRPRDYQIEFFGRLDQQIKIRGHRIE 13077	Db 14098 DRLNGSVMFATDLFQPETIQGFVAVVEEVLORGLEQPQSPIATMPLAEGIAQLRDAGALQ 14157
ò	123 122	Qy 145 144
qq	13078 PAEVEQALLSDSSINDAVVVSAQNKEGLEMVGYITTQAAQSVDKEEASNKVQEWEAHFDS 13137	Db 14158 MPKSDYPRNASLVDVFQQQAMASPSTVAVTDSTSKLTYAELDRLSDQAASYLRRQQLPAE 14217
ò	123	Qy 145 144
qq	13138 TAYANIGGIDRDALGQDFLSWTSMYDGSLIPREEMQEWLNDTMRSLLDNOPPGKVLEIGT 13197	Db 14218 TMVAVLAPRSCETIIAFLAILKANLAYMPLDVNTPSARMEAIISSVPGRRLILVGSGVRH 14277
ò	123 122	Oy 145 144
q	13198 GTGMVLFNLGKVEGLQSYAGLEPSRSVTAWVNKAIETFPSLAGSARVHVGTAEDISSIDG 13257	1427
ò	123	Ογ 145 144
qq	13258 LRSDLVVINSVAQYFPSREYLAELTANLIRLPGVKRIFFGDMRTYATNKDFLVARAVHTL 13317	Db 14338 IMRLVKDSNVVTHMPPATRMAHVTNIAFDVSLFEMCATLLNGGTLVCIDYLTLLDSTMLR 14397
ò	123 122	Oy 145 144
QQ	13318 GSNASKAMVRQQVAKLEDDEEELLVDPAFFTSLSDQFPDEIKHVEILPKRMAATNELSSY 13377	Db 14398 ETFEREQVRAAIFPPALLRQCLVNMPDAIGMLEAVYVAGDRFHSRDARATQALAGPRVYN 14457
ò	123 122	Qy 145 144
QC	13378 RYAAVIHVGGHQMPNGEDEDKQWAVKDINPKAWVDFAGTRMDRQALLQLLQDRQRGBDVV 13437	Db 14458 AYGPTENAILSTIYNIDKHDPYVNGVPIGSAVSNSGAYVMDRNQOLLPPGVMGELVVTGE 14517
ò	123 122	Qy 145 144
QQ	13438 AVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAWISRTQSRAKECPALSVADLIEIGKG 13497	Db 14518 GVARGYTDASLDTDRFVTVTIDGQRQRAYRTGBRVRYRPKGFQIBFFGRLDQQAKIRGHR 14577
ò	123 122	Ογ 145 144
g	13498 IGFEVEASWARQHSQRGGLDAVFHRFEPPRHSGHVMFRFPTEHKGRSSSSLTNRPLHLLQ 13557	Db 14578 VELGEVEHALLSENSYTDAAVVLRTMEEEDPQLVAFVTTDHEYRSGSSNEEEDPYATQAA 14637
ò	123 122	0y 145 144
අු	13558 SRRLEAKVRERLQSLLPPYMIPSRITLLDQMPLTSNGKVDRKKLARQARVIPRSAASTLD 13617	Db 14638 GDMRKRLRSLLPYYMVPSRVT1LRQMPLNANGKVDRKDLARRAQMTPTASSSGPVHVAPR 14697
ò	123 126	Oy 145GVT 147
q	13618 FVAPRTEIEVVLCEEFTDLLGVKVGITDNFFELGGHSLLATKLSARLSRRLDAGITVKQV 13677	Db 14698 NETEAAICDEFETILGVKVĞIT 14719
ò	127 126	RESULT 2
Q	13678 FDQPVLADLAASILQGSSRHRSIPSLPYEGPVEQSFAQGRLWFLDQFNIDALWYLIPFAL 13737	US-09-369-364A-7 ; Sequence 7, Application US/09369364A
ò	127 126	; Patent No. 6391610 ; GENERAL INFORMATION:
qq	13738 RMRGPLQVDALAAALVALEERHESLRTTFEERDGVGIQVVQPLRTTKDIRIIDVSGMRDD 13797	; APPLICANT: Apte, Suneel ; APPLICANT: Hurskainen, Tiina L.
ò	127	; APPLICANT: Hirohata, Satoshi ; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteages
QQ	13798 DAYLEPLQKEQQTPFDLASEPGWRVALLKLGKDDHILSIVMHHIISDGWSTEVLQRELGQ 13857	73/4007/10-30-00 NUMBER: US/09/369,364A
ò	133 132	SEQ ID NOS: 31
qq	13858 FYLAAKSGKAPLSQVAPLPIQYRDFAVWQRQEEQVAESQRQLDYWKKQLADSSPAELLAD 13917	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 7
ò	133	
QQ	13918 YTRPNVLSGEAGSVSFVINDSVYKSLVSFCRSRQVTTFTTLLAAFRAAHYRWTGSDDATI 13977	; ORGANISM: Homo sapiens ADAMTS-7 US-09-369-34A-7
ò	133	30.7%; Score 237; DB 4
	13978 GTPIANRNRPELENLIGCFVNTQCMRITIGDDETFESLVQQVRSTTATAFENQDVPFERI 14037	18.2%; Pred. No. 0.00038; vative 24; Mismatches 62;
දි සි	137 144 14038 VSTLSAGSRDTSRNPLVOLLEAVHSOOGIGETOT DEGINERAL PERINAGEN 1400	1 AAGGILHLEL
ò	THE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE THE LINE	53 AGGSFLSYELWPRALRKRDVSVRRDAPAFYELQYRGRELRFNLTANQHLLAPGFVSETRR
•	144	Qy 16 25

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6	bb 8/0 AVGGGVVFWVVSAKSAAALDAQIERLAAFASRDRTDGVDAGAVDAQAVARVLAGG 929		292 Db 990 SAVFAAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHH 115 Ov 22	1050 GVTPQAVVGHSQGEIAAAYVAGALSLDDAARVVTLRSKSIAAHLAGKGGMLSLALSEDAV	22	Db 1110 LERLAGFBGLSVAAVNGFTATVVSGDPVQIEELARACEADGVRARVIPVDYASHSRQVEI 1169 Oy 22	1170 IESELAEVLAGLSPQAPRVPFFSTLEGAWITEPVLDGGYWYRNLRHRVGFAPAVETLATD	21	QY 22HQEDTER	Db 1290 SATGHHSDLPTYAFQTERHWLGEIEALAPAGEPAVQPAVLRTEAAEPAELDRDEGLRVIL 1349	13		Db 1410 PEALAEQLLLVVHGEAAANPAGAEPAPVAAAGAVDEPVAIVGMACRLPGGVASPEDLWRL 1469	29	1470 VAGGGDAISEFPQDRGWDVEGLYHPDPEHPGTSYVRQGGFIENVAGFDAAFFGISPREAL	Db 1530 AMDPQORLLETSWEAVEDAGIDPTSLRGRQVGVFTGAMTHEYGPSLRDGGEGLDGYLLT 1589	V 4.	PHIVIG 569 Db 1590 GNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVMPT 1649 Ov 43	4  Db 1650 PGMFVEFSRQRGLAGDGRSKAFAASADGTSWSEGVGVLLVERLSDARRNGHQVLAVVRGS		Db 1710 ALNQDGASNGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQALIA 1769	4 43	1770 TYGOGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDQIDW	Oy 43	
	ARPGHAOPHVVXKROAPERLAORGDSCAPGTOGVOVVPBT.EGBPBUBODOAUD	THO BOYCE PERIODS TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL	KWVILTEPECAPNITANLTSSLLSVCGWSOTINPEDDTDPGHADLVLYITRFDL	RLVLLEDEEEDLKITHHADNTLKSFCKWQKSINMKGDAHPLHHDTAILLTRKDL ROVRGVTQLGGACSPTWSCLÍTEDTGFDLGVTI 148	38		us-us-ins-sa/-e > Sequence 6. Application US/09105537A Patent No. 6265202	GENERAL INFORMATION: APPLICANT: Sherman, D.H. APPLICANT: Liu, H.	APPLICANT: Xue, Y. APPLICANT: Zhao, L. TITLE OF INVENTION: DNA encoding methymycin and pikromycin	FILE REFERENCE: 600,438US1 CURRENT APPLICATION NUMBER: US/09/105,537A CURRENT FILING DATE: 1998-06-26	SEQ ID NOS: 43 FastSEQ for Windows Version 3.0	11877	Streptomyces venezuelae 6	e 235;	vative 21; Mismatches 36; Indels 83	AAGGAVTDVDADBWNACHEVDDDGABGBGGGGGGTGTTANTAGAAAGAAAA	100 100 100 100 100 100 100 100 100 100	DPQQRLALELGWEALERAGIDPSSLTGTRTGVFAGAIWDDYATLKHRQGGAAITF	LHRG11 ANRI SVTI CI. 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g	1950	EHRAVALGAGADDLVQALADPDGLIRGTASGVGRVAFVFPGQGTQWAGMGAELLDSSAVF	2009
ò	51	RVHLV	55
QQ	2010	AAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTP	2069
ò	96		55
DB	2070	QAVVGHSQGEIAAAYVAGALPLDDAARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERL	2129
ò	99		55
g	2130	SDFDGLSVAAVNGPTATVVSGDPVQ1EELAQACKADGFRAR11PVDXASHSRQVE11ESE	2189
ò	99	, p	55
20	2190	LAQVLAGLSPQAPRVPFFSTLEGTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFT	2249
ò	26		55
g	2250	HFVEVSAHPVLTMTLPETVTGLGTLRREQGGERLVTSLAEAWVNGLPVAWTSLLPATAS	2309
ò	26		55
a	2310	RPGLPTYAFQAERYWLENTPAALATGDDWRYRIDWKRLPAAEGSERTGLSGRWLAVTPED	2369
ò	56		55
e G	2370	HSAQAAAVLTALVDAGAKVEVLTAGADDDREALAARLTALTTGDGFTGVVSLLDGLVPQV	2429
à	26	WAYILTEPE	64
ą	2430	awvQalgDagikaplwsvTqgavsvgrldTpadpdpramlwglgrvvalehperwaglvdl	2489
à	65		64
q	2490	PAQPDAAALAHLVTALSGATGEDQIAIRTTGLHARRLARAPLHGRRPTRDWQPHGTVLIT	2549
à	65	CAPNITANLTSS	96
g	2550	GGTGALGSHAARWWAHHGAEHLLLVSRSGEQAPGATQLTAELTASGARVTIAACDVADPH	2609
à	77		76
g	2610	AMRTLLDAI PAETPLTAVVHTAGALDDGI VDTLTAEQVRRAHRAKAVGASVLDELTRDLD	2669
à	77		92
g	2670	LDAFVLFSSVSSTLGI PGQGNYAPHNAYLDALAARRRATGRSAVSVAWGPWDGGGMAAGD	2729
à	77		87
ą	2730	GVAERLRNHGVPGMDPELALAALESALGRDETAITVADIDWDRFYLAYSSGRPQPLVEEL	2789
ጵ	88		87
ą	2790	PEVRRIIDARDSATSGQGGSSAQGANPLAËRLAAAAPGERTEILLGLVRAQAAAVLRMRS	2849
à	88		87
ą	2850	PEDVAADRAFKDIGFDSLAGVELRNRLTRATGLQLPATLVFDHPTPLALVSLLRSEFLGD	2909
ጵ	88	NPED	91
ą	2910	EETADARRSAALPATVGAGAGAGAGTDADDDPIAIVAMSCRYPGDIRSPEDLWRMLSEGG	2969
à	92	DTDP	95
ą	2970	EGITPFPTDRGWDLDGLYDADPDALGRAYVREGGFLHDAAEFDAEFFGVSPREALAMDPQ	3029
à	96		95

q	3030 QRMLLTTSWEAFERAGIEPASLRGSSTGVFIGLSYQDYAARVPNAPRGVEGYLLTGSTPS 3089	63
ò	56 96	
q	3090 VASGRIAYTFGLEGPATTVDTACSSSLTALHLAVRALRSGECTMALAGGVAMMATPHMFV 3149	49
ò	56 96	
qq	3150 EFSRQRALAPDGRSKAFSADADGFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQD 3209	60
ò	56 96	
qq	3210 GASNGLTAPNGPSQQRVIRQALADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKE 3269	69
ò	56 96	
Dp	3270 RPAERPLAIGSVKSNIGHTQAAAGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGL 3329	5
ò	36 96	
g	3330 ALVTEPIDWPAGTGPRRAAVSSFGISGTNAHVVLEQAPDAAGEVLGADEVPEVSETVAMA 3389	00
ò	56 96	
qq	3390 GTAGTSEVAEGSEASEAPAAPGSREASLPGHLPWVLSAKDEOSLRGOAAALHAWLSEPAA 3449	0
ò	56 96	
qq	3450 DLSDADGPARLRDVGYTLATSRTAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTA 3509	
ò	96	_
QQ	3510 RDGTTAFLFTGQGSQRPGAGRELYDRHPVFARALDEICAHLDGHLELPLLDVMFAAEGSA 3569	6.0
ò	101	_
QQ	3570 EAALLDETRYTQCALFALEVALFRLVESWGMRPAALLGHSVGEIAAAHVAGVFSLADAAR 3629	6
ò	101	_
qq	3630 LVAARGRLMQELPAGGAMLAVQAAEDEIRVWLETEERYAGRLDVAAVNGPEAAVLSGDAD 3689	6
ò	101	_
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ò	101	_
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ò	101	_
QQ	3810 DSAAGSPVGSPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWH 3869	6.0
ò	101	_
Dp	3870 AWFAGSGAHRVDLPTYSFRRDRYWLDAPAADTAVDTAGLGLGTADHPLLGAVVSLPDRDG 3929	6
ò	101	_
g	3930 LLLTGRLSLRTHPWLADHAVLGSVLLPGAAMVELAAHAAESAGLRDVRELTLLEPLVLPE 3989	6
ò	. 101	_
q	3990 HGGVELRVTVGAPAGEPGGESAGDGARPVSLHSRLADAPAGTAWSCHATGLLATDRPELP 4049	6
ò	101	_
g G	4050 VAPDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATT 4109	ō
ò	101	
9	4110 NATEDBITANGGGABABDYGTHDBITADAGTUNFTANGGTUNFDFTUPUPFHWGGUTUHBAG 4169	6

ठे	101		100
g	4170	AAAARVRLASAGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVGGLMHRVAWRP	4229
ò	101		. 001
g	4230	YALASSGEQDPHATSYGPTAVLGKDELKVAAALESAGVEVGLYPDLAALSQDVAAGAPAP	4289
ò	101		106
g	4290	:   .     RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAGTRLLLVTRGAVRDPEGSGA	4349
ઠે	107		106
g	4350	DDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSYRTLPSVLSDAGLRDEPQLALH	4409
ò	107		106
g	4410	DGTIRLARLASVRPETGTAAPALAPEGTVLLTGGTGGLGGLVARHVVGEWGVRRLLLVSR	4469
ઠે	107		106
qq	4470	RGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAIPAEHPLTAVVHTAGVLSD	4529
à	107		106
qq	4530	GTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGGAGGGAYAAA	4589 ·
ò	107		106
ებ	4590	NATLDALAWRRRAAGLPALSLGWGLWAETSGWTGELGQADLRRMSRAGIGGISDAEGIAL	4649
ò	107		106
ය ව	4650	LDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARPSAASASTTA	4709
ò	107		106
e G	4710	GTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHARGHRIDAER	4769
6	107	EDTETEDG	114
g	4770	GFLDLGFDSLTAVELRNRLNSAGGLALPATLVFDHPSPAALASHLDAELPRGASDQDGAG	4829
ò	115		114
ą	4830	NRNGNENGTTASRSTAETDALLAQLTRLEGALVLTGLSDAPGSEEVLEHLRSLRSMVTGE	4889
ò	115		114
g	4890	TGTGTASGAPDGAGSGAEDRPWAAGDGAGGGSEDGAGVPDFMNASAEELFGLLDQDPSTD	4949
à	115		114
q	4950	MSTVNEEKYLDYLRRATADLHEARGRLRELEAKAGEPVAIVGMACRLPGGVASPEDLWRL	5009
à	115		114
g G	5010	VAGGEDAISEFPQDRGWDVEGLYDPNPEATGKSYAREAGFLYEAGEFDADFFGISPREAL	5069
ጵ	115		114
ą	5070	AMDPQQRLLLEASWEAFEHAGI PAATARGTSVGVFTGVMYHDYATRLTDVPEGI EGYLGT	5129
ጵ	115		114
ą	5130 (	GNSGSVASGRVAYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGEVDMALAGGVTVMST	5189
ते :			120
g	5190	PSTFVEFSRQRGLAPDGRSKSFSSTADGTSWSEGVGVLLVERLSDARRKGHRILAVVRGT	5249

ò	121 120	
q	5250 AVNODGASSGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQAVIA 5309	σ
ò	121 120	
요	5310 TYGQGRDGEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGVLPKTLHVEKPTDQVDW 5369	σ
ò	121 120	
qq	5370 SAGAVELLTEAMDWPDKGDGGLRRAAVSSFGVSGTNAHVVLEEAPAAEETPASEATPAVE 5429	6
ò	121 120	
qq	5430 PSVGAGLVPWLVSAKTPAALDAQIGRLAAFASQGRTDAADPGAVARVLAGGGRAEFEHRAV 5489	o
ò	121 120	
đ	5490 VLGTGQDDFAQALTAPEGLIRGTPSDVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMA 5549	6
ò	121 120	
qq	5550 ECESALSRYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVG 5609	a
ò	121	
Д	5610 HSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALSEEATRQRIENLHG 5669	σ
ò	121	
qq	5670 LSIAAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPVDYASHSAHVETIESELAEVL 5729	6
ò	121 120	
q	5730 AGLSPRTPEVPFFSTLEGAWITEPVLDGTYWYRNLRHRVGFAPAVETLATOEGFTHFIEV 5789	•
ò	121	
qq	5790 SAHPVLTMTLPETVTGLGTLRREQGGGRLVTSLAEAWTNGLTIDWAPVLPTATGHHPEL 5849	
ò	126	
g	5850 PTYAFQRRHYWLHDSPAVQGSVQDSWRYRIDWKRLAVADASERAGLSGRWLVVVPEDRSA 5909	_
ò	126 128	
ය ව	5910 EAAPVLAALSGAGADPVQLDVSPLGDRQRLAATLGEALAAAGGAVDGVLSLLAWDESAHP 5969	~
ò	126 125	
QQ	5970 GHPAPFTRGTGATLTLVQALEDAGVAAPLWCVTHGAVSVGRADHVTSPAQAMVWGMGRVA 6029	_
ò	126	
В	6030 ALEHPERWGGLIDLPSDADRAALDRWTTVLAGGTGEDQVAVRASGLLARRLVRASLPAHG 6089	•
ò	127 ACSPTW 132	
đ	6090 TASPWWQADGTVLVTGAEEPAAAEAARRLARDGAGHLLLHTTPSGSEGAEGTSGAAEDSG 6149	•
ò	133 132	
qq	6150 LAGLVAELADLGATATVVTCDLTDAEAARLLAGVSDAHPLSAVLHLPPTVDSEPLAATD 6209	_
ò	133 132	
g	6210 ADALARVVTAKATAALHLDRLLREAAAAGGRPPVLVLFSSVAAIWGGAGQGAYAAGTAFL 6269	_
ò	133 132	
qa	6270 DALAGQHRADGPTVTSVAWSPWEGSRVTEGATGERLRRLGLRPLAPATALTALDTALGHG 6329	
ò	133 132	

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8	6330	DTAVTIADVDWSSFAPGFTTARPGTLLADLPEARRALDEQQSTTAADDTVLSRELGALTG 6389	
ò	133	132	
qq	6390	AEQORRMOELVREHLAVVLNHPSPEAVDTGRAFRDLGFDSLTAVELRNRLKNATGLALPA 6449	
ò	133	132	
엄	6450	TLVFDYPTPRTLAEFLLAEILGEQAGAGEQLPVDGGVDDEPVAIVGMACRLPGGVASPED 6509	
ò	133	132	
g	6510	LWRLVAGGEDAISGFPQDRGWDVEGLYDPDPDASGRTYCRAGGFLDEAGEFDADFFGISP 6569	
ò	133	132	
gg	6570	REALAMDPOORLLLETSWEAVEDAGIDPTSLQGQQVGVFAGTNGPHYEPLLRNTAEDLEG 6629	
ò	133	132	
අු.	6630	YVGTGNAASIMSGRVSYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGECGLALAGGVT 6689	
ò	133	132	
QQ	0699	VMSTPTTFVEFSRQRGLAEDGRSKAFAASADGFGPAEGVGMLLVERLSDARRNGHRVLAV 6749	
ઠે	133	132	
q	6750	VRGSAVNQDGASNGLTAPNGPSQQRVIRRALADARLTTADVDVVEAHGTGTRLGDPIEAQ 6809	
ò	133	132	
q	6810	ALIATYGQGRDTEQPLRLGSLKSNIGHTQAAAGVSGIIKMVQAMRHGVLPKTLHVDRPSD 6869	
ò	133	132	
g	6870	QIDWSAGTVELLTEAMDWPRKQEGGLRRAAVSSFGISGTNAHIVLEEAPVDEDAPADEPS 6929	
ò	133	132	
Q	6930	VGGVVPWLVSAKTPAALDAQIGRLAAFASQGRTDAADPGAVARVLAGGRAQFEHRAVALG 6989	
ò	133	132	
g	0669	TGQDDLAAALAAPEGLVRGVASGVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAWAECE 7049	
ò	133	132	
g G	7050	AALAPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVGHSQ 7109	
ò	133	132	
q	7110	GEIAAAYVAGALSLDDAARVVTLRSKSIGAHLAGQGGMLSLALSEAAVVERLAGFDGLSV 7169	
ò	133	132	
g	7170	AAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPVDYASHSAHVETIESELADVLAGL·7229	
ò	133	132	
a	7230	SPQTPQVPFFSTLEGAWITEPALDGGYWYRNLRHRVGFAPAVETLATDEGFTHFVEVSAH 7289	
à	133	132	
අ	7290	PVLTMALPETVTGLGTLRRDNGGQHRLTTSLAEAWANGLTVDWASLLPTTTTHPDLPTYA 7349	
6	133	SCLIT137	
8	7350	:  FQTERYWPQPDLSAAGDITSAGLGAAEHPLLGAAVALADSDGCLLTGSLSLRTHPWLADH 7409	
à	138	137	

q	7410	AVAGTVLLPGTAPVELAFRAGDQVGCDLVEELTLDAPLVLPRRGAVRVQLSVGASDESGR	7469
ò	138		137
Q	7470	rtfglyahpedapgeaewtrhatgvlaaradrtapvadpeawpppgaepvdydglyerfa	7529
ò	138		137
QQ	7530	angygygplfggvrgvwrrgdevfadvalpaevagaegarfglhpalldaavqaagagrg	7589
ò	138		137
qq	7590	VRRGHAAAVRLERDLLYAVGATALRVRLAPAGPDTVSVSAADSSGQPVFAADSLTVLPVD	7649
ò	138		137
Q	7650	paqlaafsdptldalhllewtawdgaaqalpgavvlggdadglaaalraggtevlsfpdl	7709
ò	138		137
qq	7710	TOLVEAVORGETPAPATVLVACPAAGPOGPEHVREALHGSLALMQAWLADERFTOGRLVL	7769
ò	138		137
qq	7770	VTRDAVAARSGDGLRSTGQAAVWGLGRSAQTESPGRFVLLDLAGEARTAGDATAGDGLTT	7829
ò	138		137
qq	7830 (	GDATVGGTSGDAALGSALATALGSGEPQLALRDGALLVPRLARAAAPAAADGLAAADGLA	7889
ò	138		137
QQ	7890 7	alplpaapalwrlepgtdgslesltaapgdaetlapeplgpgqvriairatglnprdvli	7949
ò	138 .		137
QQ	7950 #	ALGMY PDPALMGTEGAGUVTATGPGUTHLAPGDRVMGLLSGAYAPUVVADARTVARMPEG	8009
δ	138		137
qq	8010 4	WTFAQGASVPVVFLTAVYALRDLADVKPGERLLVHSAAGGVGMAAVQLARHWGVEVHGTA	6908
ò	138 -		137
qq	80708	SHGKWDALRALGLDDAHIASSRTLDFESAFRAASGGAGMDVVLNSLAREFVDASLRLLGP	8129
ò	138 -		137
QQ	8130 G	GGRFVEMGKTDVRDAERVAADHPGVGYRAFDLGEAGPERIGEMLAEVIALFEDGVLRHLP	8189
ò	138 -	Š	137
QQ	8190 V	VTTWDVRRARDAFRHVSQARHTGKVVLTMPSGLDPEGTVLLTGGTGALGGIVARHVVGEW	8249
ò	138 -		137
qq	8250 G	GVRRLLLVSRRGTDAPGAGELVHELEALGADVSVAACDVADREALTAVLDS1PAEHPLTA	8309
ઠે	138 -		137
QQ	8310 V	VVHTAGVLSDGTLPSMTAEDVEHVLRPKVDAAFLLDELTSTPGYDLAAFVMPSSAAAVFG	8369
ò	138 -		137
q	8370 G	GAGQGAYAAANATLDALAWRRRTAGLPALSLGWGLWAETSGMTGGLSDTDRSRLARSGAT	8429
ò	138 -		137
QQ	8430 P	PMDSELTLSLLDAAMRRDDPALVPIALDVAALRAQORDGMLAPLLSGLTRGSRVGGAPVN	8489
ò	138 -	03	139
d d	8490 0	QRRAAAGGAGEADTDLGGRLAAMTPDDRVAHLRDLVRTHVATVLGHGTPSRVDLERAFRD (	3549

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    950 SVKTQPWLADHVVGGAILLPGTAFVEMLIRAADQVGCDLIEELSLTTPLVLPATGAVQVQ 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .070 VPLDSFYARAAERGFDFGPAFQGLQAAWKRGDEIFAEVGLPTÄHREDAGRFGIHPALLDA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1130 ALQALGAAEEDPDEGWLPFAWQGVSLKATGALSLRVHLVPAGANAVSVFTTDTTGQAVLS 1189
                                                                                                                                                  230 AGGISVMATPGAFVEFSRQRALASDGRCKPPADAADGTGWGGGAGMLLLERLSDARRNGH 289
                                                                                                                                                                                                                                                                         350 PIEAQALIATYGANRSADHPLLLGSLKSNIGHTQAAAGVAGVIKSVLAIRHREMPRSLHI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     770 LGEVGSEPAEIAFYSTVTGERTDTGRLDADYWYQNLRQPVRFQQTVARMADQGYRFFVEV 829
                                                                                                                                                                                                             290 PVLAAVVGSAINQDGTSNGLTAPSGPAQQRVIRQALANAGLSPAEVDVVEAHGTGTALGD 349
                                                                                                                                                                                                                                                                                                                                   410 DQPSQHVDWSAGAVRLLTDSVDWPDLGRPRRAGVSSFGMSGTNAHLIVEEVSDEPVSGST 469
                                                                                                                                                                                                                                                                                                                                                                                               470 EPTGAFPWPLSGKTETALREQAAELLSVVTEHPEPGLGDVGYSLATGRAAMEHRAVVVAD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 LAECAAATAPYVDWSLLGVLRGDPDAPALDRDDVIQLALFAMMVSLAELWRSCGVEPAAV 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 VGHSQGEIAAAHVAGALSLTDAVRIIAARCDAVSALTGKGGMLAIALPESAVVKRIAGLP 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 ELTVAAVNGPGSTVVSGEPSALEŘLQTELTAENVQTRRVGIDYASHSPQIAQVQGRLLDR 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 SPHPLLTAGIQETLEAADAGGVVVGSLRRGEGGSRRWLTSLAECOVRGLPVNWEQVFLNT 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            890 GARRVPLPTYPFQRQRYWLESAEYDAGDLGSVGLLSAEHPLLGAAVTLADAGGFLLTGKL 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 DRDSFVAGLTALAAGVPAANVVQGAADCKGKVAFVFPGQGSHWQGMARELSESSPVFRRK 589
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                                                                                          29, Indels 5123,
                                                            DB 4; Length 5588;
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                                                                          ilarity 1.7%; Pred. No. 0.6;
Conservative 25; Mismatches
                                                       Score 216; DE
                                                                                                                        2 AGGI------
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-036-987A-6
                                                                          Best Local Similarity
Matches 92; Conserv
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g	1190 I	IDSLVLRQISDKQLAAARAMEHESLFRVDWKRISPGAAKPVSWAVIGNDELARACGSALG 124	49
ò	27 -		
q	1250 T	TELHPDLTGLADPPPDVVVVPCGASRQDLDVASEARAATQRMLDLIQDWLAAARFAGSRL 130	60
ઠે	27 -	35	
g	1310 V	: :   ::: VVVTCGAASTGPAEGVSDLVHAASWGLLRSAQSENPDRFVLVDVDGTAESWRALAAAVRS 136:	69
ò	36 -	38	
qq	1370 G	GEPOLALRAGEVRVPRLARCVAAEDSRIPVPGADGTVLISGGTGLLGGLVARHLVAERGV 142	29
ò	36 -	39	
QQ	1430 R	 RRLVLAGRRGWSAPGVTDLVDELVGLGAAVEVASCDVGDRAQLDRLLTTISAEFPLRGVV 148	68
ò	40 -	39	
Q C	1490 H	HAAGALADGVVESLTPEHVAKVFGPKAAGAWHLHELTLDLDLSFFVLFSSFSGVAGAAGQ 154	4.9
ò	40 -	39	
q	1550 G	GNYAAANAFLDGLAQHRRTAGLPAVSLAWGLWEQPSGMTGALDAAGRSRIARTNPPMSAP 160	60
ò	40	43	
Q	1610 DC	 DGLRLFEMAFRVPGESLLVPVHVDLNALRADAADGGVPALLRDLVPAPVRRSAVNESADV 166	6,0
ò	44	PSLGAQFR- 51	
Db	1670 NG		59
ò	52 -	51	
q	1730 RI	RLGGVLGVRLPATAVFDYPTPRALVRFLLDKLIGGVEAPTPAPAAVAAVTADDPVVIVGM 1789	39
ò	52 -	51	
g	1790 G	GCRYPGGVSSPEELWRLVAGGLDAVAEFPDDRGWDQAGLFDPDPDRLGTSYVCEGGFLRD 1849	6.7
ò	52 -	51	
q	1850 A	AAEFDAGFFGISPREALAMDPQQRLLLEVAWETVERAGIDPLSLRGSRTGVFAGLMHHDY 1909	60
ò	52 -	84 VHL 54	
QQ	1910 G	:   GARFITRAPEGFEGYLGNGSAGGVFSGRVAYSFGFEGPAVTVDTACSSSLVALHLAGQAL 1969	6.
ò	55		
Q	1970 RS	RSGECDLALAGGVTVMATPGMFVEFSRQRGLAADGRCKSFAAAADGTGWGEGAGLVLLER 2029	6
ò	55	54	
g G	2030 LS	LSDARRNGHAVLAVVRGSAVNQDGASNGLTAPNGPSQQRVITQALASAGLSVSDVDAVEA 2089	6
ò	55	88 VKWA	
සු	2090 HG	  HGTGTRLGDP1EAQAL1ATYGQGRDSDRPLWLGSVKSNIGHTQAAAGVAGVIKMYMAMRH 2149	ø.
ò	59		
g	2150 GC	GOLPATLHVDEPTSEVDWSAGDVQLLTENTPWPGNSHPRRVGVSSFGISGTNAHVILEQA 2209	6
ò	63	- 62	
q	2210 SK	SKTPDETADKSGPDSESTVDLPAVPLIVSGRTPAALSAQASALLSYLGERGDISTLDAAF 2269	6
ò	63	62	

S S	2270 SLASSRAALEERAVVLGADRETLLSGLEALASGREASGVVSGSPVSGGVGFVFAGQGGQW	2329
ò	63	62
qq	23330 LGMGRGLYSVFPVFADAFDEACAGLDAHLGQDVGVRDVVFGSDGSLLDRTLWAQSGLFAL	2389
ò	63	65
QQ	2390 OVGLLSLLGSWGVRPGVVLGHSVGEFAAAVAAGVLSLPDAARMVAGRARLMQALPSGGAM	2449
ò	99	65
QQ	2450 LAVAAGEEQLRPLLADRVDGAGIAAVNAPESVVLSGDREVLDDIAGALDGQGIRWRRLRV	2509
ò	99	65
q	2510 SHAFHSYRMDPMLQEFAEIARSVDYRRGDLPVVSTLTGELDTAGVMATPEYWVRQVREPV	2569
ò	99	65
q	2570 RFADGVRVLAQQGVATIFELGPDATLSALIPDCHSWADQAMPIPMLRKDRTETETVVAAV	2629
ò	99	65
qq	2630 ARAHTRGVPVEWSAYFAGTGARRVELPTYAFQRQRYWLETSDYGDVTGIGLAAAEHPLLG	2689
ò	99	65
QQ	2690 AVVALADGDGMVLTGRLSVGTHPWLAQHRVLGEVVVPGTAILEMALHAGARLGCDRVEEL	2749
ò	99	65
q	2750 TLETPLVVPERAAGAGSRGPAGGTTVSIETAEERVRTNDAIEIQLLVNAPDEGGRRRVSL	2809
ò	99	65
QQ	2810 YSRPAGGSRGGGWTRHATGELVVGTTGGRAVPDWSAEGAESIALDEFYVALAGNGFEYGP	2869
ò	99	65
Q	2870 LFQGLQAAWRRGDEVLAEIAPPAEADAMASGYLLDPALLDAALQASALGDRPEQGGAWLP	2929
ò	99	65
q	2930 FSFTGVELSAPAGTISRVRLETRRPDAISVAVMDESGRLLASIDSLRLRSVSSGQLANRD	2989
ò	99	65
q	2990 AVRDALFEVTWEPVATQSTEPGRWALLGDTACGKDDLIKLATDSADRCADLAALAEKLDS	3049
ò	99	65
q	3050 SALVPDVVVYCAGEQADPGTGAAALAETQOTLALLQAWLAEPRLAEARLVVVTCAAVTTA	3109
ò	99	65
QQ	3110 PSDGASELAHAPLWGLLRAAQVENPGQFVLADVDGTAESWRALPSALGSMEPQLALRKGA	3169
ò	99	65
QQ	3170 VRAPRLASVAGQIDVPAVVADPDRTVLISGGTGLLGGAVARHLVTERGVRRLVLTGRRGW	3229
ò	66APNITCG	82
gp	3230 DAPGITELVGELNGLGAVVDVVACDVADRADLESLLAAVPAEFPLCGVVHAAGALADGVI	3289
ò	83	84
q	3290 ESLSPDDVGAVFGPKAAGAWNLHELTRDTDLSFFALFSSLSGVAGAPGQGNYAAANAFLD	3349
ò	85	34
qq	3350 ALAHYRRSOGLPAVSLAWGLWEOPSGMTETLSEVDRSRIARANPPLSTKEGLRLFDAGLA	409

≿	85		84
ð	3410	LDRAAVVPAKLDRTFLAEQARSGSLPALLTALVPPIRRNRRASGTELADEGTLLGVVREH	3469
≿.	85		84
Q	3470	AAAVLGYSSAADVGVERAFRDLGFDSLSGVELRNRLAGVLGVRLPATAVFDYPTPRALAR	3529
≿	85	GAdNILO	91
ည	3530	FLHQELADEIATTPAPVTTTRAPVAEDDLVAIVGMGCRFPGQVSSPEELWRLVAGGVDAV	3589
≿	92		91
ą	3590	ADFPADRGWDLAGLFDPDPERAČKTYVREGAFLTDADRFDAGFFGISPREALAMDPQQRL	3649
≿.	92		. 16
	3650	LLELSWEAIERAGIDPGSLRGSRTGVFAGLMYHDYGARFASRAPEGFEGYLGNGSAGSVA	3709
≿	92		91
ą	3710	SGRIAYSFGFEGPAVTVDTACSSSLVALHLAGQSLRSGECDLALAGGVTVMSTPGTFVEF	3769
≿	92		91
ą	3770	SRORGLAPDGRCKSFAESADGTGWGEGAGLVLLERLSDARRNGHRVLAVVRGSAVNQDGA	3829
2	92	QLQ.	94
ည္	3830	SNGLTAPNGPSQQRVIQQALASAGLSVSDVDAVEAHGTGTRLGDPIEAQALIATYGRDRD	3889
≿	95	PGHAD	66
ą	3890		3949
≿	100		. 66
ą	3950	LTENTPWPDSGRPCRVGVSSFGISGTNAHVILEQSTGQMDQAAEPDSSPVLDVPVVPWVV	4009
≿	100	LVLYITR	106
Q	4010	SGKTPEALSAQAATLATYLDQNVDVSPLDVGISLAVTRSALDERAVVLGSDRDTLLSGLN	4069
≥.	107		108
Q	4070	   ALAAGHEAAGVVTGPVGIGGRTGFVFAGQGGQWLGMGRRLYSEFPAFAGAFDEACAELDA	4129
≿	109		108
Q	4130	NLGREVGVRDVVFGSDESLLDRTLWAQSGLFALQVGLWELLGTWGVRPSVVLGHSVGELA	4189
≿	109		108
ą	4190	AAFAAGVLSMAEAARLVAGRARLMQALPSGGAMLAVSAŢĘARVGPLLDGVRDRVGVAAVN	4249
≿	109		108
Q	4250	APGSVVLSGDRDVLDG1AGRLDGQGIRSRWLRVSHAFHSHRMDPMLABFAELARSVDYRS	4309
≿	109		108
ą	4310	PRLPIVSTLTGNLDDVGVMATPEYWVRQVREPVRFADGVQALVDQGVDTIVELGPDGALS	4369
≿	109		108
മ	4370	SLVQECVAESGRATG1PLVRRDRDEVRTVLDALAQTHTRGGAVDWGSFFAGTRATQVDLP	4429
≿	109		108
ą	4430	TYAFQRQRYWLEPSDSGDVTGVGLTGAEHPLLGAVVPVAGGDEVLLTGRLSVGTHPWLAE	4489

à	109	111	
g	4490	HRVLGEVVVPGTALLEMAWRAGSQVGCERVEELTLEAPLVLPERGAAAVQLAVGAPDEAG 4549	
ò	112		
g	4550	RRSLQLYSRGADEDGDWRRIASGLLAQANAVPPADSTAWPPDGAGQVDLAEFYERLAERG 4609	
ઠે	121	VT	
g	4610	:   LTYGPVFQGLRAAWRHGDDIFAELAGSPDASGFGIHPALLDAALHAMALGASPDSEARLP 4669	
ò	123	125	
Q	4670	FSWRGAQLYRAEGAALRVRLSPLGSGAVSLTLVDATGRRVAAVESLSTRPVSTDQIGAGR 4729	
ò	126	132	
Ор	4730	GDQERLLHVEWVRSAESAGMSLTSCAVVGLGEPEWHAALKTTGVQVESHADLASLATEVA 4789	
ò	133	132	
q	4790	KRGSAPGAVIVPCPRPRAMQELPTAARRATQQAMAMLQQWLADDRFVSTRLILLTHRAVS 4849	
ò	133	132	
q	4850	AVAGEDVLDLVHAPLWGLVRSAQAEHPDRFALIDMDDERASQTALAEALTAGEAQLAVRS 4909	
ò	133	30 SCLITEDIG	
QD	4910	GVVLAPRLGQVKVSGGEAFRWDEGTVLVTGGTGGLGALLARHLVSAHGVRHLLLASRRGL 4969	
ò	142	141	
Ор	4970	AAPGADELVAELEQAGADVAVVACDSADRDSLARLVASVPAENPLRVVVHAAGVLDDGVL 5029	
ò	142	141	
Db	5030	MSMSPERLDAVLRPKVDAAWYLHELTRELGLSAFVLFSSVAGLFGGAGGSNYAAGNAFLD 5089	
à	142	141	
g	5090	ALAHCRQAQGLPALSLASGLWASIDGMAGDLAAADVERLSRAGIGPLSAPGGLALFDAAV 5149	
ò	142	141	
qq	5150	GSDEPLLAPVRLDVEALRVQARSVQTRIPEMLHGMAMGPSRRTPFTSRVEPLHERLAGLS 5209	
ò	142	141	
g	5210	EGERRQQVLQRVRADIAVVLGHGRSSDVDIEKPLAELGFDSLTAIELRNRLATATGLRLP 5269	
ò	142	141	
q	5270	ATLAFDHGTAAALAQHVCAQLGTATAPAPRRTDDNDATEPVRSLFQQAYAAGRILDGMDL 5329	
ò	142	141	
D D	5330	VKVAAQLRPVFGSPGELESLPKPVQLSRGPEELALVCMPALIGMPPAQOYARIAAGFRDV 5389	
ò	142	141	
q	5390	RDVSVIPMPGFIAGEPLPSAIEVAVRTQAEAVLQEFAGGSFVLVGHSSGGWLAHEVAGEL 5449	
ò	142	147 TABIGAT 147	
q	5450	ERRGVVPAGVVLLDTYIPGEITPRFSVAMAHRTYEKLATFTDMQÖVGİT 5498	

RESULT 5 US-09-370-700-6 ; Sequence 6, Application US/09370700 ; Patent No. 6274350

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 PVLAAVVGSAINQDGTSNGLTAPSGPAQQRVIRQALANAGLSPAEVDVVEAHGTGTALGD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 PIEAQALIATYGANRSADHPLLLGSLKSNIGHTQAAAGVAGVIKSVLAIRHREMPRSLHI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 DQPSQHVDWSAGAVRLLTDSVDWPDLGRPRRAGVSSFGMSGTNAHLIVEEVSDEPVSGST 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 216; DB 4; Length 5588;
Pred. No. 0.6;
25; Mismatches 29; Indels 5123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 EPTGAFPWPLSGKTETALREQAAELLSVVTEHPEPGLGDVGYSLATGRAAMEHRAVVVAD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 DRDSFVAGLTALAAGVPAANVVQGAADCKGKVAFVFPGQGSHWQGMARELSESSPVFRRK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 LAECAAATAPYVDWSLLGVLRGDPDAPALDRDDVIQLALFAMMVSLAELWRSCGVEPAAV 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650 VGHSQGEIAAAHVAGALSLTDAVRIIAARCDAVSALTGKGGMLAIALPESAVVKRIAGLP 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 SPHPLLTAGIQETLEAADAGGVVVGSLRRGEGGSRRWLTSLAECQVRGLPVNWEQVFLNT 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; GENERAL INCORMATION;
; APPLICANT: Baltz, Richard H
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Treadway, Parti J
; APPLICANT: Treadway, Parti J
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; CORRENT FILING DATE: 1998-03-09
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 39
; CRANISM: Saccharopolyspora spinosa
US-09-370-700-6
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Best Local Similarity 1.7%;
Matches 92; Conservative
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ò	у 15	14	
q	950 SVKTQPWLADHVVGGAI	LLPGTAFVEMLIRAADQVGCDLIEELSLTTPLVLPATGAVQVQ 1009	ö
ò	у 15	1717	_
g	1010 IAVGGPDEAGRRS	VRVHSCRDDAVPQDSWTCHATGTLTSSDHQDAGGGPDGIWPPNDAVA 1069	690
ò	у 18	-VFQ	10
qq	b 1070 VPLDSFYARAAERGFDFGPAFÖGLQAAWKRGDEI	PAFÓGLQAAWKRGDEIFAEVGLPTÄHREDAGRFGIHPALLDÄ 1129	
ò	у 27	56	
q	b 1130 ALQALGAAEEDPDEGWLP	FAWQGVSLKATGALSLRVHLVPAGANAVSVFTTDTTGQAVLS 1189	Θ
ò	у 27	56	
qq	1190	IDSLVLRQISDKQLAAARAMEHESLFRVDWKRISPGAAKPVSWAVIGNDELARACGSALG 1249	4
ò	у 27	56	
QQ	1250 TELHPDLTGLAD	PPPDVVVVPCGASRQDLDVASEARAATQRMLDLIQDWLAAARFAGSRL 1309	0
ò	у 27	35 35	
ф	1310	VVVTCGAASTGPAEGVSDLVHAASWGLLRSAQSENPDRFVLVDVDGTAESWRALAAAVRS 1369	9
ò	у 36	38	
qq	b 1370 GEPQLALRAGEVRVPRLAR	RCVAAEDSRIPVPGADGTVLISGGTGLLGGLVARHLVAERGV 1429	~
ò	у 36	39	
QQ	1430	RRLVLAGRRGWSAPGVTDLVDELVGLGAAVEVASCDVGDRAQLDRLLTTISAEFPLRGVV 1489	æ
ò	у 40 у	39	
q	1490 HAAGALADGVVESLTP	EHVAKVFGPKAAGAWHLHELTLDLDLSFFVLFSSFSGVAGAAGQ 1549	9
ò	у 40	68	
q	1550	GNYAAANAFLDGLAQHRRTAGLPAVSLAWGLWEQPSGMTGALDAAGRSRIARTNPPMSAP 1609	60
ò	۲ 40	11:1	
q	1610 DGLRL	FEMAFRVPGESLLVPVHVDLNALRADAADGGVPALLRDLVPAPVRRSAVNESADV 1669	69
ò	44	11 - 11 - 11 - 11 - 11 - 11 - 11 - 11	
g	1670	NGLVGRLRRLPDLDQETQLLGLVREHVSAVLGHSGAVEVGADRAFRDLGFDSLSGVEFRN 1729	53
ò	, 52	51	
g	1730	RLGGVLGVRLPATAVFDYPTPRALVRFLLDKLIGGVEAPTPAPAAVAAVTADDPVVIVGM 1789	6 8
ò	, 52		
QQ	1790 GCRYPGGVSSP	EELWRLVAGGLDAVAEFPDDRGWDQAGLFDPDPDRLGTSYVCEGGFLRD 1849	6 4
ò	, 52		
q	O 1850 AAEFDAGFFGISPREALAMD	MDPQQRLLLEVAWETVERAGIDPLSLRGSRTGVFAGLMHHDY 1909	60
ò	, 52	54 VHL 54	
qq	o 1910 GARFITRAPEGFEGYLGNGS	3SAGGVFSGRVAYSFGFEGPAVTVDTACSSSLVALHLAGQAL 1969	69
ò		54	
ď	TAMATA TATADADA OFOL	PERMEVERSED RELIABILITY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE	66

ò	55		54
g	2030	) LSDARRNGHAVLAVVRGSAVNQDGASNGLTAPNGPSQQRVITQALASAGLSVSDVDAVEA	2089
ò	5.5	\DXD\A	28
QQ	2090		2149
ò	59	10,18	62
a	2150	:      GQLPATLHVDEPTSEVDWSAGDVQLLTENTPWPGNSHPRRVGVSSFGISGTNAHVILEQA	2209
ò	63		62
a	2210	SKTPDETADKSGPDSESTVDLPAVPLIVSGRTPAALSAQASALLSYLGERGDISTLDAAF	2269
ò	63		62
qq	2270	SLASSRAALEERAVVLGADRETLLSGLEALASGREASGVVSGSPVSGGVGFVFAGQGGW	2329
ò	63		62
g	2330	· LGMGRGLYSVFPVFADAFDEACAGLDAHLGQDVGVRDVVFGSDGSLLDRTLWAQSGLFAL	. 5389
ò	63	PBG	. 59
g	2390	QVGLLSLLGSWGVRPGVVLGHSVGEFAAAVAAGVLSLPDAARMVAGRARLMQALPSGGAM	2449
ઠે	99		65
8	2450	LAVAAGEEQLRPLLADRVDGAGIAAVNAPESVVLSGDREVLDDIAGALDGQGIRWRRLRV	2509
ò	99		65
Q	2510	SHAFHSYRMDPMLOEFAEIARSVDYRRGDLPVVSTLTGELDTAGVMATPEYWVRQVREPV	
ò	99		65
g	2570	RFADGVRVLAQQGVAT1 FELGPDATLSAL1 PDCHSWADQAMP1 PMLRKDRTETETVVAAV	2629
ò	99		65
g	2630	<b>ARAHTRGVPVEWSAYFAGTGARRVELPTYAFQRQRYWLETSDYGDVTGIGLAAAEHPLLG</b>	
ò	99		65
g	2690	AVVALADGDGMVLTGRLSVGTHPWLAQHRVLGEVVVPGTAILEMALHAGARLGCDRVEEL	2749
ò	99		65
g	2750	TLETPLVVPERAAGAGSRGPAGGTTVSIETAEERVRTNDAIEIQLLVNAPDEGGRRRVSL	
ò	99		65
a	2810	YSRPAGGSRGGGWTRHATGELVVGTTGGRAVPDWSAEGAESIALDEFYVALAGNGFEYGP	2869
ò	99		65
a a	2870	LFQGLQAAWRRGDEVLAEIAPPAEADAMASGYLLDPALLDAALQASALGDRPEQGGAWLP	2929
ò	99		65
e G	2930	FSFTGVELSAPAGTISRVRLETRRPDAISVAVMDESGRLLASIDSLRLRSVSSGQLANRD	2989
ò	99		65
Q Q	2990	AVRDALFEVTWEPVATQSTEPGRWALLGDTACGKDDLIKLATDSADRCADLAALAEKLDS	3049
ò	99		65
ф	3050	SALVPDVVVYCAGEQADPGTGAAALAETQQTLALLQAWLAEPRLAEARLVVVTCAAVTTA :	3109
ò	99		

đ	3110 PSC	PSDGASELAHAPLWGLLRAAQVENPGQFVLADVDGTAESWRALPSALGSMEPQLALRKGA 3169	
ò	99	59	ī.
qq	3170 VRA	VRAPRLASVAGQIDVPAVVADPDRTVLISGGTGLLGGAVARHLVTERGVRRLVLTGRRGW 3229	229
ò	66 - AP	APNIT	C1
g	3230 DAP		583
ò	83	84	_
q	3290 ESL	: ESLSPDDVGAVFGPKAAGAWNLHELTRDTDLSFFALFSSLSGVAGAPGOGNYAAANAFLD 3349	149
ò	85	88	_
qq	3350 ALA	ALAHYRRSQGLPAVSLAWGLWEQPSGMTETLSEVDRSRIARANPPLSTKEGLRLFDAGLA 3409	60
ò	85	88	
<u>ය</u>	3410 LDR	LDRAAVVPAKLDRTFLAEQARSGSLPALLTALVPPIRRNRRASGTELADEGTLLGVVREH 3469	69
ò	85	84	_
<u>유</u>	3470 AAA	AAAVLGYSSAADVGVERAFRDLGFDSLSGVELRNRLAGVLGVRLPATAVFDYPTPRALAR 3529	62
ò	85	16OddNILD	
q	3530 FLH	FLHQELADEIATTPAPVTTTRAPVAEDDLVAIVGMGCRFPGGVSSPBELMRLVAGGVDAV 3589	68
ò	92	91	
g	3590 ADF	ADFPADRGWDLAGLFDPDPERAGKTYVREGAFLTDADRFDAGFFGISPREALAMDPQQRL 3649	4
ò	92	91	
Q	3650 LLE	LLELSWEAIERAGIDPGSLRGSRTGVFAGLMYHDYGARFASRAPEGFEGYLGNGSAGSVA 3709	60
ò	92	16 91	
a	3710 SGRIAY	IAYSFGFEGPAVTVDTACSSSLVALHLAGQSLRSGECDLALAGGVTVMSTPGTFVEF 3769	69
ò	92	16	
g	3770 SRQF	SRQRGLAPDGRCKSFAESADGTGWGEGAGLVLLERLSDARRNGHRVLAVVRGSAVNQDGA 3829	29
ò	92	96 QTQ	
đ	3830 SNGLTA	 LTAPNGPSQORVIQQALASAGLSVSDVDAVEAHGTGTRLGDPIEAQALATYGRDRD 3889	68
δ	95 PG	66	
đ	3890 PGRE	PGRPLWLGSVKSNIGHTQAAAGVAGVIKMYMAMRHGQLPRTLHVDAPSSQVDWSAGRVQL 3949	4
ò	100	66	
q	3950 LTEN	LTENTPWPDSGRPCRVGVSSFGISGTNAHVILEOSTGGMDQAAEPDSSPVLDVPVVPWVV 4009	60
ò	100	106	v
q	4010 SGKT	SGKTPEALSAQAATLATYLDQNVDVSPLDVGISLAVTRSALDERAVVLGSDRDTLLSGLN 4069	69
ò	107	108	60
qq	4070 ALAA	   ALAAGHEAAGVVTGPVGIGGRTGFVFAGQGGQWLGMGRRLYSEFPAFAGAFDEACAELDA 4129	53
ò	109	108	m
q	4130 NLGRI	EVGVRDVVFGSDESLLDRTLMAQSGLFALQVGLWELLGTWGVRPSVVLGHSVGELA 4189	68
ò	109	108	~

QY     109       DD     4250       QY     109       DD     4310       QY     109       DD     4430       QY     112       DD     4850       QY     112       DD     4850       QY     121       DD     4610       QY     121       QY     123       QY     123       QY     123       QY     123       DD     4610       QY     123       QY     123       DD     4610       QY     123       QY     123       DD     4670       QY     123       QY     123       QY     123       QY     123       QY     123       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     163       QY     164       QY     164       QY </th <th>9</th>	9
0 > 0 > 0 + 4 + 4	APGSVVLSGDRDVLDGIAGRLDGQGIRSRWLRVSHAFHSHRMDPMLAEFAELARSVDYRS
4 4	PRLPIVSTLTGNLDDVGVMATPEYWVRQVREPVRFADGVQALVDQGVDTIVELGPDGALS SLVQECVAESGRATGIPLVRRDEVRTVLDALAQTHTRGGAVDWGSFFAGTRATQVDLP TYAFQRQRYWLEPSDSGDVTGVGLTGAEHPLLGAVVPVAGGDEVLLTGRLSVGTHPWLAE
4 4	PRLPIVSTLTGNLDDVGVMATPEYWVRQVREPVRFADGVQALVDQGVDTIVELGPDGALS  SLVQECVAESGRATGIPLVRRDRDEVRTVLDALAQTHTRGGAVDWGSFFAGTRATQVDLP  TYAFQRQRYWLEPSDSGDVTGVGLTGAEHPLLGAVVPVAGGDEVLLTGRLSVGTHPWLAE
	SLVQECVAESGRATGIPLVRRDRDEVRTVLDALAQTHTRGGAVDWGSFFAGTRATQVDLP
	SLVQECVAESGRATGIPLVRRDRDEVRTVLDALAQTHTRGGAVDWGSFFAGTRATQVDLP
	TYAFQRQRYKWLEPSDSGDVTGVGLTGAEHPLLGAVVPVAGGDEVLLTGRLSVGTHPWLAE
	TYAFQRORYWLEPSDSGDVTGVGLTGAEHPLLGAVVPVAGGDEVLLTGRLSVGTHPWLAE
,	: HRVLGEVVVPGTALLEMAWRAGSQVGCERVEELTLEAPLVLPERGAAAVQLAVGAPDEAG
,	PDGNRQVRG
·	
•	TV.
	:  LTYGPVFQGLRAAWRHGDDIFAELAGSPDASGFGIHPALLDAALHAMALGASPDSEARLP
	FSWRGAQLYRAEGAALRVRLSPLGSGAVSLTLVDATGRRVAAVESLSTRPVSTDOIGAGR
Oy 126	GACSPTW
Db 4730	GDQERLLHVEWVRSAESAGMSLTSCAVVGLGEPEWHAALKTTGVQVESHADLASLATEVA
0y 133	
Db 4790	KRGSAPGAVIVPCPRPRAMQELPTAARRATQQAMAMLQQWLADDRFVSTRLILLTHRAVS
0y 133	
Db 4850	AVAGEDVLDLVHAPLWGLVRSAQAEHPDRFALIDMDDERASQTALAEALTAGEAQLAVRS
0y 133	
Db 4910	GVVLAPRLGQVKVSGGEAFRWDEGTVLVTGGTGGLGALLARHLVSAHGVRHLLLASRRGI
0y 142	
Db 4970	AAPGADELVAELEQAGADVAVVACDSADRDSLARLVASVPAENPLRVVVHAAGVLDDGVL
0y 142	
Db 5030 1	MSMSPERLDAVLRPKVDAAWYLHELTRELGLSAFVLFSSVAGLFGGAGQSNYAAGNAFLD
0y 142	
DP 2090 1	ALAHCRQAQGLPALSLASGLWASIDGWAGDLAAADVERLSRAGIGPLSAPGGLALFDAAV
0y 142 ·	
5150	GSDEPLLAPVRLDVEALRVQARSVQTRIPEMLHGMAMGPSRRTPFTSRVEPLHERLAGLS 5209
Oy 142 -	141
Db 5210 E	EGERROQVLORVRADIAVVLGHGRSSDVDIEKPLAELGFDSLTAIELRNRLATATGLRLP 5269
Oy 142 -	141
Db 5270 A	ATLAFDHGTAAALAQHVCAQLGTATAPAPRRTDDNDATEPVRSLFQQAYAAGRILDGMDL 5329

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30;
                                                                                  5330 VKVAAQLRPVFGSPGELESLPKPVQLSRGPEELALVCMPALIGMPPAQQYARIAAGFRDV 5389
                                                                                                                                                                                                                                                                           5390 RDVSVIPMPGFIAGEPLPSAIEVAVRTQAEAVLQEFAGGSFVLVGHSSGGWLAHEVAGEL 5449
                         ...... 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1057 ACTVGGEPDAAPCQAALWGMGRVAALEHPGSWGGLVDLDPEESPTEVEALVAELLSPDAE 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1117 DQLAFRQGRRRAARLVAAPPEGNAAPVSLSAEGSYLVTGGLGALGLLVARWLVERGAGHL 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1177 VLISRHGLPDREEWGRDQPPEVRARIAAIEALEAQGARVTVAAVDVADAEGMAALLAAVE 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 27.0%; Score 209; DB 3; Length 7257;
Best Local Similarity 1.5%; Pred. No. 3.1;
Matches 93; Conservative 23; Mismatches 32; Indels 6165; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1237 PPLRGVVHAAGLLDDGLLAHÖDAGRLARVLRPKVEGAWVLHTLTREQPLDLFVLFSSASG 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        877 ÄÄGGSVSWPGVFPTAGRRVPLPTYPWORQRYWIEAPAEGLGATAADALAQWFYRVDWPEM 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1297 VFGSIGGGSYAAGNAFLDALADLRRTQGLAALSIAWGLWAEGGMGSQAQRREHEASGIWA 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٤ ----- المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المناطقة المن
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                                                                                                                                                                                    142 -----
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Sequence 5, Application US/09335409

Patent No. 6121029

GENERAL INPORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Schupp, Thomas

APPLICANT: Ligar, James

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 5

LENGRIT 7257

TYPE: DATE TO 5
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ORGANISM: Sorangium cellulosum
S-09-335-409-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ------
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US-09-335-409-5
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qq	2437 EEASRGSWLVLADKGGVGEAVAALSTRGLPCVVLHAPAETSATAELVTEAAGGRSDWQV	249
ò	36	39
q	2497 VLYLWGLDAVVGAEASIDEIGDATRRATAPVLGLARFLSTVSCSPRLWVVTRGACIVGDE	2556
ò		
q	2557 PAIAPCQAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ	
ò	40	39
g	2617 LAFRHGRRHAARLVAAPPOGQAAPVSLSAEASYLVTGGLGGLGGLTVAOWLVELGARHLVL	2676
ò	40	39
ద	2677 TSRRGLPDRQAWCEQQPPEIRARIAAVEALEARGARVTVAAVDVADVEPWTALVSSVEPP	2736
ò	40	39
Q	2737 LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAVW	2796
ò	40	39
a	2797 GSHSQGAYAAANAFLDGLAHLRRSQSLPALSVAWGLWAEGGMADAEAHARLSDIGVLPMS	2856
ò	40	39
q	2857 TSAALSALQRLVETGAAQRTVTRMDWARFAPVYTARGRRNLLSALVAGRDIIAPSPPAAA	2916
ò	40	9
q	2917 TRNWRGLSVAEARVALHEIVHGAVARVLGFLDPSALDPGMGFNEQGLDSLMAVEIRNLLQ	2976
ò	40	39
q	2977 AELDVRLSTTLAFDHPTVQRLVEHLLVDVLKLEDRSDTÖHVRSLASDEPIAIVGAACRFP	3036
ò	40	39
g	3037 GGVEDLESYWQLLAEGVVVSAEVPADRWDAADWYDPDPEIPGRTYVTKGAFLRDLORLDA	3096
ò	40	39
q	3097 TFFRISPREAMSLDPQQRLLLEVSWEALESAGIAPDTLRDSPTGVFVGAGPNEYYTQRLR	3156
ò	40	39
Q	3157 GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACOSLRLGEC	3216
ò	40	39
d d	3217 DQALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRLRDAQ	3276
ò	40	2
පු	   3277 RAGDSILALIRGSAVNHDGPSSGLTVPNGPAQQALLRQALSQAGVSPVDVDFVECHGTGT	3336
ò	43 DP	4
q	3337 ALGDPIEVQALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEQIPA	3396
ò	45	4
q	3397 QPELGELNPHLPMNTLPVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP	3456
ò	45	4
qq	3457 APAAPARPVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA 3	516
ò	45	•

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seqid\_1\_15fused.rai

g	3517	1ATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP 3576	9
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Вb	3577	AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS 3636	ø
ò	45	74	
qq	3637	WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAMVAIAASEAEV 3696	9
ò	45		
g	3697	AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 3756	vo
ò	51	20	
qq	3757	PMLEDFQRVAATIAYRAPDRPVV	to.
ò	51	05	
g	3817	AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 3876	10
ò	51		
qq	3877	KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 3936	
ò	53	55	
a	3937	   IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 3996	
ò	26	55	
.q	3997	VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 4056	
à	26	55	
g	4057	IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD 4116	
à	26	55	
ą	4117	NGFAVSLLSTRSEPEDDGTPPLPFAVERVRWMRAPVGRVRCGGVPRSQAFGVSSFVLVDE 4176	
ጵ	. 95	99	
q	4177	TGEVVAEVEGFVCRRAPREVFLRQESGASTAALYRLDWPEAPLPDAPAERIEESWVVVAA 4236	
⋧	. 95	55	
ą	4237	PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL 4296	
≿	. 95	56	
ą	4297 8	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE 4356	
≿	- 95		
ă	4357 A		
≿	. 99	999	
ą	4417 I	TLDQLRLAPAQRRAPGPGEVEIKVTASGLNFRTŲLAVLGMYPGDAGPMGGDCAGVATAVG 4476	
<u>~</u>	99	9	
ũ	4477 0	QGVRHVAVGDAVMTLGTLHRFVTVDARLVVRQPAGLTPAQAATVPVAFLTAWLALHDLGN 4536	
≥	- 99	9	٠
ō	4537 L	LRRGERVLIHAAAGGVGMAAVQIARWIGAEVFATASPSKWAAVQAMGVPRTHIASSRTLE 4596	
≥	- 99	99	
۵	4597 F	FAETFROVTGGRGVDVVI.NAI AGFFVDA ST. ST. ST. CEGE ET EMCKERTERER ALLE ST. ST. ST. ST. ST. ST. ST. ST. ST. ST.	

ò	99	***************************************	65
QQ	4657	RYRVFDILELAPDRTREILERVVEGFÅAGHLRALPVHAFAITKAEAAFRFMAQARHOGKV	4716
ò	99		65
Q	4717	VLLPAPSAAPLAPTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA	4776
ò	99		65
q	4777	EIEALGARVTIAASDVADRNALEAVLQAIPAEWPLQGVIHAAGALDDGVLDEQTTDRFSR	4836
ò	99	APNIT	70
qq	4837	VLÄPKVTGAMNLHELTAGNDLAFFVLFSSMSGLLGSAGQSNYAAANTFLDALAAHRRAEG	4896
ò	7.1	ANLTSSL	77
QQ	·4897 I	LAAQSLAWGPWSDGGMAAGLSAALQARLARHGMGALSPAQGTALLGQALARPBŢOLGAMS	4956
ò	78		77
g	4957 I	LDVRAASQASGAAVPPVWRALVRAEARHTAAGAQGALAARLGALPEARRADEVRKVVQAE	5016
ò	78		77
QQ	5017 1	IARVLSWSAASAVPVDRPLSDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR	5076
ò	78 -		77
g	5077 W	WLLDKVLAVAEPSVSSAKSSPQVALDEPIAIIGIGCRFPGGVADPESFWRLLEEGSDAVV	5136
ò	- 84		77
Dp	5137 E	EVPHERWDIDAFYDPDPDVRGKMTTRFGGFLSDIDRFDPAFFGISPREATTMDPQQRLLL	5196
ò	78 -		77
qq	5197 E	:TSWEAFERAGILPERLMGSDTGVFVGLFYQEYAALAGGIEAFDGYLGTGTTASVASGRI	5256
ò	- 84		77
QQ	5257 S	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR	5316
ò	78 -		77
QQ	5317 G	GLAPDGRCKSFSAAADGVGWSEGCAMLLLKPLRDAQRDGDPILAVIRGTAVNQDGRSNGL	5376
ò	- 84	2	7.7
qq	5377 T.	TAPNGSSQQEVIRRALEQAGLAPADVSYVECHGTGTTLGDPIEVQALGAVLAQGRPSDRP	5436
ò	78 -		77
අ	5437 L	LVIGSVKSNIGHTQAAAGVAGVIKVALALERGLIPRSLHFDAPNPHIPWSELAVQVAAKP	5496
à	78 -		77
g	5497 VJ	VEWTRNGVPRRAGVSSFGVSGTNAHVVLEEAPAAFAPAARSAELFVLSAKSAALDAQ !	5556
તે	78 -		77
ą	5557 A	AARLSAHVVAHPELGLGDLAFSLATTRSPMTYRLAVAATSREALSAALDTAAQGQAPPAA !	5616
ጵ	78	3 SMSDNST	84
ą	5617 A	ARGHASTGSAPKVVFVFPGQGSQWLGMGQKLLSEEPVFRDALSACDRAIQAEAGWSLLAE !	5676
⋩	95 -		4
ą	5677 LA	LAADETTSQLGRIDVVOPALFAIEVALSALWRSWGVEPDAVVGHSMGEVAAAHVAGALSI. 9	3.6

Db 6817 RAADAFRKWAQAQHLGKLVLALEDPDVRIRVPGESGVAIRADGAYLVTGGLGGLGLSVAG 6876   Qy		127	136ITEDTG		Oy 144LGVFI 148  Db 7177 LRNRIEAVLGITM 7189	RESULT 7 US-09-568-102-5 ; Sequence 5, Application US/09568102	. S. F. F.		; APPLICANT: CYF, Devor ; APPLICANT: Goerlach, Joern ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES	; FILE REFERENCE: 4-30582A ; CURRENT APPLICATION WNMBER: US/09/568,102 ; CURRENT FILING DATE: 2000-05-10	IION NUMBER: 09/33 ATE: 1999-06-17 ID NOS: 30 DEIN VEY: 2.0		; TYPE: PRT ; ORGANISM: Sorangium cellulosum US-09-568-102-5	27.0%; Score 209; DB 4; Length 7257; nilarity 1.5%; Pred. No. 3.1;	33; Conservative 23;	87	Cy S	93	Db 997 GRNDWOGVLYLWGLDAVVEAGASAEEVAKVTHLAAAPVLALIOALGTGPRSPRLWIVTRG 1056		Db 1057 ACTVGGEPDAAPCQAALWGMGRVAALEHPGSWGGLVDLDPEESPTEVEALVAELLSPDAE 1116
EDAVAIICRRSLLLRRISGQGEMAVVELSLAEAEAALLGYEDRLSVAVSNSPRSTVLAGE	65 85	5857 STIMAGPELVASYWADNVRQPVRFAEAVQSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 85	DD 5917 KEGVAVGSEKRGQDERLSMEEALGALWVHGQAVGWERLFSAGGAGERRVPLPTYPWQRER 5976 OY 85 90	OY 91 94  Db 6037 VVFPGAAYLEMALSSGAEALGDGPLQVSDVVLAEALAFADDTPAAVQVMATEERPGRLQF 6096	OY 95 97 	Oy 98 97  Db 6157 LEYGPAFQGLVELWRGEGEALGRVRLPEAAGSPAACRLHPALLDACFHVSSAFADRGEAT 6216	Oy 98 97  Db 6217 PWVPVEIGSLRWFORPSGELWCHARSVSHCKPTPDRRSTDFWVVDSTGAIVAETSGLVAO 6276	76		9	OY 100 LVLY	Qy 107 106	Db 6457 IDLDPARRDGEVDELLAELLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516 Qy 107 FDLEL	: 6517 FRLEIDGSGVLDDLVLRATERRPPGPGEVEIAVEAAGLNFLDVMRAMGIYPGPGDGPVAL		DD 05// GAELSGEKIVAMGEGVESLKIGGDVVAVAPFSFGTHVTIDARMLAPRPAALTAAQAAALPV 6636 Qy 112	6637 AFMTAWYGLVHLGRLRAGERVLIHSATGGTGLAAVQIARHLGAEIFATAGTPEKRAWLRE	Oy 112 115	Db 6697 QGIAHVMDSRSLDFAEQVLAATKGEGVDVVLNSLSGAAIDASLSTLVPDGRFIELGKTDI 6756	v	;

ò	80	6
qq	1117	DOLAFRQGRRRAARLVAAPPEGNAAPVSLSAEGSYLVTGGLGALGLLVARWLVERGAGHL 1176
ò	80	LLVAVG 15
qq	1177	VLISRHGLPDREEWGRDQPPEVRARIAAIEALEAQGARVTVAAVDVADAEGWAALLAAVE 1236
ò	16	P
g	1237	PPLRGVVHAAGLLDDGLLAHQDAGRLARVLRPKVEGAWVLHTLTREQPLDLFVLFSSASG 1296
ò	24	
g	1297	VFGSIGOGSYAAGNAFLDALADLRRTOGLAALSIAWGLWAEGGMGSQAQRREHEASGIWA 1356
ò	24	23
අ	1357	MPTSRALAAMEWLLGTRATQRVVIQMDWAHAGAAPRDASRGRFWDRLVTATKEASSSAVP 1416
ò	24	23
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ò	24	23
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ò	24	EDTERY
qq	1537	PGGVEDLESYWQLLTEGVVVSTEVPADRWNGADGRVPGSGEAQRQTYVPRGGFLREVETF 1596
ò	30	55
g	1597	DAAFFHISPREAMSLDPQQRLLLEVSWEAIERAGQDPSALRESPTGVFVGAGPNEYAERV 1656
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qq	1657	QELADEAAGLYSGTGNMLSVAAGRLSFFLGLHGPTLAVDTACSSSLVALHLGCQSLRRGE 1716
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ò	30	56
QQ	1777	QRDRDPILAVIRGTAINHDGPSSGLTVPSGPAQEALLRQALAHAGVVPADVDFVECHGTG 1836
ò	30	55
g	1837	TALGDPIEVRALSDVYGQARPADRPLILGAAKANLGHMEPAAGLAGLLKAVLALGQEQIP 1896
ò	30	53
g	1897	AQPELGELNPLLPWEALPVAVARAAVPWPRTDRPRFAGVSSFGMSGTNAHVVLEEAPAVE 1956
ò	30	
අු	1957	LWPAAPERSAELLVLSGKSEGALDAQAARLREHLDMHPELGLGDVAFSLATTRSAMNHRL 2016
ò	30	29
8	2017	AVAVTSREGLLAALSAVAQGQTPPGAARCIASSSRGKLAFLFTGQGAQTPGMGRGLCAAW 2076 .
à	30	29
g	2077	PAFREAFDRCVALFDRELDRPLREVMWAEPGSAESLLLDQTAFTQPALFTVEYALTALWR 2136
ò	30	59
q	2137	SWGVEPELVAGHSAGELVAACVAGVFSLEDGVRLVAARGRLMQGLSAGGAMVSLGAPEAE 2196
તે	30	5

QQ .	2197 VA	VAAAVAPHAASVSIAAVNGPEQVVIAGVEQAVQAIAAGFAARGARTKRLHVSHASHSPLM 2256
ò	30	35
q	2257 EP	PMLEEFGRVAASVTYRRPSVSLVSNLSGKVVADELSAPGYWVRHVREAVRFADGVKALH 2316
ò	36	35
Q	2317 EA	EAGAGTFVEVGPKPTLLGLLPACLPEAEPTLLASLRAGREEAAGVLEALGRLWAAGGSVS 2376
ò	36	35
qq	2377 WP	WPGVPPTAGRRVPLPTYPWQRQRYWPDIEPDSRRHAAADPTQGWFYRVDWPEIPRSLQKS 2436
ò	36	35
q	2437 EE	EEASRGSWLVLADKGGVGEAVAALSTRGLPCVVLHAPAETSATAELVTEAAGGRSDWQV 2496
ò	36	1GAE39
q	2497 VL	VLYLWGLDAVVGAEASIDEIGDATRRATAPVLGLARFLSTVSCSPRLWVVTRGACIVGDE 2556
ò	40	39
ą a	2557 PA	PAIAPCQAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ 2616
ò	40	39
a	2617 LA	LAFRHGRRHAARLVAAPPQGQAAPVSLSAEASYLVTGGLGGLGLIVAQWLVELGARHLVL 2676
ò	40	39
<u>අ</u> .	2677 TS	TSRRGLPDRQAWCEQQPPEIRARIAAVEALEARGARVTVAAVDVADVEPMTALVSSVEPP 2736
ò	40	39
q	2737 LR	LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAV# 2796
ò	40	66 39
đ	2797 GSI	GSHSQGAYAAANAFLDGLAHLRRSQSLPALSVAWGLWAEGGMADAEAHARLSDIGVLPMS 2856
ò	40	663
g	2857 TS	TSAALSALQRLVETGAAQRTVTRMDWARFAPVYTARGRRNLLSALVAGRDIIAPSPPAAA 2916
ò	40	66 3
g	2917 TRI	trnwrglsvaearvalheivhgavarvlgPldpsaldpgmgFneqgldsl <b>w</b> gveirnllo 2976
ò	40	663
q	2977 AEL	LDVRLSTTLAFDHPTVQRLVEHLLVDVLKLEDRSDTQHVRSLASDEPIAIVGAACRFP 3036
ò	40	39
QQ	3037 GGVE	VEDLESYWQLLAEGVVVSAEVPADRWDAADWYDPDPEIPGRTYVTKGAFLRDLQRLDA 3096
ò	40	66 39
q	3097 TF	TFFRISPRĖAMSLDPQQRLLLEVSWEALESAGIAPDTLRDSPTGVFVGAGPNEYYTQRLR 3156
ò	40	66 39
q	3157 GF7	GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACQSLRLGEC 3216
ò	40	663
q	3217 DQA	DQALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRLRDAQ 3276
ò	40	1

ą	3277	RAGDSILALIRGSAVNHDGPSSGLTVPNGPAQQALLRQALSQAGVSPVDVDFVECHGTGT 3	3336
⋧	43	D	44
ą	3337	   ALGDP1EVQALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEQ1PA	3396
≿	45	<b>b</b>	44
ရ	3397	<b>OPELGELNPHLPWNTLPVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP</b>	3456
≿	45		44
ð	3457	APAAPARPVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA	3516
≿	4 5		44
മ	3517	IATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP	3576
≿	45		4 4
à	3577	AFREAFDRCVALFDREIDQPLREVWWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS	3636
≿	45		44
ည	3637	WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAMVAIAASEAEV	3696
≿	45	SLGAQF	20
ရွ	3697	AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD	3756
≿	51	S	20
ą	3757	PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA	3816
≿	51	5	S.O
Q	3817	AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW	3876
≿	51	. S	52
ą	3877	KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 3:	3936
≽	53	15	55
ą	3937	IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 3	3996
≿	26		55
ð	3997	VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA	4056
≥-	26		55
۵	4057	IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD	4116
≿	56		55
Q	4117	NGFAVSLLSTRSEPEDDGTPPLPFAVERVRWRAPVGRVRCGGVPRSQAFGVSSFVLVDE	4176
≿	26	15	55
ည	4177	TGEVVAEVEGFVCRRAPREVFLRQESGASTAALYRLDWPEAPLPDAPAERIEESWVVVAA	4236
≿	26	35	55
Q	4237	PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL	4296
<u>≻</u>		18	55
ą	4297	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE	4356
<b>~</b>	56	69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 69 6	9
Q	4357	ADAARSADVLLRELGRADDETQVAFRSGKRRVARLVKATTPEGLLVPDAESYRLEAGQKG	4416

ò	99		65
QQ	4417	TLDQLRLAPAQRRAPGPGEVEIKVTASGLNFRTVLAVLGMYPGDAGPMGGDCAGVATAVG	447
ò	99		65
g	4477	QGVRHVAVGDAVMTLGTLHRFVTVDARLVVRQPAGLTPAQAATVPVAFLTAWLALHDLGN	453
ò	99		65
q	4537	LRRGERVLIHAAAGGVGMAAVQIARWIGAEVFATASPSKWAAVQAMGVPRTHIASSRTLE	459
ò	99		65
QQ	4597	FAETFRQVTGGRGVDVVLNALAGEFVDASLSLLSTGGRFLEMGKTDIRDRAAVAAAHPGV	465
ò	99		9
qq	4657	RYRVFDILELAPDRTREILERVVEGFAAGHLRALPVHAFAITKAEAAFRFMAQARHQGKV	471
ò	99		65
QQ	4717	VLLPAPSAAPLAPTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA	477
ò	99		65
QQ	4777	EIEALGARVTIAASDVADRNALEAVLQAIPAEWPLQGVIHAAGALDDGVLDEQTTDRFSR	483
ò	99	APNIT	70
셤	4837	:  VLAPKVTGAWNLHELTAGNDLAFFVLFSSMSGLLGSAGOSNYAAANTFLDALAAHRRAEG	489
ò	71	ANLTSSL	77
g	4897	LAAQSLAWGPWSDGGMAAGLSAALQARLARHGMGALSPAQGTALLGQALARPETQLGAMS	495
à	78		77
g	4957	LDVRAASQASGAAVPPVWRALVRAEARHTAAGAGGALAARLGALPEARRADEVRKVVQAE	501
à	78		77
gg	5017	IARVLSWSAASAVPVDRPLSDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR	507
à	78		77
q	5077	WLLDKVLAVAEPSVSSAKSSPQVALDEPIAIIGIGCRFPGGVADPESFWRLLEEGSDAVV	513
à	78	\$	77
g	5137	EVPHERWÖIDAFYDPDPVRGKMTTRFGGFLSDIDRFDPAFFGISPREATTMDPQQRLLL	519
ò	78		77
g	5197	ETSWEAFERAGI LPERLMGSDTGVFVGLFYQEYAALAGGI EAFDGYLGTGTTASVASGRI	525
ઠે	78		77
g	5257	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR	531
ે	78		11
g	5317	GLAPDGRCKSFSAAADGVGWSEGCAMLLLKPLRDAQRDGDP1LAVIRGTAVNQDGRSNGL	537
à	78		77
g G	5377	TAPNGSSQQEVIRRALEQAGLAPADVSYVECHGTGTTLGDPIEVQALGAVLAQGRPSDRP	543
à	78		77
ź	5427	BASSWOWS 199WITHBUG SERVICES I DESTINATION AND THE SERVICES IN THE SERVICES AND THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES IN THE SERVICES I	240

qq	5497 VEWTRNGVPRRAGVSSFGVSGTNAHVVIJERAPAAFADPAAPEAPEAPET ENT CANCALATOR COLOR	Db 6577 GAECSGRI
ò	78	Oy 112
q	5557 AARLSAHVVAHPELGLGDLAFSLATTRSPMTYRLAVAATSREALSAALDTAAGGABDBA 6616	Db 6637 AFMTAWYG
ò		Oy 112
g	LLAE	Db 6697 QGIAHVMD
ò		Qy 116
g	5677 LAADETTSQLGRIDVVQPALFALEVALSALWRSWGVEPDAVVGHSMGEVAAAHVAGALSL 5736	Db 6757 YADRSLGL
ò		Qy 116
g	5737 EDAVAIICRRSLLLRRISGGGEMAVVELSLAEAEAALLGYEDRLSVAVSNSPRSTVLAGE 5796	Db 6817 RAADAFRK
ò		Qy 116
g	5797 PAALAEVLAILAAKGVFCRRVKVDVASHSPQIDPLRDELLAALGELEPRQATVSMRSTVT 5856	Db 6877 WLAEQGAG
ò		Qy 119RGVT(
q	5857 STIMAGPELVASYWADNVRQPVRFAEAVQSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 5916	Db 6937 GMPLRGVV
ò	85	Oy 127
Q	5917 REGVAVGSLRRGQDERLSMLEALGALWVHGQAVGWERLFSAGGAGLRRVPLPTYPWQRER 5976	DD 6997 GLLGSPGQ
ò		Oy 136 ITEDT
q	:: :	Db 7057 TRSLTPDEC
ò	91 DDTD 94	Oy 144
QQ	6037 VVFPGAAYLEMALSSGAEALGDGPLQVSDVVLAEALAFADDTPAAVQVMATEERPGRLOF 6096	Db 7117 LAGDRDLLE
ò	95pGH 97	Oy 144
g	6097 HVASRVPGHGGAAFRSHARGVLRQIERAEVPARLDLAALRARLQASAPAAATXAALAEMG 6156	Db 7177 LRNRIEAVL
ò	96	RESULT A
Q	6157 LEYGPAFQGLVELWRGEGEALGRVRLPEAAGSPAACRLHPALLDACFHVSSAFADRGEAT 6216	
ò	97	6.7
Q Q	6217 PWVPVEIGSLRWFQRPSGELWCHARSVSHGKPTPDRRSTDFWVVDSTGAIVAEISGLVAQ 6276	APPLICANT: Schup
ò		
g	6277 RLAGGVRRREEDDWFMEPTAVPGSEVMAGRWLLIGSGGGLGAALHSALTEAGHSVV 6336	APPLICANT: Cyr,
ò	96 OK	TITLE OF INVENTION
q	6337 HATGRGTSAAGLQALLTASFDGQAPTSVVHLGSLDERGVLDADAPFDADALEESLVRGCD 6396	CURRENT APPLI
ò	100 LVLY 106	PRIOR APPLICATION
q	;   6397 SYLWTVQAVAGAGFRDPPRLWLVTRGAQAIGAGDVSVAQAPLLGLGRVIALEHAELRCAR 6456	SOFTWARE: Patent:
ò	107 106	
g	6457 IDLDPARRDGEVDELLAELLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516	TYPE: PRT
ò	107 FDLEL111	US-09-567-969-5
g	6517 FRLBIDGSGVLDDLVLRATERRPPGPGEVEIAVEAAGLNFLDVMRAMGIYPGPGDGPVAL 6576	Query Match Best Local Similar
ò	113	CO CONTRACTOR

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27.0%; Score 209; DB 4; Length 7257;
arity 1.5%; Pred. No. 3.1;
ongervative 23; Mismatches 32; Indels 6165; Gaps 30;
RIVAMGEGVESLRIGQDVVAVAPFSFGTHVTIDARMLAPRPAALTAAQAAALPV 6636
                                                                             GLVHLGRLRAGERVLIHSATGGTGLAAVQIARHLGAEIFATAGTPEKRAWLRE 6696
                                                                                                                                                           IDSRSLDFAEQVLAATKGEGVDVVLNSLSGAAIDASLSTLVPDGRFIELGKTDI 6756
                                                                                                                                                                                                                                          LAHFRKSLSYSAVDLAGLAVRRPERVAALLAEVVDLLARGALQPLPVEIFPLS 6816
                                                                                                                                                                                                                                                                                                                          KMAQAQHLGKLVLALEDPDVRIRVPGESGVAIRADGAYLVTGGLGGLGLSVAG 6876
                                                                                                                                                                                                                                                                                                                                                                                                          GHLVLVGRSGAVSAEQQTAVAALEAHGARVTVARADVADRAQMERILREVTAS 6936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHAAĞİLDDGLLMQQTPARFRAVMAPKVRGALHLHALTREAPLSFFVLYASGA 6996
                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGNYAAANTFLDALAHHRRAQGLPÅLSIDWGLFADVGLAAGQQNRGARLVTRG 7056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EĠLWALERLLDGDRTQAGVMPFDVRQWVEFYPAAASSRRLSRLMTARRVASGR 7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRLATAEAGARAGMLQEVVRAQVSQVLRLSEGKLDVDAPLTSLGMDSLMGLE 7176
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Ligon, James
Molnar, Iervan
Zirkle, Ross
Cyr, Devon
Goerlach, Joern
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- DATE: 1999-06-17
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VLGITM 7189
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ò	-1	AAGG	
qq	877	   AAGGSVSWPGVFPTAGRRVPLPTYPWQRQRYWIEAPAEGLGATAADALAQWFYRVDWPEM	936
ò	ß	, III	7
e G	937	PRSSVDSRRARSGGWLVLADRGGVGEAAAALSSQGCSCAVLHAPAEASAVAEQVTQALG	966
ò	60		7
a a	997	GRNDWQGVLYLWGLDAVVEAGASAEEVAKVTHLAAAPVLALIQALGTGPRSPRLWIVTRG :	1056
ò	ω		7
g	1057	ACTVGGEPDAAPCQAALWGMGRVAALEHPGSWGGLVDLDPEESPTEVEALVAELLSPDAE	1116
ઠે	ω		4
Ω	1117	DOLAFROGRRRAARLVAAPPEGNAAPVSLSAEGSYLVTGGLGALGLLVARWLVERGAGHL 1	1176
ò	∞	( DNYNTT	15
a	1177	VLISRHGLPDREEWGRDQPPEVRARIAAIEALEAGGARVTVAAVDVADAEGMAALLAAVE	1236
ò	16	PDVFQAHQ	23
g G	1237	PPLRGVVHAAGLLDDGLLAHQDAGRLARVLRPKVEGAWVLHTLTREQPLDLFVLFSSASG 1	1296
ò	24		23
ap	1297	VFGSIGQGSYAAGNAFLDALADLRRTQGLAALSIAWGLWAEGGMGSQAQRREHEASGIWA 1	1356
ò	24		23
g	1357	MPTSRALAAMEWLLGTRATQRVVIQMDWAHAGAAPRDASRGRFWDRLVTATKEASSSAVP 1	1416
ò	24		23
QQ	1417	AVERWRNASVVETRSALYELVRGVVAGVMGFTDQGTLDVRRGFAEQGLDSLMAVEIRKRL 1	1476
ò	24		23
a B	1477	QGELGMPLSATLAFDHPTVERLVEYLLSQALELQDRTDVRSVRLPATEDPIAIVGAACRF 1	1536
ò	24	EDTERY	29
g	1537		. 9651
ે	30	5	29
a	1597	DAAFFHISPREAMSLDPQQRLLLEVSWEAIERAGQDPSALRESPTGVFVGAGPNEYAERV 1	1656
ò	30	2	29
q	1657	QELADEAAGLYSGTGNMLSVAAGRLSFFLGLHGPTLAVDTACSSSLVALHLGCQSLRRGE 1	1716
ઠે	30	2	29
q	1717	CDQALVGGVNMLLSPKTFALLSRMHALSPGGRCKTFSADADGYARAEGCAVVVLKRLSDA 1	1776
ò	30	5	29
g	1777	QRDRDPILAVIRGTAINHDGPSSGLTVPSGPAQEALLRQALAHAGVVPADVDFVECHGTG 1	1836
જે	30	5	. 62
g	1837	TALGDPIEVRALSDVYGQARPADRPLILGAAKANLGHMEPAAGLAGLLKAVLALGGEQIP 1	968
ò	30	2	6
a	1897	AQPELGELNPLLPWEALPVAVARAAVPWPRTDRPRFAGVSSFGMSGTNAHVVLEEAPAVE 1	926
ò	30	8	29

qq	1957	LWPAAPERSAELLVLSGKSEGALDAQAARLREHLDMHPELGLGDVAFSLATTRSAMNHRL 201	116
ò	30	29	•
qq	2017	AVAVTSREGLLAALSAVAQGQTPPGAARCIASSSRGKLAFLFTGQGAQTPGMGRGLCAAW 207	940
ò	30	- 39	_
- q	2077	PAFREAFDRCVALFDRELDRPLREVMWAEPGSAESLLLDQTAFTQPALFTVEYALTALWR 213	36
ò	30		_
q	2137	SWGVEPELVAGHSAGELVAACVAGVFSLEDGVRLVAARGRLMQGLSAGGAMVSLGAPEAE 219	96
ò	30	55	_
qq	2197	VAAAVAPHAASVSIAAVNGPEQVVIAGVEQAVQAIAAGFAARGARTKRLHVSHASHSPLM 2256	26
ò	30	VLTNLN 35	
qq	2257	EPMLEEFGRVAASVTYRRPSVSLVSNLSGKVVADELSAPGYWVRHVREAVRFADGVKALH 2310	16
ò	36	35	
පු	2317	EAGAGTFVEVGPKPTLLGLLPACLPEAEPTLLASLRAGREEAAGVLEALGRLWAAGGSVS 2371	16
ò	36	35	
g	2377	WPGVFPTAGRRVPLPTYPWQRQRYWPDIEPDSRRHAAADPTQGWFYRVDWPEIPRSLQKS 243	36
ò	36	35	
අධ	2437	EEASRGSWLVLADKGGVGEAVAAALSTRGLPCVVLHAPAETSATAELVTEAAGGRSDWQV 2496	96
ò	36	39	
අ	2497	VLYLWGLDAVVGABASIDEIGDATRRATAPVLGLARFLSTVSCSPRLWVVTRGACIVGDE 2556	
ò	40	39	
qq	2557	PAIAPCQAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ 2616	16
ò	40	39	
QQ	2617	LAFRHGRRHAARLVAAPPQGQAAPVSLSAEASYLVTGGLGGLGLIVAQWLVELGARHLVL 2676	94
ò	40	39	
qq	2677	TSRRGLPDRQAWCEQQPPEIRARIAAVEALEARGARVTVAAVDVADVEPNÆALVSSVEPP 2736	36
ò	0.4	39	
q	2737	LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAVW 2796	96
ò	40	93	
g	2797	GSHSQGAYAAANAFLDGLAHLRRSQSLPALSVAWGLWAEGGMADAEAHARLSDIGVLPMS 2856	
ò	40	39	
q	2857	TSAALSALQRLVETGAAQRTVTRMDWARFAPVYTARGRRNLLSALVAGRDIIAPSPPAAA 2916	16
ઠે	40	39	
q	2917	TRNWRGLSVAEARVALHEIVHGAVARVLGFLDPSALDPGMGFNEQGLDSLMAVEIRNLLO 2976	9,
ò	40	39	
d D	2977	AELDVRLSTTLAFDHPTVQRLVEHLLVDVLKLEDRSDTQHVRSLASDEPIAIVGAACRFP 3036	36
è	40	c	

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DD 4057 IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD 4116
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3937 IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 399  56 55  3997 VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 405  56
53
53
3877 KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 393 53
51
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3817 AGAATEVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 387 51
3817 AGAATFVEVGPRPVLLGLLPACLGEADAVLVPSLRADRSECEVYLAALGAWYAWGGALDW 51RV
51  3817 AGAATEVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51
51
3757 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51
51  3757 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3817 AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSIRADRSECEVVLAALGAWYAWGGALDW 51  1
51  3157 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3817 AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51  3817 KGVFPDGARRVALPWYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHYULS 53  3937 IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 56  56  57  3997 VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 56
3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 51 3757 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51
1697
45  3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 51  3757 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3817 AGAATFVEVGPRPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51  3817 AGAATFVEVGPRPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51  10  11  3877 KGVFPDGARRVALPWYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 53  1937 IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 56  56  3997 VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 56
3637 WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAWVAIAASEAEV 45 3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALCATFAARGIRTKRLAVSHAFHSPLMD 51 3757 PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51 3817 AGAATFVEVGRKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51 1877 KGVFPDGARRVALPWYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 53 10917 IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 56 56 57 3997 VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 56
45
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3577 AFREAFDRCVALFDREIDQPLREVWWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS 45
35.7 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQAARLDQTAYAQPALFALEYALAALWRS 45 46 47 48 48 49 49 49 49 49 49 40 40 40 40 40 40 40 40 40 40 40 40 41 41 41 41 41 41 41 41 41 41 41 41 41
45  3577 AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS 45  3637 WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRILMQALPAGGAMVAIAASEAEV 45  3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 51  31757 PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  31877 KGVFPDGARRVALGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51
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45  3517 IATTSREALRGALDAAAQOKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP 45  3577 AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS 45  3637 WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAMVAIAASEAEV 45  3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 51  3757 PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3175 PMLEDFGRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3175 PMLEDFGRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWRHVRSAVRFGDGAKALHA 51  3175 PMLEDFGRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWRHVRSAVRFGDGAKALHA 51  3175 PMLEDFGRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWRHVRSAVRFGDGAKALHA 51  3177 GGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51  1
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D 3457 APAAPARPVELVVLSAKSAAALDAAAARLSAHPELSLGDVAFSLATTRSPMEHRLA 45
3457 APAAPARPVELVVLSAKSAAALDAAAARLSAHESAHPELSLGDVAFSLATTRSPMEHRLA 45 3517 IATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP 45 3637 MGVEBHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAWVAIAASEAEV 45 3637 MGVEBHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAWVAIAASEAEV 45 3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATPEARGIRTKRLAVSHAFHSPLMD 51 3157 PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51 3817 AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 51 3817 AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 53
45  3457 APAAPARPVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA 45  3517 IATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQCAQMPGMGRGLVETWP 45  3517 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQARLDQTAYAQPALFALEYALAALWRS 45  3637 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQARLDQTAYAQPALFALEYALAALWRS 45  3637 AASVAPHAATVSIAAVNGFDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD 51  3157 PWLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3157 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3175 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 51  3175 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWRHVRSAVRFGDGAKALHA 51  3175 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWRHVRSAVRFGDGAKALHA 51  3177 KGVFPDGARRVALPWYPWORERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 52  31877 KGVFPDGARRVALPWYPWORERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 53  31997 VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 56  57  58  59  59  50  50  50  50  50  50  50  50
3457 QPELGELNPHLPMNYLLEVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP 45 45 45 45 45 45 47 48 48 48 49 48 49 49 49 49 49 49 49 49 49 49 49 49 49
b 3197 QPELGELNPHLPWNTLEVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP 45
1397 OPELGELNPHLPWNTLPVAVPRKAVPMGROARPRRAGVSAFGLSGTNVHVVLEEAPEVEP 45
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b 3337 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLKAVLALRHEOIPA  45  45  46  3197 QPELGELNPHLPWNTLPVAVPRKAVPWGRGARPRAGVSAFGLSGTNVHVVLEEAPEVEP  45  3187 APAAPARPVELLVLSAKSAAALDAAAARLSAHESAHPELSLGDVAFSLATTRSPMEHRLA  45  3187 AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDGTAYAQPALFALEYALAALWRS  45  3187 AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDGTAYAQPALFALEYALAALWRS  45  3187 AGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMOALPAGGAMVAIAASEAEV  3697 AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFARRGIRTKRLAVSHAFHSPLMD  51  3177 PMLEDFORVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA  51  3187 AGAATFVEVGBKRVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAMGGALDW  51  3187 AGAATFVEVGBKRVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAMGGALDW  51  3187 AGAATFVEVGBKRVVLDGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAMGGALDW  52  31897 KGVFPDGARRVALPWYPWQRERHWMDLTPRSAAPAGIAGRWPLACVGLCMPGAVLHHVLS  53
43 - DP  45 - DP  46 - DP  47 - DP  48 - DP  48 - DP  49 - DP  49 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  46 - DP  47 - DP  48 - DP  48 - DP  49 - DP  40 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  46 - DP  47 - DP  48 - DP  48 - DP  49 - DP  49 - DP  40 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  47 - DP  48 - DP  48 - DP  49 - DP  40 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  47 - DP  48 - DP  48 - DP  49 - DP  40 - DP  40 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  47 - DP  48 - DP  48 - DP  48 - DP  49 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  41 - DP  42 - DP  43 - DP  44 - DP  45 - DP  46 - DP  46 - DP  47 - DP  48 - DP  48 - DP  48 - DP  48 - DP  49 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40 - DP  40
43DP  3137 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA  45
1317 RAGDSILALIRGSANNHDGPSSGLTVPNGPAQQALLROALSGAGVSPVDVDFVECHGTGT 43DP 43DP 44DP 45DP 45DP 46DP 47DP 48DP 49DP 49DP 41DP 41DP 42DP 43DP 44DP 45DP 46DP 47DP 48DP 48DP 49DP 49DP 40DP 41DP 41DP 42DP 43DP 44DP 45DP 46DP 46DP 47DP 48DP 48DP 49DP 49DP 40DP 41DP 41DP 42DP 43DP 44DP 45DP 46DP 47DP 48DP 48DP 49DP 49DP 40DP 40DP 41DP 41DP 42DP 43DP 44DP 45DP 46DP 46DP 47DP 48DP 48DP 49DP 49DP 40DP 40DP 41DP 41DP 42DP 43DP 44DP 45DP 46DP 47DP 48DP 48DP 49DP 49DP 40DP 40DP 40DP 40DP 41DP 41DP 42DP 43DP 44DP 45
1217 RACDSILALIRGSAVNHDGPSSGLTVPNGPAQOALLEQALSGAGVSPVUVDFVECHGTGT 43 - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 10P - 1
1377 RAGDSILALIRGSAVNHDGPSSGLTVPNGPAQQALLRQALSQAGVSPVDVDFVECHGTGT 43
1317 DOALUGGUNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRILRDAD 40 41
1317 DOALVGGVNVLLAPETFVLLSRWRALSPDGRCKTFSADADGYARGEGCAVVVLKGLRDAQ 40
1317 DOALVGCWIVLLAPETFVLLSRWRALSPDGRCKTFSADADCYARGECAVVVLKKILRDAQ 10 1217 RACDSILALIRGSAVNHDGPSSGLTVPNGPAGOALLEGALSGLKAVLALRHEGIPA 13 1 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA 14 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA 14 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA 14 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA 14 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEGIPA 14 - DP 13 1 ALGDPIEVOALSEVYGPGRSGDRPLVLGAARANVAHLEAARGCASGLASLLKAVLALRHEAA 15 - CANADARREAFDRELVALSAKSAAALDAAARLSAHLSAHEBALSGLASLLKAVLALBABERLA 16 - SLA 17 AFREAFDRCVALFDREIDQPLREVWMAAPGLAGAARLDGTAYAQPALFALEYALAALWRS 18 1 ASVARHAATVSIAAVNGPDAVVIAGAEVOVLALGATFAARGIRTKRLAVSHAFHSPLMD 18 1 AGAATFVEVGRRYVANGRERHWMDLTPRSAAPAGIAGRWYRHVRSAVRGGGAALHA 18 1 - CHV 19 1 AGAATFVEVGRRYVALGGLAPACLGGADAVLVPSLRADRSCEVVLAALGAWYAWGGALDW 18 1 AGAATFVEVGRRYVALLGLLPACLGGADAVLVPSLRADRSCEVVLAALGAWYAWGGALDW 18 1 AGAATFVEVGRRYVALBWYRGRRHWMDLTPRSAAPAGIAGRWPLAGVYRLKAIAWEDGCS 19 1 GPRHOPPLGOBILVPGKVVVPGRRHWYLLLSIAARRWFERAIELTGVEFLKAIAWEDGCS 19 1 AGAATFVEVGRRYVARGRRHWMDLTPRSAAPAGIAGRWPLAGVPGDGARGALFRAIELTGVEFLKAIAWEDGCS 19 1 GPRHOPPLGOBILVPGKVVVPGRRHWYLLLSIAARRWFERAIELTGVEFLKAIAMEDGCS 19 1 GPRHOPPLGOBILVPGKVVVPGRRHWYLLLSIAARRWFERAIELTGVEFLKAIAMEDGCS 19 1 GPRHOPPLGOBILVPGKVVVPGRRHWYLLLSIAARRWFERAIELTGVEFLKAIAMEDGCS 19 1 GPRHOPPLGOBILVPGKVVVPGRRHWYLLLSIAARRWFERAIELTGVEFLKAIAMEDGCS 19 1 GPRHOPPLGOBILVPGKVVPGRRHWYLLLSIAARRWTTHARGRYQPTGGRQGCGCS 19 1 GPRHOPPLGOBILVPGKVVPGRRHWYLLLSIAARRWTTHARGRYQPTGGRQGCGCS 19 1 GPRHOPPLGOBILVPGKVVPGRRHWYLLAAPETERRWTTHARGRYQPTGGRQGCGCS 19 1 GPRHOPPLGOBILVPGKVVPGRRHWYLLTBARGRYGPTGGRGGCGCGCS 19 1 GPRHOPPLGOBILVPGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1317 DOALVGGVAVLLGHENTLSPELGLHGPTLANDTACSSSIVALHLACGSLALGEC  140
1157 GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPFLAMDTACSSSIVALHLACGSLRLGEC  40  1217 DOALVGGWWYLLAPETFVLLSRWRALSPDGRCKTFSADADGYARGEGCAVVYLKTLRDAQ  40  1317 RAGDSILALIRGSAVWHDGPSSGLTVPNGPAQALLRQALSGAGVSPVDVDFVECHGTGT  41  1317 ALGDPIEVOALSEVYGPGRSGDRFLLVLGAAKANVAHLEAASGLASLKAVLALRHEGIPA  45  1317 APAAPARPREVELWYLSAKSAAALDAAARLSAHPELSLGDVAFSLATTRSPWEHRLA  45  1317 APAAPARPREVELWYLSAKSAAALDAAARLSAHPELSLGDVAFSLATTRSPWEHRLA  45  1317 AFREAPDRCVALFDREIDQPLREWWAAPGLAQARLDQTAYAQPALFALEYALAALWRS  45  1317 AFREAPDRCVALFDREIDQPLREWWAAPGLAQARLDQTAYAQPALFALEYALAALWRS  45  1317 AFREAPDRCVALFDREIDQPLREWWAAPGLAQARLDQTAYAQPALFALEYALAALWRS  45  1317 AFREAPDRCVALFDREIDQPLREWWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS  45  145  145  145  146  147  148  159  169  170PHAATVSIAAVNGDDAVLAGCFSLEDAVLVPSLRAARGIRTKRLAVSHAPHSPLMD  151  151  151  151  151  151  151  1
1357 GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACQSLRLGEC  40  3217 DDALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKALRDAQ  40  413-DP  3217 DAALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKALRDAQ  43 - DP  44 LLR  45 LLR  45 LLR  45 SLAGAP  3197 APAAPAR PVELVVLSAKSAAALDAAAARLSAHPELSLGDVAFSLLKAVLALRHEGIPA  45 SLAGAP  31897 APAAPAR PVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPWEHRLA  45 SLAGAP  46 SLAGAP  3197 APAAPAR PVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPWEHRLA  45 SLAGAP  31897 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQAARLOQTAYAQPALFALEYALAALWRS  45 SLAGAP  31897 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQAARLOQTAYAQPALFALEYALAALWRS  45 SLAGAP  31897 AFREAFDRCVALFDREIDQPLREVWMAAPGLAQAARLOQTAYAQPALFALEYALAALWRS  31897 AASVAPHAATVSIAAVNGPDAVVIAGABEVQVLALGATFAARGIRTKRLAVSHAPHSPLMD  51 SLAGAP  51 SLAGAP  51
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3097 TFFRISPREMSILDPQORLILEVSWBALESAGIAPDTLRDSPTGVFVGAGDREYYTORLR   40
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1037 GGVEDLESYWOLLAECUVVSAEUPADRWDADWYDEDPELPGRITYUTKGAFLRDLORLDD 309 40 40 40 410 410 410 4117 GFTDGAGGLYGOTGARLSPEGGLAEDTRANDTROSSFTGVFVGAGRNEYTTGELR 315 410 410 4117 GFTDGAGGLYGOTGARLSPEGGLAEDTRANDTROSSFTGVFVGAGRNEYTTGELR 315 410 410 4117 GFTDGAGGLYGOTGARLSPEGGLAEDTRANDTROSSFTGVFVGAGRNEYTTGELR 315 410 410 4117 GFTDGAGGLYGOTGARLSPEGGLAEDTRANDTROSSFTGVFVGAGRGEGCAVVLKRLEDAG 317 4117 RAGDSILALIRGSAVNHDGPSSGLTVPNGAGAGALFGALSGASCHAFHEQTPA 315 4117 BAGDSILALIRGSAVNHDGPSSGLTVPNGAGAGALGALGALGALSGASGLKAVLARHEGTPA 315 4117 AAGDPIEVOALSEVYGPGRSGDRPULGAAKANVAHLEAASGLASLLKAVLALARHEGTPA 315 4117 AAGDPIEVOALSEVYGPGRSGDRPULGAAKANVAHLEAASGLASLLKAVLALARHEGTPA 315 4117 AFREAFRALRGALDAAAGOKTPOGAVRGAVSSRGKLAFFFTGGAGVRFVCHEAPER 315 4117 AFREAFRALRGALDAAAGOKTPOGAVRGAVSSRGKLAFFFTSPHEHELA 315 4117 AGAPARPRVELVULGHSTGELVAACVAGVRSGAVSSRGKLAFFFTGGAGAWATAGSEAV 315 4117 AGAATPVEVGRANDTAAVAGAETATAAARGAGAAVAHARSANGAGALARARS 315 4117 AGAATPVEVGRANDTAAVAGAETATAAARGAGAAVAHARSANGAGALDAAARSECTVLAALGARSANGAGALAATAA 315 4117 AGAATPVEVGRANDTAARADATAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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qq	Db 4237 PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL	
ò	98	5
qq	Db 4297 SVVQALRDRAVRLWWYTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE	4
ò	26	65
qq	4357 ADAARSADVLLRELGRADDETQVAFRSGKRRV	, 4
ò	99	9
qq	Db 4417 TLDQLRLAPAQRRAPGPGEVEIKVTASGLNFRTVLAVLGMYPGDAGPMGGDCAGVATAVG	
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ò	99	59
q	Db 4537 LRRGERVLIHAAAGGVGMAAVQIARWIGAEVFATASPSKWAAVQAMGVPRTHIASSRTLE	
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qq	Db 4597 FAETFROVTGGRGVDVVLNALAGEFVDASLSLL	STGGRFLEMGKTDIRDRAAVAAAHPGV 4656
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g	4717 VLLPAPSAAPLA	PTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA 4776
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В	Db 4897 LAAQSLAWGPWSDGGMAAGLSAALQARLARHGWGALSPAQGTALLGQALARPETQLGAMS	ALSPAQGTALLGQALARPETQLGAMS 4956
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Q	Db 4957 LDVRAASQASGAAVPPVWRALVRAEARHTAAGAQGALAARLGALPEARRADEVRKVVQAE	GALAARLGALPEARRADEVRKVVQAE 5016
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QQ	5017 IARVLSWSAASAVPVDRPL	SDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR 5076
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g	5077 WLLDKVLAVAEPSVSSAKSSPQVALDEPI	AIIGIGCRFPGGVADPESFWRLLEEGSDAVV 5136
ò	Оу 78	77
QQ	5137 EVPHERWDIDAFYDPDPDVRGKMTTRFGGFLS	DIDRFDPAFFGISPREATTMDPQQRLLL 5196
ò	Oy 78	77
g	Db 5197 ETSWEAFERAGILPERLMGSDTGVFVGLFYQEYAALAGGIEAFDGYLGTGTTASVASGRI	ALAGGIEAFDGYLGTGTTASVASGRI 5256

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GPELVASYWADNVR	SIIMAGPELVASYWADNVRQPVRFAEAVQSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 5916
	NECTRICOLENCY DER LOS MEDICAL MY VIGGA V GWERLFSAGGAGLRRVPLPTYPWQRER 5976
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<b>AAYLEMALSSGAEA</b> I	6037 VVFPGAAYLEMALSSGAEALGDGPLQVSDVVLAEALAFADDTPAAVQVMATEERFGRLQF 6096
PGH	26
/PGHGGAAFRSHARG	HVASRVPGHGGAAFRSHARGVLRQIERAEVPARLDLAALRARLQASAPAAATYAALAEMG 6156
	46 6
. FQGLVELWRGEGEP	LEYGPAFQGLVELWRGEGEALGRVRLPEAAGSPAACRLHPALLDACFHVSSAFADRGEAT 6216
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IGSLRWFORPSGE	PWVPVEIGSLRWFQRPSGELWCHARSVSHGKPTPDRRSTDFWVVDSTGAIVAEISGLVAQ 6276
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RRREEDDWFMEPAI	RLAGGVRRREEDDWFMEPAWEPTAVPGSEVMAGRWLLIGSGGGLGAALHSALTEAGHSVV 6336
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6337 HATGRGTSAAGLQALLTASFDGQAPTSVVHLGSLDERGVLDADAPPDADALEESLVRGCD 6396
                                                              6397 SVLWIVQAVAGAGFRDPPRLWLVIRGAQAIGAGDVSVAQAPLLGLGRVIALEHAELRCAR 6456
                                                                                                                            6457 IDLDPARRDGEVDELLAELLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516
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6877 WLAEQGAGHLVLVGRSGAVSAEQQTAVAALEAHGARVTVARADVADRAQMERILREVTAS 6936
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Patent No. 6355458
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Zirle, Ross
APPLICANT: Zirle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Getlach, Joern
APPLICANT: Getlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 4-30592A
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	qa	1777 QRDR	ORDRDPILAVIRGTAINHDGPSSGLTVPSGPAQEALLRQALAHAGVVPADVDFVECHGTG 1836
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.0.	qq	1897 AQPE	AQPELGELNPLLPWEALPVAVARAAVPWPRTDRPRFAGVSSFGMSGTNAHVVLEEAPAVE 1956
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	đ	1957 LWPA	LWPAAPERSAELLVLSGKSEGALDAQAARLREHLDWHPELGLGDVAFSLATTRSAMNHRL 2016
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	qa	2017 AVAV	AVAVTSREGLLAALSAVAQGQTPPGAARCIASSSRGKLAFLFTGQGAQTPGMGRGLCAAW 2076
	ò	30	56
	qu	2077 PAFRI	PAFREAFDRCVALFDRELDRPLREVMWAEPGSAESLLLDOTAFTQPALFTVEYALTALWR 2136
	ò	30	
	qq	2137 SWGVF	SWGVEPELVAGHSAGELVAACVAGVFSLEDGVRLVAARGRLMQGLSAGGAMVSLGAPEAE 2196
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	đ	2197 VAAAN	VAAAVAPHAASVSIAAVNGPEQVVIAGVEQAVQAIAAGFAARGARTKRLHVSHASHSPLM 2256
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_	ò	36	
	qq	2317 EAGAG	EAGAGTFVEYGPKPTLLGLLPACLPEAEPTLLASLRAGREEAAGVLEALGRLWAAGGSVS 2376
	δ	36	50
	qq	2377 WPGVF	WPGVFPTAGRRVPLPTYPWQRQRYWPDIEPDSRRHAAADPTQGWFYRVDWPEIPRSLQKS 2436
	ò	36	35
-	qq	2437 EEASR	EEASRGSWLVLADKGGVGEAVAAALSTRGLPCVVLHAPAETSATAELVTEAGGGRSDWQV 2496
	ò	36	
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	g G	2557 PAIAP(	PAIAPCOAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ 2616
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	ą a	2617 LAFRHO	LAFRHGRRHAARLVAAPPQGQAAPVSLSAEASYLVTGGLGGLGLIVAQWLVELGARHLVL 2676
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	qq	2677 TSRRGI	TSRRGLPDRQAWCEQQPPEIRARIAAVEALEARGARVTVAAVDVADVEPMTALVSSVEPP 2736
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	쇰	2737 LRGVVH	LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAVW 2796
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Q	3037	7 GGVEDLESYWQLLAEGVVVSAEVPADRWDAADWYDPDPEIPGRTYVTKGAFLRDLGRLDA	3096
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Ω	3097	7 TFFRISPREAMSLDPQQRLLLEVSWEALESAGIAPDTLRDSPTGVFVGAGPNEYYTQRLR	3156
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Q	3157	'GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACQSLRLGEC	3216
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Δ.	3217	' DQALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRLRDAQ	3276
>-	40		42
Ω	3277	 RAGDSILALIRGSAVNHDGPSSGLTVPNGPAQQALLRQALSQAGVSPVDVDFVECHGTGT	3336
>	43	da	44
۵	3337	   ALGDPIEVQALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEQIPA	3396
>	45		44
Ω	3397	. QPELGELNPHLPWNTLPVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP	3456
>-	45		44
۵	3457	' APAAPARPVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA	3516
>-	4 5		44
Ω	3517	IATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP	3576
>-	45		44
Ω	3577	AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS	3636
>-	45		44
Ω	3637	WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAMVAIAASEAEV	3696
`	4.5		. 05
Ω	3697	AASVAPHAATVSIAAVNGPDAVVIAGAEVQV	3756
_	51		50
0	3757	PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA	3816
_	51		20
0	3817	AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW	3876
_	51		52
0	3877	KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS	3936

ò	53		53
q	3937	  IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE	3996
ò	26		5.5
g	3997	VELHAVLTPEAAGDGYLPELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA	4056
ò	26		55
g	4057	IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD	4116
ò	99		55
g	4117	NGFAVSLLSTRSEPEDDGTPPLPFAVERVRWRAPVGRVRCGGVPRSQAFGVSSFVLVDE	4176
ò	56		25
g	4177	TGEVVAEVEGFVCRRAPREVFLRQESGASTAALYRLDWPEAPLPDAPAERIEESWVVVAA	4236
ò	26		55
g	4237	PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL	4296
ò	56		55
og Q	4297	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE	4356
ò	56	KAVILTEPEG	65
g	4357	3	4416
ò	99		65
Op	4417	TLDQLRLAPAQRRAPGPGEVEIKVTASGLNFRTVLAVLGMYPGDAGPMGGDCAGVATAVG	4476
ò	99		65
g	4477	<b>QGVRHVAVGDAVMTLGTLHRFVTVDARLVVRQPAGLTPAQAATVPVAFLTAMLALHDLGN</b>	4536
à	99		65
qq	4537	LRRGERVLIHAAAGGVGMAAVQIARWIGAEVFATASPSKWAAVQAMGVPRTHIASSRTLE	4596
ò	99		65
qq	4597	FAETFRQVTGGRGVDVVLNALAGEFVDASLSLLSTGGRFLEMGKTDIRDRAAVAAAHPGV	4656
ò	99	ž	65
QQ	4657	RYRVFDILELAPDRTREILERVVEGFAAGHLRALPVHAFAITKAEAAFRFMAQARHQGKV	4716
ò	99		65
QQ	4717	VLLPAPSAAPLAPTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA	4776
ò	99		65
QQ	4777	EI EALGARVTI AAS DVADRNALEAVLQAI PAEWPLQGVI HAAGALDDGVLDEQTTDR FSR	4836
ò	99	-APNIT	70
g	4837	 VLAPKVTGAWNLHELTAGNDLAFFVLFSSMSGLLGSAGOSNYAAANTFLDALAAHRRAEG	4896
ò	71	ANLTSSL	77
g	4897	LAAQSLAWGPWSDGGWAAGLSAALQARLARHGMGALSPAQGTALLGQALARPETQLGAMS	4956
ò	78		77
a	4957	LDVRAASOASGAAVPPVWRALVRAEARHTAAGAOGALAARLGALPEARRADEVRKVVOAE	5016

ò	7.8		77
ជួ	5017	IARVLSWSAASAVPVDRPLSDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR	5076
ò	7.8		77
පු	5077	WLLDKVLAVAEPSVSSAKSSPQVALDEPIAIIGIGCRFPGGVADPESFWRLLEEGSDAVV	5136
ò	78		77
g	5137	EVPHERWDIDAFYDPDPOVRGKMTTRFGGFLSDIDRFDPAFFGISPREATTMDPQQRLLL	5196
ò	78		77
8	5197	ETSWEAFERAGILPERLMGSDTGVFVGLFYQEYAALAGGIBAFDGYLGTGTTASVASGRI	5256
ò	78		7.7
q	5257	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR	5316
ò	78		77
a	5317 (	GLAPDGRCKSFSAAADGVGWSEGCAMLLLKPLRDAQRDGDPILAVIRGTAVNQDGRSNGL	5376
ò	78		77
g	5377	TAPNGSSQQEVIRRALEQAGLAPADVSYVECHGTGTTLGDPIEVQALGAVLAQGRPSDRP	5436
ò	78		. 44
g	5437 I	LVIGSVKSNIGHTQAAAGVAGVIKVALALERGLIPRSLHFDAPNPHIPWSELAVQVAAKP	5496
ò	. 87		77
g	5497 \	vewtrngvprragussfgvsgtnahvvleeapaaafapaarsaelfvlsaksaaaldao	5556
ò	78 -		77
q	5557 A	AARLSAHVVAHPELGLGDLAFSLATTRSPMTYRLAVAATSREALSAALDTAAQGQAPPAA ;	5616
ò	78 -	GMSCAST	84
g	5617 A	ARGHASTGSAPKVVFVFPGQGSQWLGMGQKLLSEEPVFRDALSACDRAIQAEAGWSLLAE !	5676
ò	85 -		
g	2677 L	LAADETTSQLGRIDVVQPALFAIEVALSALWRSWGVEPDAVVGHSMGEVAAAHVAGALSL :	5736
ò	85 -		84
g	5737 E	EDAVAIICRRSLLLRRISGQGEMAVVELSLAEAEAALLGYEDRLSVAVSNSPRSTVLAGE 5	5796
ò	85 -		84
g	5797 P	PAALAEVLAILAAKGVFCRRVKVDVASHSPQIDPLRDELLAALGELEPRQATVSMRSTVT 5	5856
ò	85 -		84
g	5857 S	STIMAGPELVASYWADNVRQPVRFAEAVOSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 5	5916
ò	85 -	8	84
8	5917 RI	REGVAVGSLRRGQDERLSMLEALGALWVHGQAVGWERLFSAGGAGLRRVPLPTYPWQRER 5	5976
ò	85 -		06
ପ୍ର	5977 YI	YWVDAPTGGAAGGSRFAHAGSHPLLGEMQTLSTQRSTRVWETTLDLKRLPWLGDHRVQGA 6	9603
ò	91 -	6	94
д	6037 VA	VVFPGAAYLEMALSSGAEALGDGPLQVSDVVLAEALAFADDTPAAVQVMATEERPGRLQF 6	9609
ò	. 36	76PGH	٠ .

g	 
ò	99
Ор	6157 LEYGPAFQGLVELWRGEGEALGRVRLPEAAGSPAACRLHPALLDACFHVSSAFADRGEAT 6216
ò	96
Q	6217 PWVPVEIGSLRWFQRPSGELWCHARSVSHGKPTPDRRSTDFWVVDSTGAIVAEISGLVAQ 6276
ò	96
q	6277 RLAGGVRRREEDDWFWEPAWEPTAVPGSEVMAGRWLLIGSGGGLGAALHSALTEAGHSVV 6336
ò	66 ΩΨ86
q	6337 HATGRGTSAAGLQALLTASFDGQAPTSVVHLGSLDERGVLDADAPFDADALEESLVRGCD 6396
ò	100 LVLY 106
οp	;     1   SVLWTVQAVAGAGFRDPPRLWLVTRGAQAIGAGDVSVAQAPLLGLGRVIALEHAELRCAR 6456
ò	107
QQ	6457 IDLDPARRDGEVDELLABLLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516
ò	107 FDLEL111
qq	6517 FRLEIDGSGVLDDLVLRATERRPPGPGEVEIAVEAAGLNFLDVMRAMGIYPGPGDGPVAL 6576
ò	112 111
Ор	6577 GAECSGRIVAMGEGVESLRIGQDVVAVAPFSFGTHVTIDARMLAPRPAALTAAQAAALPV 6636
ò	112 111
Ωp	6637 AFMTAWYGLVHLGRLRAGERVLIHSATGGTGLAAVQIARHLGAEIFATAGTPEKRAWLRE 6696
ò	112pögn pögn 115
Q	6697 QGIAHVMDSRSLDFAEQVLAATKGEGVDVVLNSLSGAAIDASLSTLVPDGRFIELGKTDI 6756
ò	116
Ор	6757 YADRSLGLAHFRKSLSYSAVDLAGLAVRRPERVAALLAEVVDLLARGALQPLPVEIFPLS 6816
ò	116 115
Q	6817 RAADAFRKMAQAQHLGKLVLALEDPDVRIRVPGESGVAIRADGAYLVTGGLGGLGLSVAG 6876
ò	116ROV 118
qq	;   6877 WLAEQGAGHLVLVGRSGAVSAEQQTAVAALEAHGARVTVARADVADRAQMERILKEVTAS 6936
ò	119RGVTQLGG 126
qq	6937 GMPLRGVVHAAGILDDGLLMQQTPARFRAVMAPKVRGALHLHALTREAPLSFFVLYASGA 6996
ò	127 ACSPTWSCL 135
Ωp	6997 GLLGSPGQGNYAAANTFLDALAHHRRAQGLPALSIDWGLFADVGLAAGQONRGARLVTRG 7056
ò	136ITEDIG 143
qq	
ò	144 143
qq	7117 LAGDRDLLERLATAEAGARAGMLQEVVRAQVSQVLRLSEGKLDVDAPLTSLGMDSLMGLE 7176
ò	144LGVTI 148

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1477 QGELGMPLSATLAFDHPTVERLVEYLLSQALELQDRTDVRSVRLPATEDPIAIVGAACRF 1536
                                                                                                      1537 PGGVEDLESYWQLLTEGVVVSTEVPADRWNGADGRVPGSGEAQRQTYVPRGGFLREVETF 1596
                                                                                                                                                                                          1597 DAAFFHISPREAMSLDPQQRLLLEVSWEAIERAGQDPSALRESPTGVFVGAGPNEYAERV 1656
                                                                                                                                                                                                                                                                         1657 QELADEAAGLYSGTGNMLSVAAGRLSFFLGLHGPTLAVDTACSSSLVALHLGCQSLRRGE 1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1957 LWPAAPERSAELLVLSGKSEGALDAQAARLREHLDMHPELGLGDVAFSLATTRSAMNHRL 2016
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PPLICANT: Goerlach, Joern
TILE OF INVENTION: GRNES FOR, THE BIOSYNTHESIS OF EPOTHILONES
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Best Local Similarity 1.5%; Pred. No. 3.1;
Matches 93; Conservative 23; Mismatches
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CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
FRIOR PELING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PTYPE: PTYPE: APPLICATION OF SEQ ID NOS: 300-05-10
                                                                                                  Sequence 5, Application US/09568486
Patent No. 6355459
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2557 PAIAPCQAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ	2617 LAFRHGRRHAARLVAAPPQGQAAPVSLSAEASYLVTGGLGGLGLIVAOWLVELGARHIVI.	04	2677 TSRRGLPDRQAWCEQQPPEIRARIAAVEALEARGARVTVAAVDVADVEPMTALVSSVEPP	40	2737 LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAVW		2797 GSHSQGAYAAANAFLDGLAHLRRSQSLPALSVAWGLWAEGGWADAEAHARLSDIGVLPMS	40	2857 TSAALSALORLVETGAAQRTVTRMDWARFAPVYTARGRRNLLSALVAGRDIIAPSPPAAA	- 40	2917 TRNWRGLSVAEARVALHEIVHGAVARVLGFLDPSALDPGMGFNEQGLDSLMAVEIRNLLQ	40	2977 AELDVRLSTTLAFDHPTVQRLVEHLLVDVLKLEDRSDTQHVRSLASDEPIAIVGAACRFP	40	3037 GGVEDLESYWQLLAEGVVVSAEVPADRWDADWYDPDPEIPGRTYVTKGAFLRDLQRLDA	40	3097 TFFRISPREAMSLDPQQRLLLEVSWEALESAGIAPDTLRDSPTGVFVGAGPNEYYTQRLR	40	3157 GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACQSLRLGEC	40	3217 DOALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRLRDAO	40LLR		43 DP		JJJ, ALGERTEVUALSEVIGFGRSGDRPLVLGAARANVAHLEAASGLASLLKAVLALRHEQIPA		5557 OF ELGELNFHLFWNILFVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP		3457 APAAPARPVELVVLSAKSAAALDAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA	45	3517 IATTSREALRGALDAAAQQKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP	45	3577 AFREAFDRCVALFDREIDOPLREVMWAAPGLAGAARLDOTAVAGERIERIEWATARTHE	45	3637 WGVEPHVLLGHSIGELVAACVAGVESI. FDAVELVAACET MONT ENGGRAMMATERS	
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g	3697	AARGIRTKRLAVSHAFHSPLMD 3
ò	51	05
g	3757	PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA 3816
ò	51	
g	3817	AGAATFVEVGPKPVLLGLLPACLGBADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW 3876
ò	51	RV
g	3877	KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS 3936
ò	53	95
g	3937	   IGPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAAERWPERAIELTGVEFLKAIAMEPDQE 3996
ò	99	55
g	3997	VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA 4056
ઠે	26	55
g	4057	IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD 4116
δ	. 95	55
g	4117	NGFAVSLLSTRSEPEDDGTPPLPPAVERVRWMRAPVGRVRCGGVPRSQAFGVSSFVLVDE 4176
ò	. 95	99
g	4177 T	TGEVVAEVEGFVCRRAPREVFLRQESGASTAALYRLDWPEAPLPDAPAERIEESWVVVAA 4236
ò	- 99	55
අ	4237 P	PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL 4296
ò	- 95	55
a a	4297 S	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE 4356
ò	- 95	65 68
qq	4357 A	
ò	- 99	59
g	4417 T	TLDQLRLAPAQRRAPGPGEVEIKVTASGLNFRTVLAVLGMYPGDAGPMGGDCAGVATAVG 4476
ò	99	59
g	4477 0	OGVRHVAVGDAVMTLGTLHRFVTVDARLVVRQPAGLTPAQAATVPVAFLTAWLALHDLGN 4536
ò	99	59
Вр	4537 LI	LRRGERVLIHAAAGGVGMAAVQIARWIGAEVFATASPSKWAAVQAMGVPRTHIASSRTLE 4596
ò	- 99	9
Dp	4597 F	FAETFRQVTGGRGVDVVLNALAGEFVDASLSLLSTGGRFLEMGKTDIRDRAAVAAAHPGV 4656
ઠે	- 99	9
a	4657 R)	RYRVFDILELAPDRTREILERVVEGFAAGHLRALPVHAFAITKAEAAFRFMAQARHQGKV 4716
ò	99	59
QQ	4717 VI	VLLPAPSAAPLAPTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA 4776

ò	99	9 9	
DD	4777	7 EIEALGARVTIAASDVADRNALEAVLQAIPAEWPLQGVIHAAGALDDGVLDEQTTDRFSR 4836	
ò	99	6APNIT 70	
QQ	4837	:  7 VLAPKVTGAWNLHELTAGNDLAFFVLFSSMSGLLGSAGQSNYAAANTFLDALAAHRRAEG 4896	
ò	71	1 77	
台	4897	7 LAAQSLAWGPWSDGGWAAGLSAALQARLARHGMGALSPAQGTALLGQALARPETQLGAMS 4956	
ò	78	77	
g	4957	7 LDVRAASQASGAAVPPVWRALVRAEARHTAAGAGGALAARLGALPEARRADEVRKVVQAE 5016	
ò	78	77	
q	5017	7 IARVLSWSAASAVPVDRPLSDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR 5076	
ò	78	77	
q	5077	7 WLLDKVLAVAEPSVSSAKSSPQVALDEPIAIIGIGCRFPGGVADFESFWRLLEEGSDAVV 5136	
ጵ	78	77	
Q	5137	PEVPHERWDIDAFYDPDDVRGKMTTRFGGFLSDIDRFDPAFFGISPREATTMDPQQRLLL 5196	
ጵ	78	77	
ရ	5197	PTSWEAFERAGILPERLMGSDTGVFVGLFYQEYAALAGGIEAFDGYLGTTTASVASGRI 5256	
ጵ	78	77	
ą	5257	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR 5316	
ጵ	78	77	
ą	. 5317	GLAPDGRCKSFSAAADGVGWSEGCAMLLLKPLRDAQRDGDPILAVIRGTAVNQDGRSNGL 5376	
⋧	78	77	
ą	5377	TAPNGSSQOEVIRRALEQAGLAPADVSYVECHGTGTTLGDPIEVQALGAVLAQGRPSDRP 5436	
⋩	78	77	
ð	5437	LVIGSVKSNIGHTQAAAGVAGVIKVALALERGLIPRSLHFDAPNPHIPMSELAVQVAAKP 5496	
≿	78	77	
ð	5497	VEWTRNGVPRRAGVSSFGVSGTNAHVVLEEAPAAAFAPAAARSAELFVLSAKSAAALDAQ 5556	
⋩	78	77	
ą	5557	AARLSAHVVAHPELGLGDLAFSLATTRSPMTYRLAVAATSREALSAALDTAAQGQAPPAA 5616	
≿	78	84 GWS B4	
۵	5617		
≿	85	8	
ð	5677	LAADETTSQLGRIDVVQPALFAIEVALSALWRSWGVEPDAVVGHSMGEVAAAHVAGALSL 5736	
≿	85.	8	
ď	5737	EDAVAIICRRSLLLRRISGQGEMAVVELSLAEAEAALLGYEDRLSVAVSNSPRSTVLAGE 5796	
<u>&gt;</u>	82	78	
ą	5797	PAALAEVLAILAAKGVFCRRVKVDVASHSPQIDPLRDELLAALGELEPRQATVSMRSTVT 5856	
ځ	85	8	

g	5857 STIMAGPELVASYWADNVRQPVRFAEAVQSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 5916
ò	85 84
qq	5917 REGVAVGSLRRGQDERLSMLEALGALWVHGQAVGWERLFSAGGAGLRRVPLPTYPWQRER 5976
ò	95 85 85
q	5977 YWVDAPTGGAAGGSRFAHAGSHPLLGEMQTLSTQRSTRVWETTLDLKRLPWLGDHRVQGA 6036
ò	91 94
gg	6037 VVFPGAAYLEMALSSGAEALGDGPLQVSDVVLAEALAFADDTPAAVQVMATEERPGRLQF 6096
ò	95PGH 97
q	6097 HVASRVPGHGGAAFRSHARGVLRQIERAEVPARLDLAALRARLQASAPAAATYAALAEMG 6156
ò	16 86
qq	6157 LEYGPAFQGLVELWRGEGEALGRVRLPEAAGSPAACRLHPALLDACFHVSSAFADRGEAT 6216
ò	96
qq	6217 PWVPVEIGSLRWFQRPSGELWCHARSVSHGKPTPDRRSTDFWVVDSTGAIVAEISGLVAQ 6276
ò	16
q	6277 RLAGGURRREEDDWFMEPAWEPTAVPGSEVMAGRWLLIGSGGGLGAALHSALTEAGHSVV 6336
ò	66 QV 86
QQ	6337 HATGRGTSAAGLQALLTASFDGQAPTSVVHLGSLDERGVLDADAPFDADALEESLVRGCD 6396
ò	100 LVLY 106
Ω	6397 SVLWTVQAVAGAGFRDPPRLWLVTRGAQAIGAGDVSVAQAPLLGLGRVIALEHAELRCAR 6456
ò	107 106
qq	6457 IDLDPARRDGEVDELLAELLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516
ò	107 FDLEL
ф	6517 FRLEIDGSGVLDDLVLRATERRPPGPGEVEIAVEAAGLNFLDVMRAMGIYPGPGDGPVAL 6576
ò	112 111
Op	6577 GAECSGRIVAMGEGVESLRIGQDVVAVAPFSFGTHVTIDARMLAPRPAALTAAQAAALPV 6636
ò	112 111
qq	6637 AFWTAWYGLVHLGRLRAGERVLIHSATGGTGLAAVQIARHLGAEIFATAGTPEKRAWLRE 6696
ò	112 PDGN 115
Ω	6697 QGIAHVMDSRSLDFAEQVLAATKGEGVDVVLNSLSGAAIDASLSTLVPDGRFIELGKTDI 6756
ò	116 115
qq	6757 YADRSLGLAHFRKSLSYSAVDLAGLAVRRPERVAALLAEVVDLLARGALQPLPVEIFPLS 6816
ò	116 115
q	6817 RAADAFRKMAQAQHLGKLVLALEDPDVRIRVPGESGVAIRADGAYLVTGGLGGLGLSVAG 6876
ò	116RQV 118
QQ	6877 WLAEQGAGHLVLVGRSGAVSAEQQTAVAALEAHGARVTVARADVADRAOMERILREVTAS 6936
ò	119RGVTQLGG 126

유	o 6937 GMPLRGVVHAAGILDDGLLMQQTPARFRAVMAPKVRGALHLHALTREAPLSFFVLYASGA 6996	
ठे व	127	
සි	o 6997 GLLGSPGGGNYAAANTFLDALAHHRRAQGLPALSIDWGLFADVGLAAGQQNRGARLVTRG 7056	
δi	136	
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ò	144 143	
යු	7117 LAGDRDLLERLATAEAGARAGMLQEVVRAQVSQVLRLSEGKLDVDAPLTSLGMDSLMGLE 7176	
ò	144	
q	7177 LRNRIEAVLGITM 7189	
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	Sequence 5, Application US/09568472 Patent No. 6358719	
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۰. ۰.	Ligon, Molnar.	
٠	APPLICANT: Zirkie, Ross APPLICANT: Cor Devon	
٠	Goriach, Joern	
٠.,	FILE REFERENCE: 4-30582A	
	T APPLICATION NUMBER: US/ T FILING DATE: 2000-05-1	
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g	   AAGGSVSWPGVFPTAGRRVPLPTYPWQRQRYWIEAPAEGLGATAADALAOWFYRVDWPPFM 916	
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g	997 GRNDWQGVLYLWGLDAVVEAGASAEEVAKVTHLAAAPVLALIQALGTGPRSPRLWIVTRG 1056	
ò	,	
g	1057 ACTVGGEPDAAPCQAALWGMGRVAALEHPGSWGGLVDLDPEESPTEVEALVAETTSPDAE	
ò	,	
g	1117 DQLAFRQGRRRAARLVAAPPEGNAAPVSLSAEGSYLVTGGLGALGLLVABWIJFBGAGH: 1126	
ò		
QQ	OGARVTVAAVDVADAEGMA	
ò	7 6	
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qq	
õ	24 23
q	1297 VFGSIGQGSYAAGNAFLDALADLRRTQGLAALSIAWGLWAEGGMGSQAORREHEASGIWA 1356
ô	24
g	1357 MPTSRALAAMEWLLGTRATQRVVIQMDWAHAGAAPRDASRGRFWDRLVTATKEASSSAVP
ò	24 23
qq	1417 AVERWRNASVVETRSALYELVRGVVAGVMGFTDQGTLDVRRGFAEQGLDSLMAVEIRKRL
ò	24 23
đ	1477 QGELGMPLSATLAFDHPTVERLVEYLLSQALELQDRTDVRSVRLPATEDPIAIVGAACRF
ò	24EDTERY 29
QQ	1537 PGGVEDLESYWQLLTEGVVVSTEVPADRWNGADGRVPGSGEAQRQTYVPRGGFLREVETF 1596
ò	30 29
đ	1597 DAAFFHISPREAMSLDPQQRLLLEVSWEAIERAGQDPSALRESPTGVFVGAGPNEYAERV 1656
ò	30 29
셤	1657 QELADEAAGLYSGTGNMLSVAAGRLSFFLGLHGPTLAVDTACSSSLVALHLGCQSLRRGE 1716
ò	30 29
qq	1717 CDQALVGGVNMLLSPKTFALLSRMHALSPGGRCKTFSADADGYARAEGCAVVVLKRLSDA 1776
ð	30 29
qq	1777 ORDRDPILAVIRGTAINHDGPSSGLTVPSGPAQEALLRQALAHAGVVPADVDFVECHGTG 1836
ò	30 29
đ	1837 TALGDPIEVRALSDVYGQARPADRPLILGAAKANLGHMEPAAGLAGLLKAVLALGQEQIP 1896
ò	30 29
q	1897 AQPELGELNPLLPWEALPVAVARAAVPWPRTDRPRFAGVSSFGMSGTNAHVVLEEAPAVE 1956
ò	30 29
Q	1957 LWPAAPERSAELLVLSGKSEGALDAQAARLREHLDMHPELGLGDVAFSLAGTRSAMNHRL 2016
ò	30 29
අ	2017 AVAVTSREGLLAALSAVAQGQTPPGAARCIASSSRGKLAFLFTGQGAQTPGMGRGLCAAW 2076
ò	30 29
Q	2077 PAFREAFDRCVALFDRELDRPLREVMMAEPGSAESLLLDQTAFTQPALFTVEYALTALWR 2136
ò	30 29
đ	2137 SWGVEPELVAGHSAGELVAACVAGVFSLEDGVRLVAARGRLMOGLSAGGAMVSLGAPEAE 2196
ò	30 29
q	2197 VAAAVAPHAASVSIAAVNGPEQVVIAGVEQAVQAIAAGFAARGARTKRLHVSHASHSPLM 2256
ò	30 35
QQ	2257 EPMLEEFGRVAASVTYRRPSVSLVSNLSGKVVADELSAPGYWVRHVREAVRFADGVKALH 2316
ò	36

a	3317 EAGAGTFVEVGPKPTLLGLLPACLPEAEPTLLASLRAGREEAAGVLEALGRLWAAGGSVS	ALGRLWAAGGSVS 2376	
	36	35	
Q D	2377 WPGVFPTAGRRVPLPTYPWQRQRYWPDIEPDSRRHAAADPTQGWFYRVDWPEIPRSLQKS	VDWPEIPRSLQKS 2436	
	36	35	
	2437 EEASRGSWLVLADKGGVGEAVAAALSTRGLPCVVLHAPAETSATAELVTEAAGGRSDWQV	VTEAAGGRSDWQV 2496	
	36IGAE	68 36	
	2497 VLYLWGLDAVVGAEASIDEIGDATRRATAPVLGLARFLSTVSCSPRLWVVTRGACIVGDE	WVVTRGACIVGDE 2556	
	40	39	
QQ	2557 PAIAPCQAALWGMGRVAALEHPGAWGGLVDLDPRASPPQASPIDGEMLVTELLSQETEDQ	LVTELLSQETEDQ 2616	
	40	39	
qq	2617 LAFRHGRRHAARLVAAPPQGQAAPVSLSAEASYLVTGGLGGLGLIVAQWLVELGARHLVL	QWLVELGARHLVL 2676	
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	2677 TSRRGLPDROAWCEQOPPEIRARIAAVEALEARGARVTVAAVDVADVEPWTALVSSVEPP	EPMTALVSSVEPP 2736	
	40	96	
	2737 LRGVVHAAGVSVMRPLAETDETLLESVLRPKVAGSWLLHRLLHGRPLDLFVLFSSGAAVW	DLFVLFSSGAAVW 2796	
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	2797 GSHSQGAYAAANAFLDGLAHLRRSQSLPALSVAWGLWAEGGMADAEAHARLSDIGVLPMS	HARLSDIGVLPMS 2856	
	40	39	
	2857 TSAALSALQRLVETGAAQRTVTRMDWARFAPVYTARGRRNLLSALVAGRDIIAPSPPAAA	GRDIIAPSPPAAA 2916	
	40	39	
	2917 TRNWRGLSVAEARVALHEIVHGAVARVLGFLDPSALDPGMGFNEQGLDSLMAVEIRNLLQ	OSLMAVEIRNLLQ 2976	
	40	39	
	2977 AELDVRLSTTLAFDHPTVQRLVEHLLVDVLKLEDRSDTQHVRSLASDEPIAIVGAACRFP	SPIAIVGAACRFP 3036	
	40	39	
	3037 GGVEDLESYWQLLAEGVVVSAEVPADRWDAADWYDPDPEIPGRTYVTKGAFLRDLQRLDA	KGAFLRDLQRLDA 3096	
	40	39	
	3097 TFFRISPREAMSLDPQQRLLLEVSWEALESAGIAPDTLRDSPTGVFVGAGPNEYYTQRLR	SAGPNEYYTQRLR 3156	
		39	
	3157 GFTDGAAGLYGGTGNMLSVTAGRLSFFLGLHGPTLAMDTACSSSLVALHLACQSLRLGEC	HLACQSLRLGEC 3216	
	40	39	
	3217 DQALVGGVNVLLAPETFVLLSRMRALSPDGRCKTFSADADGYARGEGCAVVVLKRLRDAQ	AVVVLKRLRDAQ 3276	
	40	42	
	3277 RAGDSILALIRGSAVNHDGPSSGLTVPNGPAQQALLRQALSQAGVSPVDVDFVECHGTGT	DVDFVECHGTGT 3336	÷
	43 DP	44	
	3337 ALGDPIEVQALSEVYGPGRSGDRPLVLGAAKANVAHLEAASGLASLLKAVLALRHEQIPA	AVLALRHEQIPA 3396	
	45	44	
	3397 QPELGELNPHLPWNTLPVAVPRKAVPWGRGARPRRAGVSAFGLSGTNVHVVLEEAPEVEP	HVVLEEAPEVEP 3456	

5	4	***************************************	4
g	3457	APAAPARPVELVVLSAKSAAALDAAAARLSAHLSAHPELSLGDVAFSLATTRSPMEHRLA	351
ò	45		44
QQ	3517	IATTSREALRGALDAAAQOKTPQGAVRGKAVSSRGKLAFLFTGQGAQMPGMGRGLYETWP	357
ò	4 5		4
Q	3577	AFREAFDRCVALFDREIDQPLREVMWAAPGLAQAARLDQTAYAQPALFALEYALAALWRS	363
ò	45		44
g	3637	WGVEPHVLLGHSIGELVAACVAGVFSLEDAVRLVAARGRLMQALPAGGAMVAIAASEAEV	369
ò	45	SLGAOF	20
g	3697	AASVAPHAATVSIAAVNGPDAVVIAGAEVQVLALGATFAARGIRTKRLAVSHAFHSPLMD	375
ઠે	51		20
QQ	3757	PMLEDFQRVAATIAYRAPDRPVVSNVTGHVAGPEIATPEYWVRHVRSAVRFGDGAKALHA	381
ò	51		20
g	3817	AGAATFVEVGPKPVLLGLLPACLGEADAVLVPSLRADRSECEVVLAALGAWYAWGGALDW	387
ò	51	RV	22
QQ	3877	KGVFPDGARRVALPMYPWQRERHWMDLTPRSAAPAGIAGRWPLAGVGLCMPGAVLHHVLS	393(
ò	53	HLV	55
qq	3937	  GPRHQPFLGDHLVFGKVVVPGAFHVAVILSIAABRWPBRAIBLTGVEFLKAIAMEPDQE	3996
ò	99		55
QQ	3997	VELHAVLTPEAAGDGYLFELATLAAPETERRWTTHARGRVQPTDGAPGALPRLEVLEDRA	4056
ò	99		55
g	4057	IQPLDFAGFLDRLSAVRIGWGPLWRWLQDGRVGDEASLATLVPTYPNAHDVAPLHPILLD	4116
ò	56		55
g	4117	NGFAVSLLSTRSEPEDDGTPPLPPAVERVRWWRAPVGRVRCGGVPRSQAFGVSSFVLVDE	4176
ò	26		ខ្ល
g	4177	TGEVVAEVEGFVCRRAPREVFLRQESGASTAALYRLDWPEAPLPDAPAERIEESWVVVAA	4236
ò	99		55
엄	4237	PGSEMAAALATRLNRCVLAEPKGLEAALAGVSPAGVICLWEAGAHEEAPAAAQRVATEGL	4296
à	. 95		55
g G	4297	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVMGLGRTVMQERPELSCTLVDLEPE	4356
ò	. 95	KMVILTEPEG	65
g	4357 7	adaarsadvilrelgraddetqvafrsgkrrvarlvkattpegilvpdaesyrleagokg	4416
ò	. 99		65
g G	4417 7	TLDQLRLAPAQRRAPGPGEVE1KVTASGLNFRTVLAVLGMYPGDAGPMGGDCAGVATAVG	4476
ò	99		65
g G	4477	OGVRHVAVGDAVMTLGTLHRFVTVDARL.VVROPAGI TPANAATVPVAFI TAWI ATHDI CN	7636

ò	99	59
đ	4537	LRRGERVLIHAAAGGVGMAAVQIARWIGAEVPATASPSKWAAVQAMGVPRTHIASSRTLE 4
ò	99	9
qq	4597	FAETFROVTGGRGVDVVLNALAGEFVDASLSLLSTGGRFLEMGKTDIRDRAAVAAAHPGV 4
ò	99	99
g	4657	RYRVFDILELAPDRTREILERVVEGFAAGHLRALPVHAFAITKAEAAFRFWAQARHQGKV 4716
ò	. 66	99
a	4717	VLLPAPSAAPLAPTGTVLLTGGLGALGLHVARWLAQQGVPHMVLTGRRGLDTPGAAKAVA 4776
ò	99	9
q	4777	EIEALGARVTIAASDVADRNALEAVLQAIPAEWPLQGVIHAAGALDDGVLDEQTTDRFSR 4836
ò	99	APNIT 70
q	4837	VLAPKVTGAMNLHELTAGNDLAFFVLFSSMSGLLGSAGQSNYAAANTFLDALAAHRRAEG 4896
ò	71	77
Q	4897	LAAQSLAWGPWSDGGWAAGLSAALQARLARHGMGALSPAQGTALLGQALARPETQLGAMS 4956
ò	78	77
QQ	4957	LDVRAASQASGAAVPPVWRALVRAEARHTAAGAQGALAARLGALPEARRADEVRKVVQAE 5016
ò	78	22
Ор	5017	IARVLSWSAASAVPVDRPLSDLGLDSLTAVELRNVLGQRVGATLPATLAFDHPTVDALTR 5076
ò	78	24
QQ	5077	WLLDKVLAVAEPSVSSAKSSPQVALDEPIAIIGIGCRFPGGVADPESFWRLLEEGSDAVV 5136
ò	78	22
Ор	5137	EVPHERWDIDAFYDPDPDVRCKMTTRFGGFLSDIDRFDPAFFGISPREATTMDPQQRLLL 5196
ò	78	44
g	5197	ETSWEAFERAGILPERLMGSDTGVFVGLFYQEYAALAGGIEAFDGYLGTGTTASVASGRI 5256
ò	7.8	77
g	5257	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR 5316
ò	78	44
QQ	5317 (	GLAPDGRCKSFSAAADGVGWSEGCAMLLLKPLRDAQRDGPILAVIRGTAVNQDGRSNGL 5376
ò	78	44
Dp	5377	TAPNGSSQQEVIRRALEQAGLAPADVSYVECHGTGTTLGDPIEVQALGAVLAQGRPSDRP 5436
ò	78	26
QD	5437 1	LVIGSVKSNIGHTQAAAGVAGVIKVALALERGLIPRSLHFDAPNPHIPWSELAVQVAAKP 5496
ò	78	77
සු	5497	VEWTRNGVPRRAGVSSFGVSGTNAHVVLEEAPAAAFAPAARSAELFVLSAKSAAALDAQ 5556
ò	78	11
QQ	5557	AARLSAHVVAHPELGLGDLAFSLATTRSPMTYRLAVAATSREALSAALDTAAQGQAPPAA 5616
ò	78	84

a	
ò	85 84
Q	5677 LAADETTSQLGRIDVVQPALFAIEVALSALWRSWGVEPDAVVGHSMGEVAAAHVAGALSL 5736
ò	85 84
q	5737 EDAVAIICRRSLLRRISGQGEMAVVELSLAEAEAALLGYEDRLSVAVSNSPRSTVLAGE 5796
ò	85 84
රු	5797 PAALAEVLAILAAKGVFCRRVKVDVASHSPQIDPLRDELLAALGELEPRQATVSMRSTVT 5856
ò	8584
q	5857 STIMAGPELVASYWADNVRQPVRFAEAVQSLMEDGHGLFVEMSPHPILTTSVEEIRRATK 5916
ò	85 84
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ò	30	53
g	2137	SWGVEPELVAGHSAGELVAACVAGVFSLEDGVRLVAARGRLMQGLSAGGAMVSLGAPEAE
ò	30	5
Ωp	2197	VAAAVAPHAASVSIAAVNGPEOVVIAGVEQAVQAIAAGFAARGARTKRLHVSHASHSPLM
ठे	30	3EATINTN38
g	2257	:::  : EPMLEEFGRVAASVTYRRPSVSLVSNLSGKVVADELSAPGYWVRHVREAVRFADGVKALH
ò	36	
g	2317	EAGAGTFVEVGPKPTLLGLLPAC
ò	36	35
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à	36	35
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q	2497	
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Ω	3037	GGVEDLESYWQLLAEGVVVSAEVPADRWDAADWYDPDPEIPGRTYVTKGAFLRDLQRLDA 3096
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ò	9639	
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qq	 3277 RAGDSILALIRGSAVNHDGPSSGLTVPNGPAOQALLRQALSQAGVSPVDVDFVECHGTGT 3336	ب
ò	43 DP	
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ò	45 SLCAAQF 50	
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ò	51 50	
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ò	95	
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ò	95	
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ò	99		55	
음	4297 S	SVVQALRDRAVRLWWVTMGAVAVEAGERVQVATAPVWGLGRTVMQERPELSCTLVDLEPE	4356	
ò	- 95	KMVIL/TEPEG		
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g	4477 0	<b>OGVRHVAVGDAVMTLGTLHRFVTVDARLVVRQPAGLTPAQAATVPVAFLTAWLALHDLGN</b>	4536	
ò	- 99		65	
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ò	- 99		. 59	
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ò	. 48		77	
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ò	- 84		77	
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ò	78		77	
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g	5257 8	SYVLGLKGPSLTVDTACSSSLVAVHLACQALRRGECSVALAGGVALMLTPATFVEFSRLR	5316	
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q	6397	:   SVLWTVQAVAGAGFRDPPRLWLVTRGAQAIGAGDVSVAQAPLLGLGRVIALEHAELRCAR 645	99
ò	107	106	9

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Query Match
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6457 IDLDPARRDGEVDELLAELLADDAEEEVAFRGGERRVARLVRRLPETDCREKIEPAEGRP 6516
                                                            6517 FRLEIDGSGVLDDLVLRATERRPPGPGEVEIAVEAAGLNFLDVMRAMGIYPGPGDGPVAL 6576
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APPLICANT: Reders, Michael
APPLICANT: Schneider, Michael
APPLICANT: Gluckemann, Sander
TITLE OF INVENTION: DENTRICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08460751
Patent No. 5891628
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 SGLEAAYSIVALGEEPARAVHPLCPSDTEIFPGNGHCYRLVVEKAAWLQAQEQCQAWAGA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 QQVRVVQPEAATCAGPGSLAGQPLLGIPLLDSGCGEEYVACLPDNSSGTVAAVSFSAAHE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 GLLQPEACSAFCFSTGGGLAALSEQGWCLCGAAQPSSASFACLSLCSGPPAPPAPTCRGP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 TLLQHVFPASPGATLVGPHGPLASGQLAAFHIAAPLPVTDTRWDFGDGSAEVDAAGPAAS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 HRYVLPGRYHVTAVLALGAGSALLGTDVQVEAAPAALELVCPSSVQSDESLDLSIQNRGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 ALAMVDSPAVQRFLVSRVTRSLDVWIGFSTVQGVEVGPAPQGEAFSLESCQNWLPGEPHP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 ATAEHCVRLGPTGWCNTDLCSAPHSYVCELQPGGPVQDAENLLVGAPSGDLQGPLTPLAQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 ODGLSAPHEPVEVMVFPGLRLSREAFLTTAEFCTQELRRPAQLRLOVYRLLSTAGTPENG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AGGPGRGCGPCEPPCLCGPAPGAACRVNCSGRGLRTLGPALRIPADATELDVSHNLLRAL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 2; Length 4303;
0.89;
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 -DVFQAHQEDTERYV-----LINLNIGAELLRDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 208; DB
Pred. No. 0.89;
9; Mismatches
                                                                                                                                                                                                                                               NAME: COLUZZI, LGURA A.
REGIGTRATION UNUBER: 30,742
REFRENCE/DOCKET NUMBER: 7638-005
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PRINIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4303 amino acids
TYPE: amino acid
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,580
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: procein
US-08-460-751-2
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Ω	683	WREFLFSVPAGPPAQYSVTLHGQDVLMLPGDLVGLQHDAGPGALLHCSPAPGHPGPRAPY 742	
_	45	44	
0	743.	LSANASSWLPHLPAQLEGTWGCPACALRLLAQREQLTVLLGLRPNPGLRLPGRYEVRAEV 802	
<b>&gt;</b> -	45	44	
0	803	GNGVSRHNLSCSFDVVSPVAGLRVIYPAPRDGRLYVPTNGSALVLQVDSGANATATARWP 862	
`	4 5	SLGAQFR58	
0	863	GGSLSARFENVCPALVATFVPACPWETNDTLFSVVALPWLSEGEHVVDVVVENSASRANL 922	
>-	93	85	
Ω	923	SLRVTAEEPICGLRATPSPEARVLQGVLVRYSPVVEAGSDMVFRWTINDKQSLTFQNVVF 982	
>-	5	85	
	983	NVIYQSAAVFKLSLTASNHVSNVTVNVTVERMNRMQGLQVSTVPAVLSPNATLALTAG 1042	~
>-	59	85	
Ω	1043	VLVDSAVEVAFLWTFGDGEQALHQFQPPYNESFPVPDPSVAQVLVEHNVTHTYAAPGEYL 1102	2
`	59	89	
Ω	1103	LTVLASNAFENLTQQVPVSVRASLPSVAVGVSDGVLVAGRPVTFYPHPLPSPGGVLYTWD 1162	2
>-	59	89	
.0	1163	FGDGSPVLTQSQPAANHTYASRGTYHVRLEVNNTVSGAAAQADVRVFEELRGLSVDMSLA 1222	2
<b>&gt;</b> -	59	64	
Ω	1223	VEQCAPVVVSAAVQTGDNITWTFDMGDGTVLSGPEATVEHVYLRAQNCTVTVGAGSPAGH 1282	2
>-	9	99 VD	
۵	1283	LARSLHVLVFVLEVLRVEPAACIPTQPDARLTAYVTGNPAHYLFDWTFGDGSSNTTVRGC 1342	7
>-	67	PNITANLISS	
Ω	1343		2
>-	82	81	
Ω	1403	CAWPPFPYRYTWDFGTEEAAPTRARGPEVTFIYRDPGSYLVTVTASNNISAANDSALVEV 1462	2
>-	82	81	
۵	1463	QEPVLVTSIKVNGSLGLELQQPYLFSAVGRGRPASYLWDLGDGGWLEGPEVTHAYNSTGD 1522	2
>-	82		
Ω	1523		2
>-	88	18	
Ω	1583	VLCDRCTPIPGGPTISYTFRSVGTFNIIVTAENEVGSAQDSIFVYVLQLIEGLQVVGGGR 1642	2
>	88	81	
Ω	1643	YFPTNHTVQLQAVVRDGTNVSYSWTAWRDRGPALAGSGKGFSLTVLEAGTYHVQLRATNM 1702	2
>-	88	87	
۵	1703	LGSAWADCTMDFVEPVGWLMVAASPNPAAVNTSVTLSAELAGGSGVVYTWSLEEGLSWET 1762	2
>	88	87	

g	1763	SEPFTTHSFPTPGLHLVTMTAGNPLGSANATVEVDVQVPVSGLSIRASEPGGSFVAAGSS 1822
ò	88	89
QQ	1823	VPFWGQLATGTNVSWCWAVPGGSSKRGPHVTMVFPDAGTFSIRLNASNAVSWVSATYNLT 1882
ò	88	06
αg	1883	AEEPIVGLVLWASSKVVAPGQLVHFQILLAAGSAVTFRLQVGGANPEVLPGPRFSHSFPR 1942
ò	91	06
q	1943	VGDHVVSVRGKNHVSWAQAQVRIVVLEAVSGLQVPNCCEPGIATGTERNFTARVQRGSRV 2002
ò	91	06
q	2003	AYAWYFSLQKVQGDSLVILSGRDVTYTPVAAGLLEIQVRAFNALGSENRTLVLEVQDAVQ 2062
ò	91	96PG96.
g	. 2063	YVALQSGPCFTNRSAQFEAATSPSPRRVAYHWDFGDGSPGQDTDEPRAEHSYLRPGDYRV 2122
ò	97	104 L. L. L. L. L. L. L. L. L. L. L. L. L.
QQ	2123	QVNASNLVSFFVAQATVTVQVLACREPEVDVVLPLQVLMRRSQRNYLEAHVDLRDCVTYQ 2182
ò	105	1R
g	2183	 TEYRWEVYRTASCORPGRPARVALPGVDVSRPRLVLPRLALPVGHYCFVFVVSFGDTPLT 2242
ò	101	114
q	2243	SIQANVTVAPERLVPIIEGGSYRVWSDTRDLVLDGSESYDPNLEDGDGTPLSFHWACVA 2302
ò	115	118
QQ	2303	STOREAGGCALNFGPRGSSTVTIPRERLAAGVEYTFSLTVWKAGRKEEATNOTVLIRSGR 2362
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ò	119	128RGVTQ
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ò	129	128
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ò	129	128
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ò	129	128
qq	2603	ADPQHVIEYSLALVTVLNEYERALDVAAEPKHERQHRAQIRKNITETLVSLRVHTVDDIQ 2662
ò	129	131
qq	2663	11 QIAAALAQCMGPSRELVCRSCLKQTLHKLEAMMLILQAETTAGTVTPTAIGDSILNITGD 2722
ò	132	131
q	2723	LIHLASSDVRAPQPSELGAESPSRMVASQAYNLTSALMRILMRSRVLNEEPLTLAGEEIV 2782
ò	132	131
q	2783	AQGKRSDPRSLLCYGGAPGPGCHFSIPEAFSGALANLSDVVQLIFLVDSNPFPFGYISNY 2842
ò	132	131
q	2843	TVSTKVASMAFQTQAGAQIPIERLASERAITVKVPNNSDWAARGHRSSANSANSVVVQPQ 2902

INCSASRR  COYFSEED  TAHVGIML  THLOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHVIV  TELOHV	Qy 144LGVTI 148 Db 3983 VSSAARGLAASLLFLLLVKAAQHVRFVRQWSVFGKTLCRALPELLGVTL 4031	RESULT 14 US-09-120-878-1	; Sequence 1, Application US/09320878A ; Patent No. 6117659	; GENERAL INFORMATION: ; APPLICANT: ASHLEY, Gary		; APPLICANT: TANG, Li ; APPLICANT: TANG, Li ; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE	FERENCE: 30062 APPLICATION N	; CURRENT FILING DATE: 1999-05-27 ; EARLIER APPLICATION NUMBER: CIP OF 09/141,908	; EARLIER FILING DATE: 1998-08-28 ; EARLIER APPLICATION NUMBER: CIP OF 09/073,538	; EARLIER FILING DATE: 1998-05-06 ; EARLIER APPLICATION NUMBER: CIP OF 08/846,247	; EARLIER FILING DATE: 1997-04-30 ; EARLIER APPLICATION NUMBER: 60/119,139	; EARLIER FILING DATE: 1999-02-08 ; EARLIER APPLICATION NUMBER: 60/100,880	; EARLIER FILING DATE: 1998-09-22 ; EARLIER APPLICATION NUMBER: 60/087,080	FILING DATE: 1995 F SEQ ID NOS: 34		; Oktanism: Streptomyces venezuelae US-09-320-878-1	26.8%; Score 207;	Debt. Docal Similarity 1.9%; Fred. NO. 1.2; Matches 84; Conservative 19; Mismatches 42; Indels 4181; Gaps	Oy 1 AAGG	   52 AAGGQAVTDVPADRWNAGDFYDPDRSAPGRSNSRWGGFIEDVDRFDAAFFGISPREAAEM 111	ογ 5	Db 112 DPQQRLALELGWEALERAGIDPSSLTGTRTGVFAGAIWDDYATLKHRQGGAAITPHTVTG 171	δγ 5	Db 172 LHRGIIANRLSYTLGLRGPSMVVDSGQSSSLVAVHLACESLRRGESELALAGGVSLNLVP 231	δy 5	Db 232 DSIIGASKFGGLSPDGRAYTFDARANGYVRGEGGGFVVLKRLSRAVADGDPVLAVIRGSA 291	φ	Db 292 VNNGGAAQGMTTPDAQAQEAVLREAHERAGTAPADVRYVELHGTGTPVGDPIEAAALGAA 351	6 6 6 6 6 6 6 6	Db 352 LGTGRPAGOPLLVGSVKTNIGHLEGAAGIAGLIKAVLAVRGRALPASLNYETPNPAIPFE 411	Ογ 10 9	Db 412 ELNLRVNTEYLPWEPEHDGQRMVVGVSSFGMGGTNAHVVLEEAPGVVEGASVVESTVGGS 471	0y 10 9
	HNCSASRR	WS	IRPESLOGADHRPYTFFISPGSRDPAGSYHLNLSSHFRWSALQVSVGLYTSLCQYFSEED	MVMRTEGIA. DI RETS DROAVCI TREIL TRECASI EVIDGALIVE RUEDE DER MINIVITANI TON	THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF THE TRACES OF TH	AHVGIML		FLQHVIV		GPFDKHI		SPLSVDT		LDSSFLT	FSGLHAEQAFVGQMKSDLFLDDSKSLVCWPSGEGTLSWPDLLSDPSIVGSNLRQLARGQA		rrssrss		TPGEKTETLALQRLGELGPPSPGLNWEQPQAARLSRTGLVEGLRKRLLPAWCASLAHGLS			ED	VYMLFLL	13	HGNQSSP 374	13	ELGPPRLROVRLQEALYPDPPGPRVHTCSAAGGFSTSDYDVGWESPHNGSGTWAYSAPDL		LGAMSWGSCAVYDSGGYVQELGLSLEESRDRLRFLQLHNWLDNRSRAVFLELTRYSPAVG		LHAAVTLRLEFPAAGRALAALSVRPFALRRLSAGLSLPLLTSVCLLLFAVHFAVAEARTW	TGFD	3923 HREGRWRVLRLGAWARWLLVALTAATALVRLAQLGAADRQWTRFVRGRPRRFTSFDQVAH 3982

23;

ò	Oy 51RVHLV	99
QQ	Db 1612 AAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVT	MVSLARVWOHHGVTP 1671
ò	ογ 56	55 58
තු	Db 1672 QAVVGHSQGEIAAAYVAGALPLDDAARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERL	MLSLALNEDAVLERL 1731
ò	ολ 26	55
đ	1732 SDFDGLSVAAVNGPTATVVSGDPVQIEELAQACKADGFRARI	IPVDYASHSRQVEIIESE 1791
ò	ολ 26	55 85
g	Db 1792 LAQVLAGLSPQAPRVPFFSTLEGTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFT	FAPAIETLAVDEGFT 1851
ò	, vo	55
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ò	Оу 56	55 88
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ò	26	KMVILTEPE 64
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ò	ολ 65	64
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ò	Oy 65GAPNITANLTSS	94 18
d d	Db 2152 GGTGALGSHAARWAHHGAEHLLLVSRSGEQAPGATQLTAELTASGARVTIAACDVADPH	SARVTIAACDVADPH 2211
ò	ογ 77	92 19
qq	Db 2212 AMRTLLDAIPAETPLTAVVHTAGALDDGIVDTLTAEQVRRAHRAKAVGASVLDELTRDLD	AVGASVLDELTRDLD 2271
ò	Oy 77	92 16
Q	Db 2272 LDAFVLFSSVSSTLGIPGGGNYAPHNAYLDALAARRRATGRSAVSVAWGPWDGGGMAAGD	/AWGPWDGGGMAAGD 2331
ò	Oy 77	18
q	Db 2332 GVAERLRNHGVPGMDPELALAALESALGRDETAITVADIDWDRFYLAYSSGRPQPLVEEL	AYSSGRPQPLVEEL 2391
ò	Оу 88	18 87
a	Db 2392 PEVRRIIDARDSATSGQGGSSAQGANPLAERLAAAAPGERTEILLGLVRAQAAAVLRMRS	SLVRAQAAAVLRMRS 2451
ò	Оу 88	8 87
QC	Db 2452 PEDVAADRAFKDIGFDSLAGVELRNRLTRATGLQLPATLVFDHPTPLALVSLLRSEFLGD	PLALVSLLRSEFLGD 2511
ò	Ογ 88	NPED 91
qq	DD 2512 EETADARRSAALPATVGAGAGAGTDADDDPIAIVAMSCRYPGDIRSPEDLWRMLSEGG	:     RSPEDLWRMLSEGG 2571
ò	Qy 92DIDP	56
qq	Db 2572 EGITPFPTDRGWDLDGLYDADPDALGRAYVREGGFLHDAAEFDAE	FFGVSPREALAMDPQ 2631
ò	ογ 96 γο	56
g	Db 2632 ORMLLTTSWEAFERAGIEPASLRGSSTGVFIGLSYODYAARVPNA	RGVEGYLLTGSTPS 2691

ò	96	Db 3772 AAAARVRLASAGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVGGLMHRVAWRP 3831
පු	2692 VASGRIAYTFGLEGPATTVDTACSSSLTALHLAVRALRSGECTMALAGGVAMMATPHMFV 2751	
ò	56 96	3832 VALASSGEODPHATEVGPTAVICKDELKVANALESAGVEVGLYPDLANISODVANGADAD
g G	2752 EFSRQRALAPDGRSKAFSADADGFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQD 2811	10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000 p. 10.000
ò	56 96	אייייין אייייין זייייין אייייין אייייין אייייין זייייין זייייין אייייין אייייין אייייין זיייין אייייין איייין אייייין אייייין אייייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין אייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין אייין איין אייין איין אייין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין איין אי
g	2812 GASNGLTAPNGPSQQRVIRQALADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKE 2871	3892 KIVLARLKAGPADGGAEGVRGIVARILELLQAWLADEHLAGIRLLLVIRGAVRDFEGSGA
ò	56 96	135
g	2872 RPAERPLAIGSVKSNIGHTQAAAGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGL 2931	Db 3952 DDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSYRTLPSVLSDAGLRDEPQLALH 4011
ò	56 96	Oy 135 141
Q	2932 ALVTEPIDWPAGTGPRRAAVSSFGISGTNAHVVLEQAPDAAGEVLGADEVPEVSETVAMA 2991	Db 4012 DGTIRLARLASVRPETGTAAPALAPEGTVLLTGGTGGLGGLVARHVVGEWGVRRLLLVSR 4071
ò		Qy 142 141
g	2992 GTAGTSEVAEGSEASEAPAAPGSREASLPGHLPWVLSAKDEOSLRGOAAALHAWLSEPAA 3051	Db 4072 RGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAIPAEHPLTAVVHTAGVLSD 4131
·ò		Oy 142 141
q	3052 DLSDADGPARLRDVGYTLATSRTAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTA 3111	Db 4132 GTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGGAGGGAYAAA 4191
ઠે	96102	Qy 142 141
<u>a</u>	RDGTTAFLFTGGGSORPGAGRELYDRHPVFARALDEICAHLDGHLELPLLDVWFAAEGSA	Db 4192 NATLDALAWRRRAAGLPALSLGWGLWAETSGWTGELGQADLRRMSRAGIGGISDAEGIAL 4251
ò		Oy 142 141
: යු	EAALLDETRYTOCAL FALEVAL FRLVESMGMR PAALLGHSVGET AAAHVAGVEST.ADAAR	Db 4252 LDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARPSAASASTTA 4311
ò	Cachiy	Oy 142 141
3 6	CINITY	Db 4312 GTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHARGHRIDAER 4371
3 8	LYAARGELINGELFAGGANILAYQAAEDEIKYWLEIEERIAGKLUVAAVNGFEAAVLSGDAD	Qy 142FDLG 145
ò	109	Db 4372 GFLDLG 4377
සු	3292 AAREAEAYWSGLGRRTRALRVSHAFHSAHMDGMLDGFRAVLETVEFRRPSLTVVSNVTGL 3351	
ò	109	RESULT 15
g	3352 AAGPDDLCDPEYWVRHVRGTVRFLDGVRVLRDLGVRTCLELGPDGVLTAMAADGLADTPA 3411	US-09-105-537-31 ; Sequence 31, Application US/09105537A
ò	109	; Patent No. 6265202 ; GENERAL INFORMATION:
Q	3412 DSAAGSPVGSPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWH 3471	; APPLICANT: Sherman, D.H. ; APPLICANT: Liu, H.
ò	109	
đ	:     3472 AWFAGSGAHRVDLPTYSFRRDRYWLDAPAADTAVDTAGLGLGTADHPLLGAVVSLPDRDG 3531	; TITLE OF INVENTION: DNA encoding methymycin and pikromycin ; FILE REFERENCE: 600.438US1
ò		; CURRENT APPLICATION NUMBER: US/09/105,537A ; CURRENT FILING DATE: 1998-06-26
. 음	EPLVLPE	NUMBER OF SEO ID NOS: 43
ò		
· 유		TYPE: PRT CRGANISM: Streptomyces venezuelae
ò	;	-31
g	3652 VAPDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATT 3711	atch 26.8%; Score 207; DB 4; Length 4613; cal Similarity 1.9%; Pred. No. 1.2;
ò	135 134	Matches 84; Conservative 19; Mismatches 42; Indels 4181; Ga
q	3712 NATAPATANGGGSAAAAPYGIHPALLDASLHAIAVGGLVDEPELVRVPFHWSGVTVHAAG 3771	Oy 1 AAGG
ò	135 134	II4 AAGGGAVIDVFADKWNAGDFIDFDKOAFGKSNOKWGGFIEDVDKFDAAFFGISKKEAAEM

23;

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ဂ္က	174	DPQQRLALELGWEALERAGIDPSSLTGTRTGVFAGAIWDDYATLKHRQGGAAITPHTVTG	233
≿	ស		4
ဂ္ဂ	. 234	LHRGI IANRLSYTLGLRGPSMVVDSGQSSSLVAVHLACESLRRGESELALAGGVSLNLVP	293
≥.	រប		4
ထူ	294	DSIIGASKFGGLSPDGRAYTFDARANGYVRGEGGGFVVLKRLSRAVADGDPVLAVIRGSA	353
≿.	S		4
ą	354	VNNGGAAQGMTTPDAQAQEAVLBEAHERAGTAPADVRYVELHGTGTPVGDPIEAAALGAA	413
≿	ß	ILHUE	o.
ą	414	LGTGRPAGQPLLVGSVKTNIGHLEGAAGIAGLIKAVLAVRGRALPASLNYETPNPAIPFE	473
<u>&gt;</u>	10		σ
Q	474	ELNLRVNTEYLPWEPEHDGQRMVVGVSSFCMGGTNAHVVLEEAPGGCRGASVVESTVGGS	533
<u>&gt;</u> -	10		6
۵	534	<b>AVGGGVVPWVVSAKSAAALDAQIERLAAFASRDRTDGVDAGAVDAGAVDAGAVARVLAGG</b>	593
≽	10	LVAVGPD	17
۵	594	RAQFEHRAVVVGSGPDDLAAALAAPEGLVRGVASGVGRVAFVFPGQGTQWAGMGAELLDS	653
<u>&gt;</u>	18	VPQA	21
۵	654	 SAVFAAAWAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHH	713
<u>~</u>	22		21
م	714	GVTPQAVVGHSQGEIAAAYVAGALSLDDDAARVVTLRSKSIAAHLAGKGGMLSLALSEDAV	773
<u>&gt;</u> -	22		21
۾	774	LERLAGFDGLSVAAVNGPTATVVSGDPVQ1EELARACEADGVRARV1PVDYASHSRQVE1	833
>	22		21
Ω	834	IESELAEVLAGLSPQAPRVPFFSTLEGAWITEPVLDGGYWYRNLRHRVGFAPAVETLATD	893
ج	22		21
Ω	894	EGFTHFVEVSAHPVLTMALPGTVTGLATLRRDNGGQDRLVASLAEAWANGLAVDWSPLLP	953
>	22	HQEDTER	28
Ω	954	SATGHHSDLPTYAFQTERHWLGEIEALAPAGEPAVQPAVLRTEAAEPAELDRDEQLRVIL	1013
>	29		28
Д	1014	DKVRAQTAQVLGYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAFGVRMAPSMIFDFPT	1073
>	29		28
ρ	1074	PEALAEQLLLVVHGEAAANPAGAEPAPVAAAGAVDEPVAIVGMACRLFGGVASPEDLWRL	1133
>-	29		28
Ω	1134	VAGGGDAISEFPQDRGWDVEGLYHPDPEHPGTSYVRQGGFIENVAGFDAAFFGISPREAL	1193
>	29	170X	32
Ω	1194	:   AMDPQQRLLLETSWEAVEDAGIDPTSLRGRQVGVFTGAMTHEYGPSLRDGGEGLDGYLLT	1253
>	33	NLNIGAELLR	42

94	77	ò
2333	2274 AMRTLLDAIPAETPLTAVVHTAGALDDGIVDTLTAEQVRRAHRAKAVGASVLDELTRDLD	qq
94	77	ò
2273	2214 GGTGALGSHAARWAHHGAEHLLLVSRSGEQAPGATQLTAELTASGARVTIAACDVADPH	qq
91	65GAPNITANLTSS	ò
2213	2154 PAQPDAAALAHLVTALSGATGEDQIAIRTTGLHARRLARAPLHGRRPTRDWQPHGTVLIT	qq
64		ઠે
2153	2094 AWVQALGDAGIKAPLWSVTQGAVSVGRLDTPADPDRAMLWGLGRVVALEHPERWAGLVDL	g
64	56KMVILTEPE	ò
2093	2034 HSAQAAAVLTALVDAGAKVEVLTAGADDDREALAARLTALTTGDGFTGVVSLLDGLVPQV	qq
55	95	ò
2033	1974 RPGLPTYAFQAERYWLENTPAALATGDDWRYRIDWKRLPAAEGSERTGL&GRWLAVTPED	QQ
55		ò
1973	1914 HFVEVSAHPVLTMTLPETVTGLGTLRREQGGGRLVTSLAEAWVNGLPVAWTSLLPATAS	QQ
55	26	ð,
1913	1854 LAQVLAGLSPQAPRVPFFSTLEGTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFT	g
55	99	ò
1853	1794 SDFDGLSVAAVNGPTATVVSGDPVQIEELAQACKADGFRARIIPVDYASHSRQVEIIESE	Q
55	95	ò
1793	1734 QAVVGHSQGEIAAAYVAGALPLDDAARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERL	qq
55	26	ò
1733	1674 AAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWOHHGVTP	q
55	51RVHLV	ò
1673	1614 EHRAVALGAGADDLVQALADPDGLIRGTASGVGRVAFVFPGQGTQWAGMGAELLDSSAVF	q
20	51	ò
1613	1554 SAVGGGVTPWVVSAKSAAALDAQIERLAAFASRDRTDDADAGAVDAGAVAHVLADGRAQF	QC
20	48	ò
1553		q
47	. 43DPSLG-	ò
1493	1434 TYGGGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDQIDW	QQ
42	43	ò
1433	1374 ALNODGASNGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQALIA	g
42	43	ò
1373	1314 PGMFVEFSRQRGLAGDGRSKAFAASADGTSWSEGVGVLLVERLSDARRNGHOVLAVVRGS	QQ
4 2	43	ò
1313	:: :       1254 GNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVMPT	g

2393	. 87	. 2453	. 87	3 2513	. 87	2573	. 91	3 2633	. 95	2693	95	2753	95	2813		2873	95	2933	95	2993	95	3053	95	3113	95	3173	102	3233	102	3293	108	3353	108	3413	108	3473
LDAFVLFSSVSSTLGI PGQGNYAPHNAYLDALAARRRATGRSAVSVAWGPWDGGGMAAGD	TLSVCGWSQTI			PEVRRIIDARDSATSGQGGSSAQGANPLAERLAAAAPGERTEILLGLVRAQAAAVLRMRS		PEDVAADRAFKDIGFDSLAGVELRNRLTRATGLQLPATLVFDHPTPLALVSLLRSBFLGD	NPEDNPED-	:    EETADARRSAALPATVGAGAGAGAGTDADDDP1AIVAMSCRYPGD1RSPEDLWRMLSEGG	- DTDP	 EGITPFPTDRGWDLDGLYDADPDALGRAYVREGGFLHDAAEFDAEFFGVSPREALAMDPQ		<b>Ormllitsweaferagiepaslrgsstgvfiglsyqdyaarvpnaprgvegylltgstps</b>		VASGRIAYTFGLEGPATTVDTACSSSLTALHLAVRALRSGECTMALAGGVAMMATPHMFV		EFSRQRALAPDGRSKAFSADADGFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQD		GASNGLTAPNGPSQQRVIRQALADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKE		RPAERPLAIGSVKSNIGHTQAAAGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGL		alvtepidwpagtgprraavssfgisgtnahvvleqapdaagevlgadevpevsetvama		GTAGTSEVAEGSEAPAAPGSREASLPGHLPWVLSAKDEQSLRGQAAALHAWLSEPAA		DLSDADGPARLRDVGYTLATSRTAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTA	CHADLVL	:     RDGTTAFLFTGGGSQRPGAGRELYDRHPVFARALDEICAHLDGHLELPLLDVMFAAEGSA		<b>EAALLDETRYTQCALFALEVALFRLVESWGMRPAALLGHSVGEIAAAHVAGVFSLADAAR</b>	YITRED	LVAARGRLMQELPAGGAMLAVQAAEDEIRVWLETEERYAGRLDVAAVNGPEAAVLSGDAD		AAREAEAYWSGLGRRTRALRVSHAFHSAHMDGMLDGFRAVLETVEFRRPSLTVVSNVTGL		AAGPDDLCDPEYWVRHVRGTVRFLDGVRVLRDLGVRTCLELGPDGVLTAMAADGLADTPA
2334 1	. 77	2394 (	88	2454	88	2514	88	2574 E	- 26	2634 E	96	2694	- 96	2754 V	- 96	2814 E	- 96	2874 G	- 96	2934 R	- 96	2994 A	- 96	3054 G	- 96	3114 D	- 96	3174 R	103 -	3234 E	103 -	3294 L	109	3354 A	109 -	3414 A
g	ò	qq	ò	q	ò	q	ò	q	ò	qq	ò	QQ	ò	ପ୍ର	ò	q	ò	Q	ò	<del>Q</del>	ò	6	ò	QQ	ò	q	ò	ορ	ò	q	ò	g	ò	QQ	ò	අ

ò	109
qq	3474 DSAAGSPVGSPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWH 3533
ò	109
qq	_g_
ò	114 124
qq	3594 LLLTGRLSLRTHPWLADHAVLGSVLLPGAAMVELAAHAAESAGLRDVRRLTLLEPLVLPE 3653
ò	
Q	
ò	135 134
qq	3714 VAPDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATT 3773
ò	135 134
쉽.	3774 NATAPATANGGGSAAAAPYGIHPALLDASLHAIAVGGLVDEPELVRVPFHWSGVTVHAAG 3833
ò	135 134
q	3834 AAAARVRLASAGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVGGLMHRVAWRP 3893
ò	135 134
qq	3894 YALASSGEQDPHATSYGPTAVLGKDELKVAAALESAGVEVGLYPDLAALSQDVAAGAPAP 3953
ò	135 134
q	3954 RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAGTRLLLVTRGAVRDPEGSGA 4013
ò	135 134
QQ	4014 DDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSYRTLPSVLSDAGLRDEPQLALH 4073
ò	13511TEDTG141
QQ	
ò	142 141
QQ	4134 RGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAIPAEHPLTAVVHTAGVLSD 4193
ò	142
qq	4194 GTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGGAGGGAYAAA 4253
ò	142 141
С	4254 NATLDALAWRRRAAGLPALSLGWGLWAETSGMTGELGQADLRRMSRAGIGGISDAEGIAL 4313
ò	142 141
QQ	4314 LDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARPSAASASTTA 4373
ò	142 141
qq	4374 GTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHARGHRIDAER 4433
ò	142 FDLG 145
С	4434 GFLDLG 4439

Search completed: March 20, 2003, 12:41:25 Job time : 149 secs

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March 20, 2003, 12:37:58 ; Search time 18 Seconds (without alignments) 439.578 Million cell updates/sec
                                                                                                                                                                                                                                                                              SEQID_1_1SFUSED
773
1 AAGGILHLELLVAVGPDVFQ......SPTWSCLITEDTGFDLGVTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Ggn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/NEO7_PUBCOMB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/NEO8_PUBCOMB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221153 segs, 53462247 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                      OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match	100.0	100.0	100.0	100.0	9.66	99.6	95.6	90'8	35.2	30.7	30.4	30.4	29.9	29.6	29.6	29.5	28.7	28.5	0 40	9
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Ouery Match 100.0%; Score 773; DB 10; Length 148; Best Local Similarity 100.0%; Pred. No. 4.4e-31; Matches 148; Conservative 0; Mismatches 0; Indels 0.

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2 2 2 3 3 3	206	'n	4303	<b>D</b> O	US-10-014-717-5 US-09-904-968A-2	Sequence 5, Appli Segmence 2, Appli
24	208	7	5701	2	0 US-09-864-761-37319	Sequence 1, Appli
25	207	5 6	950	20	US-09-965-631-4	Sequence 4, Appli
27	202	7 6	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	nσ	US-10-160-758-13	Sequence 13, Appl
28	207	ñ	4613	'n	US-09-860-846-31	Segmence 14, Appl
53	207	5	4613	10	US-09-861-289-31	Sequence 31, Appl
30	206	2 2	5405	σ,	US-10-025-380-1116	Sequence 1116, Ap
35	205	7 7	4999	7 6	US-09-976-0141116 US-09-976-059-15	Sequence 1116, Ap
33	204	56	1882	10,	US-09-918-171A-13	Sequence 13, Appl Sequence 13, Appl
3.4	202	56	947	10	US-09-788-043C-7	Sequence 7, Appli
3. C	202	7 2	1629	9 9	US-09-972-467-2	Sequence 2, Appli
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. 39	198	25	1249	10	US-09-938-330-22	Segmence 27 April
40	198	25	1252	2	US-09-938-330-20	Sequence 20, Appl
41	197	25	507	2	US-09-963-791-10	Sequence 10, Appl
45	197	25	289	10	US-09-963-791-12	Sequence 12, Appl
4	197	22	828	2	US-09-918-171A-5	Seguence 5, Appli
4 4 4 A	197		806	9 5	US-09-963-791-2	Sequence 2, Appli
7	121	7	000	2	US-UY-321-987B-4	Sequence 4, Appli
RESULT 1 US-09-833-228-4 Sequence 4, A Patent No. US GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	3-328- No. U. 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US-09-833	-328-4	ıdınarı				

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Sequence 2, Application US/09836712
Patent No. US20010049106A1
GENERAL INFORMATION
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC10851A
CURRENT APPLICATION NUMBER: US/09/836,712
CURRENT FILE OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNROVRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 242;
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,979
FILING DATE: 16-OCC-2001
CLASSIFICATION NUMBER: US/60/241,469
FILING DATE: CUNKNOWN>
APPLICATION DATA:
APPLICATION NUMBER: US/60/241,469
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REFERENCE/DOCKET NUMBER: GI 5435p
TELECOMUNICATION INFORMATION:
TELEPHONE: (973) 660-5000
TELEPHONE: (973) 660-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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ORGANISM: Human
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Matches 148;
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                                                                                                                                                                    Sequence 6, Application US/09833328

Patent No. US20020136713A1

GENERAL INFORMATION

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Luigina

APPLICANT: Tagliavacca, Luigina

APPLICANT: Tagliavacca, Luigina

APPLICANT: Tagliavacca, Luigina

APPLICANT: Gerritsen, Helena E.

TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act

TITLE OF INVENTION: Composition Exhibiting a Polypeptide Chain with the Amino Acid Sequence AAGG

FILE REFERENCE: 247.00CIP

TITLE OF INVENTION NUMBER: US/09/833,328

CURRENT FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1
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Patent No. US20020151702A1;
GENERAL INFORMATION:
APPLICANT: Racie, Lisa, A.
Mortian, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
Wolfman, Naichael, J.
STREET OF INVENTION: Aggrecanase Molecules
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
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4.6e-31;
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Best Local Similarity 100.0%; Pred. No. 4
Matches 148; Conservative 0; Mismatche
                               121 VTQLGGACSPTWSCLITEDTGFDLGVTI 148
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     121 VTQLGGACSPTWSCLITEDTGFDLGVTI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: New Jersey
COUNTRY: USA
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-833-328-6
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APPLICANT: Furlan, Miha APPLICANT: Furlan, Miha APPLICANT: Furlan, Miha APPLICANT: Turecek, Peter APPLICANT: Turecek, Peter APPLICANT: Turecek, Helena E. TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protea TITLE OF INVENTION: Composition a Polypeptide Chain with the Amino Acid Sequenc FILE REPERENCE: 247.00CIP US. 100CIP CURRENT APPLICATION NUMBER: 09/9833,328 CURRENT APPLICATION NUMBER: 09/121,254 PRIOR PILING DATE: 2000-11-22 NUMBER OF SEQ ID NOS: 15
                                                                                                                             TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG 120
                                                                                                                                                      61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLXITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                              1 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVIL 60
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100.0%; Pred. No. 2.4e-28;
iive 0; Mismatches 0;
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US-09-833-328-2
Sequence 2, Application US/09833328
Patent No. US20020136713A1
GENERAL INFORMATION:
APPLICANT: Laemmle, Bernhard
APPLICANT: Schwarz, Hans-Peter
APPLICANT: Schwarz, Hans-Peter
APPLICANT: Antoine, Gerhard
APPLICANT: Artoine, Gerhard
APPLICANT: Artoine, Luigina
APPLICANT: Tagliavacca, Luigina
APPLICANT: Zimmermann, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NT: Schwarz, Hans-Peter
NT: Scheiflinger, Friedrich
NT: Arciole, Gerhard
NT: Kerschbaumer, Randolf
NT: Tagliavacca, Luigina
NT: Zimmermann, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09833328
; Patent No. US20020136713A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Laemmle, Bernhard APPLICANT: Schwarz, Hans-Pei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.61
Best Local Similarity 100.0
Matches 136; Conservative
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ORGANISM: human
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SOFTWARE: Pater
SEQ ID NO 15
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158 TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG 217
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                                                                                                                                                                                                               Sequence 2, Application US/09781080B
Pacent No. US20020142439A1
GENERAL INFORMATION:
APPLICANT: HOLLOWAY, JIM
APPLICANT: SHEPPARD, PAUL
APPLICANT: YAMAMOTO, GAYLE
TITLE OF INVENTION: Anti-Anglogenic Intestinal Peptides,
TITLE OF INVENTION: Zdint5
FILE REFERENCE: 99-82
CURRENT APPLICATION NUMBER: US/09/781,080B
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: SHEPPARD, PAUL
APPLICANT: SHEPPARD, PAUL
APPLICANT: YAMAMOTO, GAYLE
TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides,
TITLE OF INVENTION: Actints
FILE REFERENCE: 99-82
CURRENT APPLICATION NUMBER: US/09/781,0808
CURRENT FILING NUMBER: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FRAESO for Windows Version 3.0
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99.6%; Score 770; DB 10;
Best Local Similarity 99.3%; Pred; No. 6.7e-29;
Matches 147; Conservative 1; Mismatches 0;
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COCATION: (1)...(1120)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-781-080B-11
                                                                          218 VTQLGGACSPTWSCLITEDTGFDLGVTI 245
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Patent No. US20020142439A1
GENERAL INFORMATION:
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US-09-781-080B-2
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LENGTH: 203
TYPE: PRT
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370 IRTEERWEGRYGVQEQVTISGAAGAAASVSASASYAAEAVATGAKEVKQDADKSAAVATV 429
                                                                          430 VAAVDMARVREPVISAVEQTAQRTTTTAVHIQPAQEQVRKEAEKTAVTKVVVAADKAKEQ 489
                                                                                                                                             490 ELKSRTKEIITTKQEQMHVTHEQIRKETEKTFVPKVVISAAKAKEQETRISEEITKKQKQ 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                           730 HIKTTDOKGMHISSQIKKTTDLTTERLVHVDKRPRTASPHFTVSKISVPKTEHGYEASIA 789
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       APPLICANT: Turecek, Peter APPLICANT: Turecek, Peter APPLICANT: Turecek, Peter APPLICANT: Gerritern, Helena E. APPLICANT: Gerritern, Helena E. TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act TITLE OF INVENTION: Composition a Polypeptide Chain with the Amino Acid Sequence AAGG CURRENT APPLICATION NUMBER: US/09/833,328 CURRENT FILING DATE: 2001-04-12 PRIOR PILING DATE: 2000-11-22 PRIOR FILING DATE: 2000-11-22 PRIOR PILING DATE: 2000-11-22 SOFTWARE: Patentin version 3.1 ENUMBER: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                      250 PHKTPPRIPPKPKSRSPTPPSIAAKAQLARQOSPSPIRHSPSPVRHVRAPTPSPVRSVSP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 AARISTSPIRSVRSPLLMRKTQASTVATGPEVPPPWKQEGYVASSSBAEMRETTLTTSTQ 369
                                                                                                                                                                                                                                                                                                                                                                                             16 PDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fishman, Mark C.
TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REFERENCE: 007086/381002
CURRENT APPLICATION NUMBER: US/09/759,508B
PRIOR APPLICATION NUMBER: US 60/175,787
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VERSION 3.1
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US-09-759-508B-2
Sequence 2, Application US/09759508B
Publication No. US20020182599A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 133; Conservative
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Best Local Similarity 0.4*
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-508B-2
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                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: human
US-09-833-328-2
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37	36
1570 KI	KIDSTVSQDSAWYTATAINKAGRDTTRCKVNVEVEFAEPEPERKLIIPRGTYRAKEIAAP 1629
37	36
1630 EL	ELEPLHLRYGQEQWEEGDLYDKEKQQKPFFKKKLTSLRLKRFGPAHFECRLTPISDPTMV 1689
37	36
690 VE	VEWLHDGKPLEAANRLRMINEFGYCSLDYGVAYSRDSGIITCRATNKYGTDHTSATLIVK 1749
37	
1750 DE	 DEKSLVEESQLPEGRKGLQRIEELERMAHEGALTGVTTDQKEKQKPDIVLYPEPVRVLEG 1809
39	38
1810 ET	ETARFRCRVTGYPQPKVNWYLNGQLIRKSKRFRVRYDGIHYLDIVDCKSYDTGEVKVTAE 1869
39	38
1870 NP	NPEGVIEHKVKLEIQQREDFRSVLRRAPEPRPEFHVHEPGKLQFEVQKVDRPVDTTETKE 1929
39	
1930 W	 VVKLKRAERITHEKVPEESBELRSKFKRRTEEGYYEAITAVELKSRKKDESYEELLRKTK 1989
43	42
1990 DE	DELLHWTKELTEEEKKALAEEGKITIPTFKPDKIELSPSMEAPKIFERIQSGTVGQGSDA 2049
43	15 DPS
2050 HF	
46	45
2110 IA	IAGETSSHAFLLVQAKQLITFTQELQDVVAKEKDTWATFECETSEPFVKVKWYKDGMEVH 2169
46	45
2170 EG	EGDKYRMHSDRKVHFLSILTIDTSDAEDYSCVLVEDENVKTTAKLIVEGAVVEFVKELQD 2229
46	45
2230 IE	IEVPESYSGELECIVSPENIEGKWYHNDVELKSNGKYTITSRRGRQNLTVKDVTKEDQGE 2289
46	. 45
2290 YS	YSFVIDGKKTTCKLKMKPRPIAILQGLSDQKVCEGDIVQLEVKVSLESVEGVWMKDGQEV 2349
46	. 45
2350 QP	QPSDRVHIVIDKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSGRVSVYSVDVITPLKDVN 2409
46	45
2410 VI	VIEGTKAVLECKVSVPDVTSVKWYLNDEQIKPDDRVQAIVKGTKQRLVINRTHASDEGPY 2469
46	45
2470 KL	KLIVGRVETNCNLSVEKIKIIRGLRDLTCTETQNVVFEVELSHSGIDVLMNFKDKEIKPS 2529
46	45

ò	46		45
qq	2590	EAVFECEVANPDSKGEWLRDGKHLPLTNNIRSESDGHKRRLIIAATKLDDIGEYTYKVAT	2649
ò	46		45
q	2650	SKTSAKLKVEAVKIKKTLKNLTVTETQDAVFTVELTHPNVKGVQWIKNGVVLESNEKYAI	2709
ò	4	LGAQFRVHLVKMV	28
q	2710	SVKGTIYSLRIKNCAIVDESVYGFRLGASARLHVETVKIIKKPKDVTALENATVAFE :	2769
ò	65		58
qq	2770	VSVSHDTVPVKWFHKSVEIKPSDKHRLVSERKVHKLMLQNISPSDAGEYTAVVGQLECKA	2829
ò	29		28
qq	2830	KLFVETLHITKTMKNIEVPETKTASFECEVSHFNVPSMMLKNGVEIEMSEKFKIVVQGKL	2889
ò	29		28
q	2890 1	HQLIIMNTSTEDSAEYTFVCGNDQVSATLTVTPIMITSMLKDINAEEKDTITFEVTVNYE	2949
ò	59		58
QQ	2950 (	GISYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGDAADYTFVAGKATSTATLYVEA	3009
ò	29		58
đ	3010	RHIEFRKHIKDIKVLEKKRAMFECEVSEPDITVQMMKDDQELQITDRIKIQKEKYVHRLL ;	3069
ò	. 89		88
ď	3070	IPSTRMSDAGKYTVVAGGNVSTAKLFVEGRDVRIRSIKKEVQVIEKQRAVVEFEVNEDDV ;	3129
ò	. 65		58
qq	3130 1	DAHWYKDGI EINFQVQERHKYVVERRIHRMFI SETRQSDAGEYTFVAGRNRSSVTLYVNA	3189
ò	65		88
qq	3190 1	PEPPQVLQELQPVTVQSGKPARFCAMISGRPQPKISWYKBEQLLSTGFKCKFLHDGQEYT :	3249
ò	. 65		28
q	3250 1	LLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEVPEVVSPDQEMPVYPPAIITPLQDTV	3309
ò	. 65		28
Ġ	3310 7	TSEGGPARFOCRVSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLEIAEAYPEDEGTYT	3369
ò	. 65		58
qq	3370	FVANNAVGQVSSTANLSLEAPESILHERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLS	3429
ò	. 65		28
qq	3430 1	KINETLELLSESPVYPTKFDSEKEGTGPIFIKEVSNADISMGDVATLSVTVIGIPKPKIQ :	3489
ò	. 65		28
q	3490 1	WFFNGVLLTPSADYKFVFDGDDHSLIILFTKLEDEGEYTCMASNDYGKTICSAYLKINSK ;	3549
ò	. 65		8
qq	3550	GEGHKDTETESAVAKSLEKLGGPCPPHFLKELKPIRCAQGLPAIFEYTVVGEPAPTVTWF	3609
ò	. 65		28
QQ	3610 1	KENKOLCTSVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENMLGESTCAAELLVLLED	3669
ò	. 69		28

		qq	4750 DGKIVVEKP
đ	3670 TDMTDTPCKAKSTPEAPEDFPQTPLKGPAVEALDSEQEIATFVKDTILKAALITEENQOL 3729	ò	70
ò	85 65	qq	4810 WLVKPIRDQ
අු	3730 SYEHIAKANELSSQLPLGAQELQSILEQDKLTPESTREFLCINGSIHFQPLKEPSPNLQL 3789	ò	
ò	59	셤	4870 KNAMPEDIA
Q	3790 QIVQSQKTFSKEGILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPLKTLLAEPEGN	ò	70
ò	99	g	4930 GOWKLKGEL
Q	3850 YPQSSIEPPMHSYLTSVAEEVLSLKEKTVSDTNREQRVTLQKQEAQSALILSQSLAEGHV 3909	ò	70
ò	99	ති	4990 DFAVPLKDV
g	3910 ESLQSPDVMISQVNYEPLVPSEHSCTEGGKILIESANPLENAGQDSAVRIEEGKSLRFPL 3969	ò	70
ò	5999	අු	5050 QFDDEGVYT
පු	3970 ALEEKQVLLKEEHSDNVVMPPDQIIESKREPVAIKKVQEVQGRDLLSKESLLSGIPEEQR 4029	ò	
ò	99	g	5110 FKNDAKLHT
g	4030 LNLKIQICRALQAAVASEQPGLFSEWLRNIEKVEVEAVNITQEPRHIMCMYLVTSAKSVT	ò	70
ò		g	5170 VKLHDKTAV
q	4090 EEVTIIIEDVDPQMANLKMELRDALCAIIYEEIDILTAEGPRIQQGAKTSLQEEMDSFSG	ò	70
ò		qq	5230 DKGEYVCDC
g	4150 SQKVEPITEPEVESKYLISTEEVSYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKP 4209	ò	70
ò	99	q	5290 GQPLTASPI
đ	4210 SEEKEESSSESGTEEVATVKIQEAEGGLIKEDGPMIHTPLVDTVSEEGDIVHLTTSITNA 4269	ò	70
ò	99	<u>අ</u>	5350 SDVKVFEKI
g	4270 KEVNWYFENKLVPSDEKFKCLQDQNTYTLVIDKVNTEDHQGEYVCEALNDSGKTATSAKL 4329	ò	
ò	99	셤	5410 AKYMFEAE
a	4330 TVVKRAAPVIKRKIEPLEVALGHLAKFTCEIQSAPNVRFQWFKAGREIYESDKCSIRSSK 4389	ò	70
ò	. 70 69	q	5470 RLHTTRSV
q	3 4390 YISSLEILRTQVVDCGEYTCKASNEYGSVSCTATLTVTVPGGEKKVRKLLPERKPEPKEE 4449	ò	70
ò	70	g	5530 YTGVEKDE
đ	4450 VVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPKPVEEVEVPTVTKRERKIPEPTK	ò	70
ò	70	q	5590 YTCDCGTD
g	4510 VPEIKPAIPLPAPEPKPKPEAEVKTIKPPPVEPEPTPIAAPVTVPVVGKKAEAKAPKEEA	ò	70
ò	70	g	S650 LQTPDCEI
a	4570 AKPKGPIKGVPKKTPSPIEAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDIIL	ò	70
ò		qq	5710 VTAGETAT
g	4630 TESEFVGSSAIFECLVSPSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAG	ò	70
ò	10	q <sub>Q</sub>	5770 LTAKDFKT
d	4690 EYTCVLRLGNKEKTSTAKLVVEELPVRFVKTLEEEVTVVKGOPLYLSCELNKERDVVWRK	δ	70
à.	69	g	5830 SKKYEIVA

g G	4750	DCKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYTVTVENANNLECSSCVKVVEVIRD 4	4809
ò	70	9	69
QQ	4810	WLVKPIRDQHVKPKGTAIFACDIAKDTPNIKWFKGYDEIPAEPNDKTEILRDGNHLYLKI 4	4869
ò	70	9	69
g	4870	KNAMPEDIAEYAVEIEGKRYPAKLTLGEREVELLKPIEDVTIYEKESASFDAEISEADIP 4	4929
ò	70	9	69
g	4930	GOWKLKGELLRPSPTCEIKAEGGKRFLTLHKVKLDQAGEVLYQALNAITTAILTVKEIEL 4	4989
ò	70	9	69
g	4990	DFAVPLKDVTVPERRQARFECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILVINDS S	5049
ò	70	9	69
qq	5050	QPDDEGVYTAEVEGKKTSARLFVTGIRLKFMSPLEDQTVKEGETATFVCELSHEKMHVVW 5	5109
ò	70	9	69
Db	5110	FKNDAKLHTSRTVLISSEGKTHKLEMKEVTLDDISQIKAQVKELSSTAQLKVLEADPYFT \$	5169
ò	70		69
g	5170	VKLHDKTAVEKDEITLKCEVSKDVPVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLK \$	5229
ò	70	9	69
엄	5230	DKGEYVCDCGTDKTKANVTVEARLIEVEKPLYGVEVFVGETAHFEIELSEPDVHGOWKLK §	5289
જે	70	)	69
D D	5290	GQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKELPLIFITPL 9	5349
ò	70	9	. 69
g	5350	SDVKVFEKDEAKFECEVSREPKTFRWLKGTQEITGDDRFELIKDGTKHSMVIKSAAFEDE 9	5409
ò	70		69
g	5410	AKYMFEAEDKHTSGKLIIEGIRLKFLTPLKDVTAKEKESAVFTVELSHDNIRVKWFKNDQ	5469
ò	70		69
qq	5470	RLHTTRSVSMQDEGKTHSITFKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGKLQD	5529
ò	70		69
g	5530	YTGVEKDEVILQCEISKADAPVKWFKDGKEIKPSKNAVIKTDGKKRMLILKKALKSDIGQ	5589
ò	70		69
g	5590	YTCDCGTDKTSGKLDIEDREIKLVRPLHSVEVMETETARFETEISEDDIHANWKLKGEAL	5649
ò	70		69
g	5650	LQTPDCEIKEEGKIHSLVLHNCRLDQTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVT	5709
ò	7.0		69
g	5710	VTAGETATFDCELSYEDI PVEWYLKGKKLEPSDKVVPRSEGKVHTLTLRDVKLEDAGEVO	5769
ò	70		69
g	5770	LTAKDFKTHANLFVKEPPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFKNGTEILK	5829
ò	70		69
g	5830	SKKYEIVADGRVRKLVIHDCTPEDIKTYTCDAKDFKTSCNLNVVPPHVEFLRPLTDLQVR	5889

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ò	γ 70 69	ð :	
Ω	Db 6070 EKAEFVCSISKESFPVQWKRDDK†LESGDKYDVIADGKKRVLVVKDATLQDMGTYVVMVG 6129	g d	EVIGLEEGKWYAIKVKILNKUCASKKSKPIEBLUAVUIUBAFEIFLUVNLLAGEIVNAGI
o	69 69	à á	82
ם	Db 6130 AARAAAHLTVIEKLRIVVPLKDTRVKEQQEVVFNCEVNTEGAKAKWFRNEEAIFDSSKYI 6189	8 8	NIELFAIVIGAFERNIIMINAUMILUKUNALIIENVENNIIVILA
J	ογ 7069	ें है	52
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Ω	Db 6430 ADVVFLAELNKDKVEVQWLRNNMVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIAK 6489	සු ර	PEHDGGAKIESYVIEMLKTGTDEWVRVAEGVPTTOHLLPGLMEGGETSFRVKAVNNAGES 750
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J	δο 20 20 Αδ	q	7750 DVIEGTEVQFQVRAENEAGVGHPSEPTEILSIEDPTSPPSPPLDLHVTDAGRKHIAIAWK 7809
រ	Db 6670 RNRVGTGEPVETDNPVEARSKYDVPGPPLNVTITDVNRFGVSLTWEPPEYDGGAEITNYV 6729	ò	82 81
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u	6790 DPIERPSPPVNLTSSDQTQSSVQLKWEPPLKDGGSPILGYIIERCEEGKDNWIRCNMKLV	ò	82 81
J	77	qq	7930 VKASDRLTMKNDHISAHLEVPKSVRADAGIYTITLENKLGSATASINVKVIGLPGPCKDI 7989
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J (		qq	7990 KASDITKSSCKLTWEPPEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWTVKDLIPN 8049
_	DB 6910 IVPNPITILVPSTGYPRPTATWCFGDKVLETGDRVKMTLSAYAELVISPSEKSDKGIYT 6969	ò	82 81

മ	8050	GEYFFRVKAVNKVGGGEYIELKNPVIAQDPKQPPDPPVDVEVHNPTAEAMTITWKPPLYD	8109
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ą	8170	RATPPTKAVDPIDAPKVILRTSLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEEIK	8229
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ą	8230	KRAAPLVRRRKGEVQEEEPFVLPLTQRLSIDNSKKGESQLRVRDSLRPDHGLYMIKVEND	8289
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ą	8290	HGIAKAPCTVSVLDTPGPPINFVFEDIRKTSVLCKWEPPLDDGGSEIINYTLEKKDKTKP	8349
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දි	8350	DSEWIVVTSTLRHCKYSVTKLIEGKEYLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAP	8409
à	82		81
g	8410	DKPIVEDVTSNSMLVKWNEPKDNGSPILGYWLEKREVNSTHWSRVNKSLLNALKANVDGL	8469
⋩	82		81
g	8470	LEGLTYVFRVCAENAAGPGKFSPPSDPKTAHDPISPPGPPIPRVTDTSSTTIELEWEPPA	8529
ત્	82		81
q	8530	FNGGGEIVGYFVDKQLVGTNKWSRCTEKMIKVRQYTVKEIREGADYKLRVSAVNAAGEGP	8589
તે	82		81
q <sub>0</sub>	8590	PGETQPVTVAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGRPVPTKVWTKEEGELD	8649
ò	82		81
g	8650	KDRUVI DNVGTKSELI I KDALRKDHGRYVI TATNSCGSKFAAARVEVFDVPGPVLDLKPV	8709
ò	82		81
g	8710	VTNRKMCLLNWSDPEDDGGSEITGFIIERKDAKMHTWRQPIETERSKCDITGLLEGQEYK	8769
ò	82		81
g	8770	FRVIAKNKFGCGPPVEIGPILAVDPLGPPTSPERLTYTERQRSTITLDWKEPRSNGGSPI	8829
ò	82		81
g G	8830	QGYIIEKRRHDKPDFERVNKRLCPTTSFLVENLDEHQMYEFRVKAVNEIGESEPSLPLNV	8889
ò	82		81
g	9890	VIQDDEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPMPKIEWSKNETVIEKPTDAL	8949
ò	82		81
Op	8950	QITKEEVSRSEAKTELSIPKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPPRNLAV	6006
ò	82		81
qq	9010	TDIKAESCYLTWDAPLDNGGSEITHYVIDKRDASRKKAEWEEVTNTAVEKRYGIWKLIPN	6906
ò	82		81
g	9070	GQYEFRVRAVNKYGISDECKSDKVVIQDPYRLPGPPGKPKVLARTKGSMLVSWTPPLDNG	9129
ò	83		81

g	9130 GSPITGYWL)	tgywlekreegspywsrvsrapitkvglkgvefnvprllegvkyQframainaagi 9	9189
ò	82	88	83
qq	9190 GPPSEPSDP)	EVAGDP1 FPPGPPSCPEVKDKTKSS1SLGWKPPAKDGGSP1KGY1VEMQEE	9249
ò	84	8	83
q	9250 GTTDWKRVNEPDKL	ITTCECVVPNLKELRKYRFRVKAVNEAGESEPSDTTGEIPATDIQE	9309
ò	84	60	83
q	9310 EPEVFIDIG	IGAQDCLVCKAGSQIRIPAVIKGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQ 9	9369
ò	84	8	83
QQ	9370 LETAENSSV	LETAENSSVIIIPECKRSHTGKYSITAKNKAGQKTANCRVKVMDVPGPPKDLKVSDITRG 9	9429
ò	84	60	83
g	9430 SCRLSWKMP	SCRLSWKMPDDDGGDRIKGYVIEKRTIDGKAWTKVNPDCGSTTFVVPDLLSEQQYFFRVR 9	9489
ò	84		83
q	9490 AENRFGIGP	AENRFGIGPPVETIQRTTARDPIYPPDPPIKLKIGLITKNTVHLSWKPPKNDGGSPVTHY 9	9549
ò	84		83
QQ	9550 IVECLAWDP	IVECLAWDPTGTKKEAWRQCNKRDVEELQPTVEDLVEGGEYEFRVKAVNAAGVSKPSATV 9	6096
ò	84		83
QQ	9610 GPCDCQRPD	GPCDCQRPDMPPSIDLKEFMEVEEGTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLY \$	6996
ò	84	8	83
qq	9670 DTHVNKLVV	DTHVNKLVVDDTCTLVI PQSRRSDTGLYTITAVNNLGTASKEMRLNVLGRPGPPVGPIKF 9	9729
ò	84	8	83
qq	9730 ESVSADOMT	ESVSADQMTLSWFPPKDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTIPKLLEGHE 9	9789
ò	84		88
ф	9790 YVFRIMAQN	YVFRIMAQNKYGIGEPLDSEPETARNLFSVPGAPDKPTVSSVTRNŠMTVNWEEPEYDGGS 9	9849
ò	89		88
g	9850 PVTGYWLEM	PVTGYWLEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGSDYQFRVYAINAAGVGPA 9	6066
ò	68	8	88
QQ	9910 SLPSDPATA	SLPSDPATARDPIAPPGPPFPKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEGKEE \$	6966
ò	68		88
qq	9970 WEKGKDKEV	WEKGKDKEVRGTKLVVTGLKEGAFYKFRVSAVŅIAGIGEPGEVTDVIEMKDRLVSPDLQL	10029
ò	68		88
g	10030 DASVRDRIV	DASVRDRIVVHAGGVIRIIAYVSGKPPPTVTWNMNERTLPQEATIETTAISSSMVIKNCO :	10089
ò	68		92
Q	10090 RSHQGVYSL	RSHQGVYSLLAKNEAGERKKTIIVDVLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGS	10149
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QQ	10150 PITNYVIEK	PITNYVIEKRESDRRAWTPVTYTVTRQNATVQGLIQGKAYFFRIAAENSIGMGPFVETSE	10209
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3 8	rnsbegskiidimekkevidamvkvnnifiahlekfkvidbifenijeffkvfaenLagls	ò	102
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ò	102		101
g	11350	TAQWNRINKDELIRQCAFRVPGLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILHPP	11409
ò	102		101
g	11410	EVELDVTCRDVITVRVGQTIRILARVKGRPEPDITWTKEGKVLVREKRVDLIQDLPRVEL	11469
ò	102		101
q	11470	QIKEAVRADHGKYIISAKNSSGHAQGSAIVNVLDRPGPCQNLKVTNVTKENCTISWENPL	11529
ò	102		101
g	11530	DNGGSEITNFIVEYRKPNOKGWSIVASDVTKRLIKANLLANNEYYFRVCAENKVGVGPTI	11589
ò	102		101
qq	11590	ETKTP1 LAINPIDR PGEPENLHIADKGKTFVYLKWRRPDYDGGSPNLSYHVERRLKGSDD	11649
ò	102		101
qq	11650	WERVHKGSIKETHYMVDRCVENOIYEFRVQTKNEGGESDWVKTEEVVVKEDLOKPVLDLK	11709
ò	102		101
g	11710	LSGVLTVKAGDTIRLEAGVRGKPFPEVAWTKDKDATDLTRSPRVKIDTRADSSKFSLTKA	11769
ò	102		101
පු	11770	KRSDGGKYVVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSDRCTVCWDPPEDDGGC	11829
ò	102		101
q	11830	EI ONY I LEKCETKRMVASTYSATVLTPGTTVTRLI EGNEY I PRVRAENKI GTGPPTESKP	11889
ò	102		101
a	11890	VIAKTKYDKPGRPDPPEVTKVSKEEMTVVMNPPEYDGGKSITGYPLEKKEKHSTRWVPVN	11949
ò	102		101
q	11950	KSAI PERRMKVQNLLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEPPGPPTNFRVV	12009
ò	102		101
q	12010	DTTKHSITLGWGKPVYDGGAPIIGYVVEMRPKIADASPDEGWKRCNAAAQLVRKEFTVTS	12069
ò	102		101
QQ	12070	LDENOEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEIDLDASMRKLVIVRAGCPIRL	12129
ò	102		101
q	12130	FAIVRGRPAPKVTWRKVGIDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLVNPAGE	12189
ò	102		101
Q	12190	KAVEVNVRVLDTPGPVSDLKVSDVTKTSCHVSWAPPENDGGSQVTHYIVEKREADRKTWS	12249
ò	102		101
q	12250	TVTPEVKKTSFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLASDPLSEPDPPRKLE :	12309
ò	102		101
g	12310	ATEMTKNSATLAWLPPLRDGGAKIDGYIISYREEEQPADRWTEYSVVKDLSLVVTGLKEG	12369
ò	102		101
d	12370	KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKILMPEQITIKAGKKLRIEAHVYGKP 1	12429
ò	102		101

q	12430 HPTC	HPTCKWKKGEDEVVTSSHLAVHKADSSS1L11KDVTRKDSGYYSLTAENSSGTDTQK1KV	12489
ò	102		101
Q	12490 VVMD	VVMDAPGPPQPPFDISDIDADACSLSWHIPLEDGGSNITNYIVEKCDVSRGDWVTALASV	12549
ò	102		101
g	12550 TKTS	TKTSCRVGKLI PGQEYI FRVRAENRFGI SEPLTSPKMVAQFPFGVPSEPKNARVTKVNKD	12609
ò	102		101
QQ	12610 CIFV	CIFVAWDRPDSDGGSP11GYL1ERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEYSFR1	12669
ò	102	•	101
g	12670 YALN	YALNKAGSSPPSKPTEYVTARMPVDPPGKPEVIDVTKSTVSLIWARPKHDGGSKIIGYFV	12729
ò	102		101
q	12730 EACK	EACKL PGDKWVRCNTAPHQI PQEEYTATGLEEKAQYQFRA I ARTAVNI S PPSEPSDPVTI	12789
ò	102		101
g	12790 LAEN	LAENVPPRIDLSVAMKSLLTVKAGTNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAM	12849
ò	102		101
g	12850 QRNL	QRNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLKVLDKPGPPASVKINKMYSDRAM	12909
ò	102		101
q	12910 LSWE	LSWEPPLEDGGSEITNYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEYQFRICAEN	12969
ò	102		101
g	12970 KYGV	KYGVGDPVFTEPAIAKNPYDPPGRCDPPVISNITKDHMTVSWKPPADDGGSPITGYLLEK	13029
ò	102		101
Q	13030 RETC	RETQAVNWTKVNRKPI I ERTLKATGLQEGTEYEFRVTAINKAGPGKPSDASKAAYARDPQ	13089
ò	102		101
g	13090 YPPA	YPPAPPAFPKVYDTTRSSVSLSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPQNLQK	13149
ò	102		101
q	13150 TRFE	TRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPDKHYPKDILIPPEGEHDADLRKTLILR	13209
ò	102		101
g	13210 AGVT	AGVTMRLYVPVKGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCENVNKYDAGKYIL	13269
ò	102		101
g	13270 TLEN	TLENSCGKKEYTIVVKVLDTPGPPINVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKR	13329
ò	102		101
q	13330 DAER	DAERKSWSTVTTECSKTSFRVPNLEEGKSYFFRVFAENEYGIGDPGETRDAVKASQTPGP	13389
ò	102		101
පු	13390 VVDI	VVDLKVRSVSKSSCSIGWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLT	13449
ò	102		101
Q	13450 EGKE	EGKEYTFRVSAENENGEGTPSE1TVVARDDVVAPDLDLKGLPDLCYLAKENSNFRLKIPI	13509
ò	102		101

14649	) IPVLGRPKPTVTWKKGDQILKQTQRVNFETTATSTILNINECVRSDSGPYPLTARNIVGE	14590	Ωp
107		108	ò
14589	) LTEGEEYTFQVMAVNSAGRSAPRESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE	14530	g
107		108	ò
14529	) PPDSLNIMDITKSTVSLAMPKPKHDGGSKITGYVIBAQRKGSDQWTHITTVKGLECVVRN	14470	qq
107		108	ò
14469	) REATRKSYSTATTKCHKCTYKVTGLSEGCEYFFRVMAENEYGIGEPTETTEPVKASEAPS	14410	qq
107		108	ò
14409	) MIIENPAGKKSGFVNVRVLDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITNYIVEK	14350	q
107		108	ò
14349	) VVRAGLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTESFTLLIIPECNRYDTGKFV	14290	QQ
107		108	ò
14289	:    ALRITQFVVPDLQTKEKYNFRISAINDAGVGEPAVIPDVEIVEREMAPDFELDAELRRTL	14230	qq
101	-LYIT	102	ò
14229	) KDAAYPPGPPSNPHVTDTTKKSASLAWGKPHYDGGLEITGYVVEHQKVGDEAWIKDTTGT	14170	q
101	2	102	ò
14169	0 HVERREKKSLRWVRAIKTPVSDLRCKVTGLOEGSTYEFRVSAENRAGIGPPSEASDSVLM	14110	d d
101		102	ò
14109	SAVNHYGKGEPVQSEPVKMVDRFGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSEITGY	14050	g
101	2	102	ò
14049	) EKATLIWIPPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRHVATKLIQGNEYIFRV	13990	g
101	2	102	ò
13989	) QITSTPTSSMLTIKYATRKDAGEYTITATNPFGTKVEHVKVTVLDVPGPPGPVEISNVSA	13930	qq
101		102	ò
13929	) IICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDIRPSDIT	13870	d d
101		102	ò
13869	O GYIVEKRDLPSKSWMKANHUNVPECAFTVTDLVEGGKYEFRIRAKNTAGAISAPSESTET	13810	g
101	2	102	ò
13809	O EFRVMAINLAGVGKPSLPSEPVVALDPIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLT	13750	qq
101	2	102	ò
13749	) VRHDSVSLTWTDPKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDFKVTGLTEGLEY	13690	q
101		102	ò
13689	) ASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPNIVD	13630	qq
101		102	ò
13629	) TISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWVTC	13570	q
101		102	ò
13569	) KGKPAPSVSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGKYTITLKNVAGTKEG	13510	පු

14650	0 VGDVITIQVHDIPGPPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVEMRQTDSTTW 14709	
108		
14710	0 VELATTVIRTTYKATRLTTGLEYQFRVKAQNRYGVGPGITSAWIVANYPFKVPGPPGTPO 14769	
108	107	
14770	O VTAVTKDSMTISWHEPLSDGGSPILGYHVERKERNGILWQTVSKALVPGNIFKSSGLTDG 14829	
108	107	
14830	JAYEFRVIAENWAGKSKPSKPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEYTGGF 14889	
108	8	
14890	O KITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEP 14949	
108	8	
14950	O SDAITCRDDVEAPKIKVDVKFKDTVILKAGEAFRLEADVSGRPPPTMEWSKDGKELEGTA 15009	
108	8	
15010	O KLEIKIADFSTNLVNKDSTRRDSGAYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTE 15069	
108	3 107	
15070	) VTSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTNVASEVQVTKLKVTKLLKGNEYI 15129	
108	3 107	
15130	) FRVMAVNKYGVGEPLESEPVLAVNPYGPDPPKNPEVTTITKDSMVVCWGHPDSDGGSEI 15189	
108	3 107	
15190	) INYIVERRDKAGQRWIKCNKKTLTDLRYKVSGLTEGHEYEFRIMAENAAGISAPSPTSPF 15249	
108	107	
15250	) YKACDTVFKPGPPGNPRVLDTSRSSISIAWNKPIYDGGSEITGYMVEIALPEEDEWQIVT 15309	
108	3 107	
15310	) PPAGLKATSYTITGLTENQEYKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELDADL 15369	
108	3 107	
15370	) RKVVTIRACCTLRLFVPIKGRPDPEVKWARDHGESLDKASIESASSYTLLIVGNVNRFDS 15429	
108	3 107	
15430	) GKYILTVENSSGSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTWDPPLLDGGSKIKNY 15489	
108	107	
15490	) IVEKRESTRKAYSTVATNCHKTSWKVDQLQEGCSYYFRVLAENEYGIGLPAETAESVKAS 15549	
108	107	
15550	) ERPLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIVEMQTKGSDKWATCATVKVTEA 15609	
108	3	
15610	) TITGLIQGEEYSFRVSAQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTVLAGEDLK 15669	
108	3 107	

ò	108		107
đ	15730	GEAIETLNVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGGSSINNYIVEKRDTSTT	15789
ò	108		107
g	15790	TWQIVSATVARTTIKACRLKTGCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPPGT	15849
ò	108		107
qo	15850	PVVTLSSRDSMEVQWNEP1SDGGSRVIGYHLERKERNSILWVKLNKTP1PQTKFKTTGLE	15909
ò	108		107
qq	15910	EGVEYEFRVSAENIVGIGKPSKVSECYVARDPCDPPGRPEAIIVTRNSVTLQWKKPTYDG	15969
ò	108		101
qq	15970	GSKITGYIVEKKELPEGRWMKASFTNIIDTHFEVTGLVEDHRYEFRVIARNAAGVFSEPS	16029
ò	108		101
qq	16030	ESTGAITARDEVDPPRISMDPKYKDTIVVHAGESFKVDADIYGKPIPTIQWIKGDQELSN	16089
ò	108		101
QQ	16090	TARLEIKSTDFATSLSVKDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPPEGPVVI	16149
ò	108		107
a	16150	SGVTAEKCTLAWKPPLQDGGSDIINYIVERRETSRLVWTVVDANVQTLSCKVTKLLEGNE	16209
ò	108		107
q	16210	YTFRIMAVNKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKDSMIVVWERPASDGGS	16269
ò	108		101
q	16270	EILGYVLEKRDKEGIRWTRCHKRLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPPS	16329
ò	108		107
QQ	16330	AYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPIYDGGCEIQGYIVEKCDVNVGEWTM	16389
ò	108	JO	109
đ	16390	CTPPTGINKTNIEVEKLLEKHEYNPRICAINKAGVGEHADVPGPIIVEEKLEAPDIDLDL	16449
ò	110	ZL	111
a	16450		16509
ò	112		111
đ	16510	DSGKYTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITKDSVSITWEPPLLDGGSKIK	16569
ò	112		111
g	.16570	NYIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIK	16629
ò	112		111
đ	16630	VAEVPQPPGKITVDDVTRNSV3LSWTKPEHDGGSKIIQYIVEMQAKHSEKWSECARVKSL	16689
ò	112		111
g	16690	QAVITNLTQGEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDVKPAFSSYSVQVGQD	16749
ò	112		111
g	16750	LKIEVPISGRPKPTITWTKDGLPLKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN	16809
ò	112		111

Q	16810	VVGQKTASIEIVTLDKPDPPKGPVKFDDVSAESITLSWNPPLYTGGCQITNYIVQKRDTT	16869	
ò	112		111	
q	16870	TTVWDVVSATVARTTLKVTKLKTGTEYQFRIFAENRYGQSFALESDPIVAQYPYKEPGPP	16929	
ò	112		111	
qq	16930	GTPFATAISKDSMVIQWHEPVNNGGSPVIGYHLERKERNSILWTKVNKTIIHDTQFKAQN	16989	
ò	112		111	
q	16990	LEEGIEYEFRVYAENIVGVGKASKNSECYVARDPCDPPGTPEPIMVKRNEITLQWTKPVY	17049	
ò	112	•	111	
Q	17050	DGGSMITGYIVEKRDLPDGRWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAGAISK	17109	
ò	112		111	
qq	17110	PSDSTGPITAKDEVELPRISMDPKFRDTIVVNAGETFRLEADVHGKPLPTIEWLRGDKEI	17169	
ò	112	PDGNR 	116	
g	17170	EESÄRCEIKNTDFKALLIVKDAIRIDGGQYILRASNVAGSKSFPVNVKVLDRPGPPEGPV	17229	
ò	117	QVRGVTQLGGQLGG	126	
CC	17230		17289	
ò	127		126	
QQ	17290	NEYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKSLEVTNIAKDSMTVCWNRPDSDG	17349	
ò	127		126	
QΩ	17350	) GSEIIGYIVEKRDRSGIRWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENAAGVGEPSP	17409	
ò	127	ACSP.	130	
g	17410		17469	
ò	131		130	
g	17470	OIVTPQTGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSVPGTVKPEDKLEAPELDL	17529	
ò	131	SML	133	
qq	17530	) DSELRKGIVVRAGGSARIHIPFKGRPMPEITWSREEGEFTDKVQIEKGVNYTQLSIDNCD	17589	
ò	134		133	
q	17590	) RNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQNLAVKEVRKDSAFLVWEPPIIDGGAK	17649	
ò	134		133	
q	17650	) VKNYVIDKRESTRKAYANVSSKCSKTSFKVENLTEGAIYYFRVMAENEFGVGVPVETVDA	17709	
ò	134		133	
g	17710	) VKAAEPPSPPGKVTLTDVSQTSASLMWEKPEHDGGSRVLGYVVEMQPKGTEKWSIVAESK	17769	
ò	134		133	
g	17770	) VCNAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIAKDLTIQPSLKLPFNTYSIQAG	17829 .	
ò	134		133	
g	17830	O EDLKIEIPVIGRPRPNISWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDFGKYTVTA	17889	
ò	134		133	

g	17890	TNSAGTATENLSVIVLEKPGPPVGPVRFDEVSADFVVISWEPPAYTGGCQISNYIVEKRD 1794	949
ò	134	133	m
q	17950	TTTTTWHMVSATVARTTIKITKLKTGTEYQFRIFAENRYGKSAPLDSKAVIVQYPFKEPG 18009	600
ò	134	133	м
q	18010	PPGTPFVTSISKDQMLVQWHEPVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIODTKFKT 1806	690
ò	134	133	m
QQ	18070	TGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARDPCDPPGRPEAIVITRNNVTLKWKKP 1812	129
ò	134	133	е
qq	18130	AYDGGSKITGYIVEKKDLPDGRWMKASFTNVLETEFTVSGLVEDQRYEFRVIARNAAGNF 1818	189
ò	134	133	m
QQ	18190	SEPSDSSGAITARDEIDAPNASLDPKYKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGK 1824	249
ò	134	133	м
QQ	18250	ELEETAARMEIKSTIQKTTLVVVKDCIRTDGGQYILKLSNVGGTKSIPITVKVLDRPGSPE 1836	309
ò	134	133	е.
QQ	18310	GPLKVTGVTAEKCYLAMNPPLQDGGANISHYIIEKRETSRLSWTQVSTEVQALNYKVTKL 1836	369
ò	134	133	m
g	18370	LPGNEYIFRVMAVNKYGIGEPLESGPVTACNPYKPPGPPSTPEVSAITKDSMVVTWARPV 1842	429
ò	134	133	<b>с</b>
q	18430	DDGGTEIEGYILEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHSYEFRVAAENAAGVGE 1848	489
ò	134	133	m
q	18490	PSEPSVFYRACDALYPPGPPSNPKVTDTSRSSVSLAWSKPIYDGGAPVKGYVVEVKEAAA 1854	549
ò	134	133	<b>m</b>
q	18550	DEWTTCTPPTGLQGKQFTVTKLKENTEYNFRICAINSEGVGEPATLPGSVVAQERIEPPE 1860	609
ò	134	133	<b>.</b>
Q	18610	IELDADLRKVVVLRASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEVTSSFTMLVID 1866	699
ò	134	133	m
qq	18670	NVTRFDSGRYNLTLENNSGSKTAFVNVRVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDG 187	729
ò	134	133	eņ.
Q	18730	GAKITNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCSYYFRVLASNEYGIGLPAET 1878	189
ò	134	133	m
qq	18790	TEPVKVSEPPLPPGRVTLVDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEKWSTCT 1884	849
ò	134	133	<u>m</u>
qq	18850	QVKTLEATISGLTAGEEYVFRVAAVNEKGRSDPRQLGVPVIARDIEIKPSVELPFHTFNV	18909
ò	134	133	m
Q	18910	KAREQLKIDVPFKGRPQATVNWRKDGGTLKETTRVNVSSSKTVTSLSIKEASKEDVGTYE 1896	6961
ò	134	133	en.
g	18970	LCVSNSAGSITVPITIIVLDRPGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIVEK 1902	029

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a	b 19090	) PGPPGTPKVVHATKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSKANKILIADTQV 19149	ò	134 -
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qa	b 19270	SVSEPSESTGPIIVKDDVEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPVISWAKD 19129	3 8	
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g	b 19330	GIEIEERARTEIISTDNHTLLTVKDCIRRDTGQYVLTLKNVAGTRSVAVNCKVLDKPGPP 19389	an (	20410
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ò	у 134		o Q	20650 G
đ	b 19570	LPSETSPLIRAEDPVFLPSPPSKPKIVDSGKTTITIAWVKPLFDGGAPITGYTVEYKKSD 19629	2	
ò	у 134	133	i d	
අ	b 19630	DIDWKTSIQSLRGTEYTISGLTTGAEYVFRVKSVNKVGASDPSDSSDPQIAKEREEEPLF 19689	an d	01/07
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· £	19690	DIDSEMBRITIVKAGASETWTVPERGRPVDNVIMSKPOTOLISTRANDGRTGSTGSTTSLTIEN 19749	අ	20770 E
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a †	4	IVRAGSNLKVDIPISGKFLFKVILSKUGVFLKAIMKFNIELIAENLIINLKESVIADAGK	ò	138
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Ω	Db 20050	) YEITAANSSGTTKAFINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYDGGSQVTNYI 20109	ò	138

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ପୁ	20170	YTTPGPPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEMKDRNSILWQKANKLVIRT	20229
ò	134		133
qq	20230	THFKVTTISAGLIYEFRVYAENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKNSVSL	20289
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qq	20290	SWQQPAFDGGSKITGYIVERRDLPDGRWTKASFTNVTETQFTISGLTQNSQYEFRVFARN	20349
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Ωp	20350	AVGSISNPSEVVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLRAGISGKPAPTIEW	20409
ò	134		133
QQ	20410	YKDDKELQTNALVCVENTTDLASILIKDADRLNSGCYELKLRNAMASASATIRVQILDKP	20469
ò	134	LITD	137
QC	20470	GPPGGPIEFKTVTAEKITLLWRPPADDGGAKITHYIVEKRETSRVVWSMVSEHLEECIIT	20529
δ	138		137
qu	20530	TTKI I KGNEYI FRVRAVNKYGI GEPLESDSVVAKNAFVT PGPPGI PEVTKI TKNSMTVVM	20589
ò	138		137
qq	20590	SRPIADGGSDISGYFLEKRDKKSLGWFKVLKETIRDTRQKVTGLTENSDYQYRVCAVNAA	20649
ò	138		137
q	20650	GQGPFSEPSEFYKAADPIDPPGPPAKIRIADSTKSSITLGWSKPVYDGGSAVTGYVVEIR	20709
ò	138		137
q	20710	QGEEEEWTTVSTKGEVRTTEYVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAKDIL	20769
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ò	138		137
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ò	138		137
q	20890	DPPLIDGGSPIINYVIEKRDATKRTWSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENEIG	20949
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ò	138		137
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Db 21790	990 GYIIEMCKTDLGDWHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGAGKGDSCEVTGTI 21849	
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Db 21850	350 KAVDRLTAPELDIDANFKQTHVVRAGASIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHT 21909	
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Db 22030	310 EYGVGEPYEMPEPIVATEQPAPPRRLDVVDTSKSSAVLAWLKPDHDGGSRITGYLLEMRQ 22089	
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Db 22090	)90 KGSDLWVEAGHTKOLTFTVERLVEKTEYEFRVKAKNDAGYSEPREAFSSVIIKEPQIEPT 22149	
0,	138 137	
Db 22150	ISO ADLIGITNQLITCKAGSPPTIDVPISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLT 22209	
o,	138 137	
Db 22210	110 VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGPVTGPIEVSSVSAESCVLSWGEPK 22269	

23409	50 TELTISMEDDEL DGG DI SGYVVEORDAHR PGWI PVSESVTRSTFKFTRL TEGNEYVPRV	2335	ć
141	21	14	ò
23349	 30 VETHTKVAKLTIRETTIRDTGEYTLELKNVTGTTSETIKVIILDKPGPPTGPIKIDEIDA	2329	g
141	98	13	ò
23289	30 VTVQDLRVLPTIDLSTMPQKTIHVPAGRPVELVIPIAGRPPPAASWFFAGSKLRESERVT	2323	g
137	88	13	ò
23229	70 TGYVLEACKAGTERWMKVVTLKPTVLEHTVTSLNEGEQYLFRIRAQNEKGVSEPRETVTA	2317	g
137	88	13	ò
23169	10 HYFRVLPENIYGIGEPCETSDAVLVSEVPLVPAKLEVVDVTKSTVTLAWEKPLYDGGSRL	2311	DP
137	81	13	ò
23109	O KEVSRDSVTITWEIPTIDGGAPINNYIVEKREAAMRAFKTVTTKCSKTLYRISGLVEGTM	23050	g
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23049	00 LASRAIIDTTESYSLLIVDKVNRYDAGKYTIEAENQSGKKSATVLVKVYDTPGPCPSVKV	2299	a
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22989	30 EYSESIAEIEPVERIEIPDLELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQGID	2293	qq
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22569	10 SEGDTYEFRVLAKNAAGVISKGSESTGPVTCRDEYAPPKAELDARLHGDLVTIRAGSDLV	22510	g
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137	88	13	ò
22449	30 WVKENKVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASEASRPIMAQNPVDAPGRPE	2239	g
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22389	10 LESAPIIAEHPFVPPSAPTRPEVYHVSANAMSIRWEEPYHDGGSKIIGYWVEKKERNTIL	2233	g
137	81	13	ò
22329	10 DGGGTEITNYIVEKRESGTTAWQLVNSSVKRTQIKVTHLTKYMEYSFRVSSENRFGVSKP	2227	g

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g	23410	AATNRFGIGSYLQSEVIECRSSIRIPGPPETLQIFDVSRDGMTLTWYPPEDDGGSOVTGY 23469	qo	2449
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ò	142	141		2473
a	23650	FVRQGGVIRLTIPIKGKPFPICKWTKEGQDISKRAMIATSETHTELVIKEADRGDSGTYD 23709	2 6	
ò	142	141	δ i	FT
Q	23710	LVLENKCGKKAVYIKVRVIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADILGYILE 23769	an d	2479
ò	142	141	ò	14
d	23770	RREVPKAAWYIIDSRVRGTSLVVKGLKENVEYHFRVSAENQFGISKPLKSEEPVTPKTPL 23829	ପ୍ର	2485
ò	142	141	ò	14
ОP	23830	NPPEPPSNPPEVLDVTKSSVSLSWSRPKDDGGSRVTGYYIERKETSTDKWVRHNKTQITT 23889	ପ୍	2491
ò	142	141	ò	14
g	23890	TMYTVTGLVPDAEYQFRIIAQNDVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKDS 23949	qa	2497
ò	142		<i>\doldo</i>	14
a	23950	VTLQWEKPECDGGKEILGYWVEYRQSGDSAWKKSNKERIKDKQFTIGGLLEATEYEFRVF	qq	2503
ò	142		ò	14
С	24010	AENETGLSRPRRTAMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQIVGRPLPDIKW 24069	qa ·	2509
ò	142	141	δ	14
q	24070	YRFGKELIQSRXYKMSSDGRTHTLTVMTEEQEDEGVYTCIATNEVGEVETSSKLLLQATP 24129	ପ୍ର	2515
ò	142	141	ò	14
Q	24130	OFHPGYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQKLLQNSENITIENTEHYTHL 24189	QQ —	2521
ò	142	141	RES	RESULT 1
Q	24190	VMKNVQRKTHAGKYKVQLSNVFGTVDAILDVEIQDKPDKPTGPIVIEALLKNSAVISWKP 24249	- SO	equence
ò	142	141	a. ()	SENERA
С	24250	PADDGGSWITNYVVEKCEAKEGAEWQLVSSAISVTTCRIVNLTENAGYYFRVSAQNTFGI 24309		APPLI
ò	142	141		TITLE
q	24310	SDPLEVSSVVIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDGGAKIRNYYLEKREK 24369		CURRE
ò	142	141		PRIOR
g	24370	KONKWISVTTEEIRETVFSVKNLIEGLEYEFRVKCENLGGESEWSEISEPITPKSDVPIQ 24429	•• ••	NUMBER
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අධ	24430	APHFKEELRNLNVRYOSNATLVCKVTGHPKPIVKWYRQGKEIIADGLKYRIQEFKGGYHQ 24489		TYPE

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90 LIIASVTDDDATVYQVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAVHALRGEVVS 24549
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Sequence 7, Application US/09918171A
Patent No. US20020110894A1
GENERAL INFORMATION:
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APPLICANT: NEURINON NUMBER: US/09/918,171A
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ORGANISM: Homo sapiens ADAMTS-7
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GNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVMPT 1649
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                                               690 VNNGGAAQGMTTPDAQAQEAVLREAHERAGTAPADVRYVELHGTGTPVGDPIEAAALGAA 749
                                                                                                                                                                                             ELNIRVNTEYLPWEPEHDGQRMVVGVSSFGMGGTNAHVVLEEAPGGCRGASVVESTVGGS 869
                                                                                                                                                                                                                                                                   870 AVGGGVVPWVVSAKSAAALDAQIERLAAFASRDRTDGVDAGAVDAGAVDAGAVARVLAGG 929
                                                                                                                                                                                                                                                                                                                                       930 RAQFEHRAVVVGSGPDDLAAALAAPEGLVRGVASGVGRVAFVFPGOGTQWAGMGAELLDS 989
                                                                                                                     LGTGRPAGQPLLVGSVKTNIGHLEGAAGIAGLIKAVLAVRGRALPASLNYETPNPAIPFE
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                                                                                                                                                                                                                                                                                                                                                233 LHQRSVSKEKWCETLVVADAKMVEYHGQPQVESYVLTIMNMVAGLFHDPSIGNPIHITIV 292
                                                                                                                                                                                                                                                                                                                                                                                                 KMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                          293 RLVLLEDEEEDLKITHHADNTLKSFCKWQKSINMKGDAHPLHHDTAILLTRKDL-CAAMN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 AAGGQAVTDVPADRWNAGDFYDPDRSAPGRSNSRWGGFIEDVDRFDAAFFGISPREAAEM 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 DPQQRLALELGWEALERAGIDPSSLTGTRTGVFAGAIWDDYATLKHRQGGAAITPHTVTG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570 LHRGIIANRLSYTLGLRGPSMVVDSGQSSSLVAVHLACESLRRGESELALAGGVSLNLVP 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 DSIIGASKFGGLSPDGRAYTFDARANGYVRGEGGGFVVLKRLSRAVADGDPVLAVIRGSA 689
                                                                                                                                           53 AGGSFLSYELWPRALRKRDVSVRRDAPAFYELQYRGRELRFNLTANQHLLAPGFVSETRR 112
                                                                                                                                                                                                                 13 RGGLGRAHIRAHTPACHLLGEVQDPELEGGLAAISACDGLKGVFQLSNEDYFIEPLDSAP 172
                                                                                                                                                                                                                                                                                       173 ARPGHAOPHVVYKROAPERLAORGDSSAPSTCGVOVYPELESRRERWEORQOWRRPRLRR 232
                                                                       Gaps
                                                                                                                                                                               16 .....VFQAHQED---- 25
                                  30.7%; Score 237; DB 10; Length 997;
18.2%; Pred. No. 0.011;
ive 24; Mismatches 62; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Score 235; DB 9; Length 11877; Pred. No. 4.1; 21; Mismatches 36; Indels 8329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/860,846

CORRENT FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R--QVRGVTQLGGACSPTWSCLITEDTGFDLGVTI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.09-860-846-6
Sequence 6, Application US/09860846
Patent No. US20020164742A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Streptomyces venezuelae
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llarity 1.1%; E
Conservative 21
                                  Query Match
Best Local Similarity 18.2
Matches 61; Conservative
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US-09-918-171A-7
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a &	1770 TYGQGRDDEQPLF	TYGQGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDOIDW	1829
ò			
	43	-būsda	47
g	1830 SAGAVELLTEAVE	SAGAVELLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPVVVEGASVVEPSVGG	1889
ò	48	AQF	20
g	1890 SAVGGGVTPWVVS	   SAVGGGVTPWVVSAKSAAALDAQIERLAAFASRDRTDDADAGAVDAGAVAHVLADGRAQF	1949
ò	51		50
g	1950 EHRAVALGAGADD	EHRAVALGAGADDLVQALADPDGLIRGTASGVGRVAFVFPGQGTQWAGMGAELLDSSAVF	2009
ò	51	RVHLV	55
g	2010 AAAMAECEAALSP	AAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTP	2069
ઠે	26		55
q	2070 QAVVGHSQGEIAA	QAVVGHSQGEIAAAYVAGALPLDDAARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERL	2129
ò	96		55
g	2130 SDFDGLSVAAVNG	SDFDGLSVAAVNGPTATVVSGDPVQ1EELAQACKADGFRAR11PVDYASHSRQVE11ESE	2189
ò	26		55
g	2190 LAQVLAGLSPQAP	LAQVLAGLSPQAPRVPFFSTLEGTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFT	2249
ઠે	56		55
g	2250 HFVEVSAHPVLTM	HFVEVSAHPVLTMTLPETVTGLGTLRREQGGQERLVTSLAEAWVNGLPVAWTSLLPATAS	2309
ò	26		. 55
g	2310 RPGLPTYAFQAER	RPGLPTYAFQAERYWLENTPAALATGDDWRYRIDWKRLPAAEGSERTGLSGRWLAVTPED	2369
ò	26 38		55
g	2370 HSAQAAAVLTALV	HSAQAAAVLTALVDAGAKVEYLTAGADDDREALAARLTALTTGDGFTGVVSLLDGLVPQV	2429
ò	26	BdalilyMy	64
g	2430 AWVQALGDAGIKA	AWVQALGDAGIKAPLWSVTQGAVSVGRLDTPADPDRAMLWGLGRVVALEHPERWAGLVDL	2489
ò			64
g	2490 PAQPDAAALAHLV	PAQPDAAALAHLVTALSGATGEDQIAIRTTGLHARRLARAPLHGRRPTRDWQPHGTVLIT	. 548
ò		GAPNITANLTSS	92
g G	2550 GGTGALGSHAARWN	GGTGALGSHAARWMAHHGAEHLLLVSRSGEQAPGATQLTAELTASGARVTIAACDVADPH	. 5092
ò	44		76
qq	2610 AMRTLLDAIPAETE	AMRTLLDA I PAETPLTAVVHTAGALDDG I VDTLTAEQVRRAHRAKAVGASVLDELTRDLD	2669
ò	77		91
셤	2670 LDAFVLFSSVSSTI	LDAFVLFSSVSSTLGI PGQGNYAPHNAYLDALAARRRATGRSAVSVAWGFWDGGGMAAGD	2729
ò	44	LLSVCGWSQTI	87
g	2730 GVAERLRNHGVPGN	GVAERLRNHGVPGMDPELALAALESALGRDETAITVADIDWDRFYLAYSSGRPQPLVEEL :	2789
ò	88		87
g G	2790 PEVRRIIDARDSAT	PEVRRIIDARDSATSGQGGSSAQGANPLAERLAAAAPGERTEILLGLVRAQAAAVLRMRS :	2849
ò	88		87

g	2850 PEDVAADRAFKDIGFDSLAGVELRNRLTRATGLQLPATLVFDHPTPLALVSLLRSEFLGD 2909	
ò	16 NPED 91	
Q	2910 EETADARRSAALPATVGAGAGAGAGTDADDPIAIVAMSCRYPGDIRSPEDLWRMLSEGG 296	69
ò	, 92 DTDP 95	
Q	2970 EGITPFFTDRGWDLDGLYDADPDALGRAYVREGGFLHDAAEFDAEFFGVSPREALAMDPQ 3029	59
ò	56	
QQ	3030 QRMLLTTSWEAFERAGIEPASLRGSSTGVFIGLSYQDYAARVPNAPRGVEGYLLTGSTPS 308	68
ò	56 96 .	
Q	3090 VASGRIAYTFGLEGPATTVDTACSSSLTALHLAVRALRSGECTWALAGGVAMMATPHMFV 314	0.
ò	56	
셤	3150 EFSRQRALAPDGRSKAFSADADGFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQD 320	60
ò	56 96	
Q	3210 GASNGLTAPNGPSQORVIRQALADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKE 326	6.5
ò	96	
qq	3270 RPAERPLAIGSVKSNIGHTQAAAGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGL 332	6
ò	96	
q	3330 ALVTEPIDWPAGTGPRRAAVSSFGISGTNAHVVLEQAPDAAGEVLGADEVPEVSETVAMA 3389	6
ò	56 96	
qq	3390 GTAGTSEVAEGSEASEAPAAPGSREASLPGHLPWVLSAKDEQSLRGQAAALHAWLSEPAA 3449	
ò	56 96	
qq	3450 DLSDADGPARLRDVGYTLATSRTAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTA 3509	9
ò	96 100	_
QQ	3510 RDGTTAFLFTGQGSQRPGAGRELYDRHPVFARALDEICAHLDGHLELPLLDVMFAAEGSA 3569	
ò	101 100	
q	3570 EAALLDETRYTQCALFALEVALFRLVESWGMRPAALLGHSVGEIAAAHVAGWFSLADAAR 3629	6
ò	101 100	
q	3630 LVAARGRLMQELPAGGAMLAVQAAEDEIRVWLETEERYAGRLDVAAVNGPEAAVLSGDAD 3689	6
ò	101 100	_
Op	3690 AAREAEAYWSGLGRRTRALRVSHAFHSAHMDGMLDGFRAVLETVEFRRPSLTVVSNVTGL 3749	σ
ò	101 100	-
qq	3750 AAGPDDLCDPEYWVRHVRGTVRFLDGVRVLRDLGVRTCLELGPDGVLTAMAADGLADTPA 3809	6
ò	101 100	
g	3810 DSAAGSPYGSPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWH 3869	6
ò	101 100	
අ	3870 AWFAGSGAHRVDLPTYSFRRDRYWLDAPAADTAVDTAGLGLGTADHPLLGAVVSLPDRDG 3929	6
è	101	

AESAGLRDVRELTLLEPLVLPE 3989	100	PAGTAWSCHATGLLATDRPELP 4049		SLNAVWRYEGEVFADIALPATT 4109	100	/DEPELVRVPFHWSGVTVHAAG 4169	100	/TADQAAASRVGGLMHRVAWRP 4229	100	SVGLYPDLAALSQDVAAGAPAP 4289	VLYITR 106	.  :  :   .AGTRLLLVTRGAVRDPEGSGA. 4349	106	KRTLPSVLSDAGLRDEPQLALH 4409	106	3GLVARHVVGEWGVRRLLLVSR 4469	106	LDAIPAEHPLTAVVHTAGVLSD 4529	106	FVMFSSAAAVFGGAGQGAYAAA 4589	106	ADLRRMSRAGIGGISDAEGIAL 4649	106	RDVVGARTVRARPSAASASTTA 4709	106	FVVGEVAEVLGHARGHRIDAER 4769	FDLELPDG 114	AALASHLDAELPRGASDQDGAG 4829	114	DAPGSEEVLEHLRSLRSMVTGE 4889	114	PDFMNASAEELFGLLDQDPSTD 4949	114	AIVGMACRLPGGVASPEDLWRL 5009	114	
LLLTGRLSLRTHPWLADHAVLGSVLLPGAAMVELAAHAAESAGLRDVRELTLLEPLVL		HGGVELRVTVGAPAGEPGGESAGDGARPVSLHSRLADAPAGTAWSCHATGLLATDRPELP		VAPDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATT		NATAPATANGGGSAAAAPYGIHPALLDASLHAIAVGGLVDEPELVRVPFHWSGVTVHAAG		AAAARVRLASAGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVGGLMHRVAWRP		YALASSGEQDPHATSYGPTAVLGKDELKVAAALESAGVEVGLYPDLAALSQDVAAGAPAP		RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAGTRLLLVTRGAVRDPEGSGA		DDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSYRTLPSVLSDAGLRDEPQLALH		DGTIRLARLASVRPETGTAAPALAPEGTVLLTGGTGGLGGLVARHVVGEWGVRRLLLVSR		RGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAIPAEHPLTAVVHTAGVLSD		GTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGGAGQGAYAAA		NATLDALAWRRRAAGLPALSLGWGLWAETSGMTGELGQADLRRMSRAGIGGISDAEGIAL		LDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGI PALFRDVVGARTVRARPSAASASTTA		GTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHARGHRIDAER		GFLDLGFDSLTAVELRNRLNSAGGLALPATLVFDHPSPAALASHLDAELPRGASDQDGAG		NRNGNENGTTASRSTAETDALLAQLTRLEGALVLTGLSDAPGSEEVLEHLRSLRSMVTGE		TGTGTASGAPDGAGSGAEDRPWAAGDGAGGSEDGAGVPDFMNASAEELFGLLDQDPSTD		MSTVNEEKYLDYLRRATADLHEARGRLRELEAKAGEPVAIVGMACRLPGGVASPEDLWRL		
3930	101	3990	101	4050	101	4110	101	4170	101	4230	101	4290	107	4350	107	4410	107	4470	107	4530	101	4590	107	4650	101	4710	101	4770	115	4830	115	4890	115	4950	115	
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_	5070	AMDPQQRLLLEASWEAFEHAGIPAATARGTSVGVFTGVMYHDYATRLTDVPEGIEGYLGT	5128
_	115		114
0	5130	GNSGSVASGRVAYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGEVDMALAGGVTVMST	5185
_	115	- NRQ	120
0	5190	   PSTFVEFSRQRGLAPDGRSKSFSSTADGTSWSEGVGVLLVERLSDARRKGHRILAVVRGT	524
_	121		120
0	5250	AVNQDGASSGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQAVIA	530
_	121		120
0	5310	TYGOGRDGEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGVLPKTLHVEKPTDQVDW	5365
_	121		120
0	5370	SAGAVELLTEAMDWPDKGDGGLRRAAVSSFGVSGTNAHVVLEEAPAAEETPASEATPAVE	542
_	121		120
0	5430	PSVGAGLVPWLVSAKTPAALDAQIGRLAAFASQGRTDAADPGAVARVLAGGRAEFEHRAV	5485
`	121		120
0	5490	VLGTGQDDFAQALTAPEGLIRGTPSDVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMA	5545
ν.	121		120
0	5550	<b>ECESALSRYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVG</b>	2605
`	121		120
0	5610	HSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALSEEATRQRIENLHG	5995
۶.	121		120
Ω	5670	LSIAAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPVDYASHSAHVETIESELAEVL	572
>-	121		120
Ω	5730	AGLSPRTPEVPFFSTLEGAWITEPVLDGTYWYRNLRHRVGFAPAVETLATDEGFTHFIEV	578
٠.	121	VITQLG	125
Ω	5790	SAHPVLTMTLPETVTGLGTLRREQGGOERLVTSLAEAWTNGLTIDWAPVLPTATGHHPEL	584
>-	126		125
۵	5850	PTYAFQRRHYWLHDSPAVQGSVQDSWRYRIDWKRLAVADASERAGLSGRWLVVVPEDRSA	290
>-	126		125
Ω	5910	EAAPVLAALSGAGADPVQLDVSPLGDRQRLAATLGEALAAAGGAVDGVLSLLAWDESAHP	296
>-	126		125
۵	5970	GHPAPFTRGTGATLTLVQALEDAGVAAPLWCVTHGAVSVGRADHVTSPAQAMVWGMGRVA	602
>-	126	9-	126
Ω	6030	ALEHPERWGGLIDLPSDADRAALDRMTTVLAGGTGEDQVAVRASGLLARRLVRASLPAHG	609
>	127	ACSPTW	132
	000	TERMINATION VICER PARABBARA PROGRESSION TO SECURITE SEGREGIS CAREDS C	614

ò	133 132	_	
q	6150 LAGLVAELADLGATATVVTCDLTDAEAAARLLAGVSDAHPLSAVLHLPPTVDSEPLAATD 6209	qa	7230 SPQTPQVPFFSTLEGAW
ò	133 132	ò	133
đ	6210 ADALARVVTAKATAALHLDRLLREAAAAGGRPPVLVLFSSVAAIWGGAGQGAYAAGTAFL 6269	qa	7290 PVLTMALPETVTGLGTL
ò	133 132	ò	133
g	6270 DALAGQHRADGPTVTSVAWSPWEGSRVTEGATGERLRRLGLRPLAPATALTALDTALGHG 6329	අධ	7350 FQTERYWPQPDLSAAGD
ò	133 132	ò	138
g	6330 DTAVTIADVDWSSFAPGFTTARPGTLLADLPEARRALDEQQSTTAADDTVLSRELGALTG 6389	qa	7410 AVAGTVLLPGTAFVELA
ò	133 132	ò	138
qq	6390 AEQQRRMQELVREHLAVVLNHPSPEAVDTGRAFRDLGFDSLTAVELRNRLKNATGLALPA 6449	අු	7470 RTFGLYAHPEDAPGEAE
ò	133 132	ò	138
q	6450 TLVFDYPTPRTLAEFLLAEILGEQAGAGEQLPVDGGVDDEPVAIVGMACRLPGGVASPED 6509	ය	7530 ANGYGYGPLFQGVRGVW
ò	133 132	ò	138
 qq	6510 LWRLVAGGEDAISGFPQDRGWDVEGLYDPDPBASGRTYCRAGGFLDEAGEFDADFFGISP 6569	ପ୍ର	7590 VRRGHAAAVRLERDLLY.
ò	133 132	ò	138
q	6570 REALAMDPOORLLLETSWEAVEDAGIDPTSLQGQQVGVFAGTNGPHYEPLLRNTAEDLEG 6629	q <sub>0</sub>	7650 PAQLAAFSDPTLDALHL
ò	133 132	ò	138
q	6630 YVGTGNAASIMSGRVSYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGECGLALAGGVT 6689	qa	7710 TDLVEAVDRGETPAPAT
ò		ò	138
q	6690 VMSTPTTFVEFSRQRGLAEDGRSKAFAASADGFGPAEGVGMLLVERLSDARRNGHRVLAV 6749	qa	7770 VTRDAVAARSGDGLRST
ò		ò	138
Ор	VRGSAVNQDGASNGLTAPNGPSQQRVIRRALADARLTTADVDVVEAHGTGTRLGDPIEAQ	qa	7830 GDATVGGTSGDAALGSAI
ò	133	ò	138
q	6810 ALIATYGGGRDTEQPLRLGSLKSNIGHTQAAAGVSGIIKMVQAMRHGVLPKTLHVDRPSD 6869	qa	7890 ALPLPAAPALWRLEPGTI
ò		δ	138
q	6870 QIDWSAGTVELLTEAMDWPRKQEGGLRRAAVSSFGISGTNAHIVLEEAPVDEDAPADEPS 6929	අු	7950 ALGMYPDPALMGTEGAGN
ò	133 132	ò	138
q	6930 VGGVVPWLVSAKTPAALDAQIGRLAAFASQGRTDAADPGAVARVLAGGRAQFEHRAVALG 6989	සු	8010 WTFAQGASVPVVFLTAVY
ò	133 132	ò	
q	6990 TGQDDLAAALAAPEGLVRGVASGVGRVAFVPPGQGTQWAGWGAELLDVSKEFAAAMAECE 7049	ପ୍	8070 SHGKWDALRALGLDDAHI
ò	133 132	ò	138
đ	7050 AALAPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVGHSQ 7109	q	8130 GGRFVEMGKTDVRDAERV
ò	133 132	ò	138
qq	7110 GEIAAAYVAGALSLDDAARVVTLRSKSIGAHLAGQGGMLSLALSEAAVVERLAGFDGLSV 7169	셤	8190 VITWDVRRARDAFRHVSC
ò	133 132	ò	138
đ	7170 AAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPVDYASHSAHVETIESELADVLAGL 7229	අධ	8250 GVRRLLLVSRRGTDAPGA
ò	133 132	ò	138

LRRDNGGQHRLTTSLAEAWANGLTVDWASLLPTTTHPDLPTYA 7349 AFRAGDQVGCDLVEELTLDAPLVLPRRGAVRVQLSVGASDESGR 7469 WITEPALDGGYWYRNLRHRVGFAPAVETLATDEGFTHFVEVSAH 7289 DITSAGLGAAEHPLLGAAVALADSDGCLLTGSLSLRTHPWLADH 7409 EWTRHATGVLAARADRTAPVADPEAWPPPGAEPVDVDGLYERFA 7529 WRRGDEVFADVALPAEVAGAEGARFGLHPALLDAAVQAAGAGRG 7589 YAVGATALRVRLAPAGPDTVSVSAADSSGQPVFAADSLTVLPVD 7649 LLEWTAWDGAAQALPGAVVLGGDADGLAAALRAGGTEVLSFPDL 7709 TVLVACPAAGPDGPEHVREALHGSLALMQAWLADERFTDGRLVL 7769 TGQAAVWGLGRSAQTESPGRFVLLDLAGEARTAGDATAGDGLTT 7829 ALATALGSGEPQLALRDGALLVPRLARAAPAAADGLAAADGLA 7889 SVVTATGPGVTHLAPGDRVMGLLSGAYAPVVVADARTVARMPEG 8009 VYALRDLADVKPGERLLVHSAAGGVGMAAVQLARHWGVEVHGTA 8069 HIASSRTLDFESAFRAASGGAGMDVVLNSLAREFVDASLRLLGP 8129 137 TDGSLESLTAAPGDAETLAPEPLGPGQVRIAIRATGLNFRDVLI 7949 RANDANDENGYRAFOLGEAGPERIGEMLAEVIALFEDGVLRHLP 8189 SQARHTGKVVLTMPSGLDPEGTVLLTGGTGALGGIVARHVVGEW 8249 137 137 3AGELVHELEALGADVSVAACDVADREALTAVLDSIPAEHPLTA 8309 137 137 137

1290 SATGHHSDLPTYAFQTERHWLGEIEALAPAGEPAVQPAVLRTEAAEPAELDRDEQLRVIL 1349 1470 VAGGGDAISEFPQDRGWDVEGLYHPDPEHPGTSYVRQGGFIENVAGFDAAFFGISPREAL 1529 990 SAVFAAAMAECEAALSPYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHH 1049 1050 GVTPQAVVGHSQGEIAAAYVAGALSLDDAARVVTLRSKSIAAHLAGKGGMLSLALSEDAV 1109 1230 EGFTHFVEVSAHPVLTMALPGTVTGLATLRRDNGGQDRLVASLAEAWANGLAVDWSPLLP 1289 1350 DKVRAQTAQVLGYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAFGVRMAPSMIFDFPT 1409 1410 PEALAEQLLLVVHGEAAANPAGAEPAPVAAAGAVDEPVAIVGMACRLPGGVASPEDLWRL 1469 1530 AMDPQQRLLLETSWEAVEDAGIDPTSLRGRQVGVFTGAMTHEYGPSLRDGGEGLDGYLLT 1589 1110 LERLAGFDGLSVAAVNGPTATVVSGDPVQIEELARACEADGVRARVIPVDYASHSRQVEI 1169 1170 IESELAEVLAGLSPQAPRVPFFSTLEGAWITEPVLDGGYWYRNLRHRVGFAPAVETLATD 1229 510 DPQQRLALELGWEALERAGIDPSSLTGTRTGVFAGAIWDDYATLKHRQGGAAITPHTVTG 569 570 LHRGIIANRLSYTLGLRGPSMVVDSGQSSSLVAVHLACESLRRGESELALAGGVSLNLVP 629 630 DSIIGASKFGGLSPDGRAYTFDARANGYVRGEGGGFVVLKRLSRAVADGDPVLAVIRGSA 689 690 VNNGGAAQGMTTPDAQAQEAVLREAHERAGTAPADVRYVELHGTGTPVGDPIEAAALGAA 749 750 LGTGRPAGQPLLVGSVKTNİGHLEGAAGIAGLIKAVLAVRGRALPASLNYETPNPAIPFE 809 310 ELNIRVNTEYLPWEPEHDGQRMVGVSSFGMGGTNAHVVLEEAPGGCRGASVVESTVGGS 869 870 AVGGGVVPWVVSAKSAAALDAQIERLAAFASRDRTDGVDAGAVDAGAVDAGAVARVLAGG 929 930 RAQFEHRAVVVGSGPDDLAAALAAPEGLVRGVASGVGRVAFVFPGQGTQWAGMGAELLDS 989 ----- 28 -----LLVAVGPD----- 17 18 --VFQA-----22 ----HQED-----TER---5 5 -----..... 5 10 -----10 10 22 유 g g a q g ò a ò g ò g g g ઠે a ò a a 셤 g ò ŝ ò õ ò 8 8 ò ò ò ò

ò	33 N 42		2670 T.DAFULFSSVSSTITEDGOONYA
යි <b>.</b>	1590 GNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVMPT	· &	77
ò		g	2730 GVAERLRNHGVPGMDPELALAALI
음 (	1650 PGMFVEFSRQRGLAGDGRSKAFAASADGTSWSEGVGVLLVERLSDARRNGHQVLAVVRGS	ò	88
ò 1	1310 NINDARGAGE BARANCACATA SANA MACAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANAMATANA	đ	2790 PEVRRIIDARDSATSGQGGSSAQO
ž	1/10 ALNQUGASNGLIAFNGFSQQRVIRRALADARLIISDVDVVEAHGIGIRLGDVIEAQALIA 1/09	ò	88
ò	43 42	. 6	2850 PEDVAADBAFKDIGFDSLAGVEL
a a	1770 TYGOGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDQIDW 1829	} &	
ò	43DDSLG- 47	<b>5</b>	
qq	) 1830 SAGAVELLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPVVVEGASVVEPSVGG 1889	9 (	EETADARRSAALPATVGA
ò	48AQF 50	ò	05
qq		<u>ප</u>	2970 EGITPFPTDRGWDLDGLYDADPD
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i é	TO CONTRACT THE STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTRACT TO STANDARD CONTR	QQ —	3030 QRMLLTTSWEAFERAGIEPASLR0
i d	1950 BRAYALGAGADDEVQALADEDGEIRGIASGVGRYAFVFFGGGIQMAGRGABELLDSSAVF	ò	96
à à	1:   :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	QQ —	3090 VASGRIAYTFGLEGPATTVDTACS
20 1	ZOIO AAAMAECEAALSPIVUMSLEAVVRQAPGAPILERVUVVQPVIFAVMVSLARVMUHHGVIP	ò	96
ò		<u>8</u>	3150 EFSRQRALAPDGRSKAFSADADG
අ	2070 QAVVGHSQGEIAAAYVAGALPLDDAARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERL 2129	ò	96
ò	. 56	· 8	3210 GASNGLTAPNGPSOORVIROALA
걾	2130 SDFDGLSVAAVNGPTATVVSGDPVQIEELAQACKADGFRARIIPVDYASHSRQVEIIESE 2189	8 8	
ò	. 56 55	5 6	SedeOmmonio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiorio Superiori
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ò	. 56 55	<b>⇒</b> †	
da .	2250 HFVEVSAHPVLTMTLPETVTGLGTLRREQGQERLVTSLAEAWVNGLPVAWTSLLPATAS 2309	qq ,	3330 ALVIEPIDWPAGIGPRRAAVSSFG
ò.	55 95 /	<del>}</del> 1	
đ	2310 RPGLPTYAFQAERYWLENTPAALATGDDWRYRIDWKRLPAAEGSERTGLSGRWLAVTPED 2369	<b>Q</b>	3390 GTAGTSEVAEGSEASEAPAAPGSE
ò		ò	
Q	2370 HSAQAAAVLTALVDAGAKVEVLTAGADDDREALAARLTALTTGDGFTGVVSLLDGLVPQV 2429	<u>අ</u>	3450 DLSDADGPARLRDVGYTLATSRT
ò	, 56KMVILTEPE64	ò	96
3 6	2430 AWVOALGDAGTKAPLWSVTOGAUSTGEDDRAMIWG.GRVVALEHPERMAGTVDI.	8	3510 RDGTTAFLFTGQGSQRPGAGREL)
3 8		ò	101
ં ત		Q <sub>C</sub>	3570 EAALLDETRYTQCALFALEVALFI
g (	2490 PAQPDAAALAHUVIALSGATGEDQIALKITGLHARKLAKAPLHGKRPIRDWQPHGIVLII	ò	101
ਤੇ <i>ਹ</i>	ob	q	3630 LVAARGRLMQELPAGGAMLAVQAJ
<u> </u>	2550 GGIGALGSHAARWMAHHGAEHLLLVSRSGEQAFGAIQLIAELIASGARVIIAACDVADPH	ò	101
ð í		qq	3690 AAREAEAYWSGLGRRTRALRVSH
Q O	2610 AMRTLLDAIPAETPLTAVVHTAGALDDGIVDTLTAEQVRRAHRAKAVGASVLDELTRDLD	ò	101
ò	17	_	

LESALGRDETAITVADIDWDRFYLAYSSGRPOPLVEEL 2789 QGANPLAERLAAAAPGERTEILLGLVRAQAAAVLRMRS 2849 LRNRLTRATGLQLPATLVFDHPTPLALVSLLRSEFLGD 2909 RGSSTGVFIGLSYQDYAARVPNAPRGVEGYLLTGSTPS 3089 GFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQD 3209 ADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKE 3269 AGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGL 3329 FGISGTNAHVVLEQAPDAAGEVLGADEVPEVSETVAMA 3389 TAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTA 3509 | | :| LYDRHPVFARALDEICAHLDGHLELPLLDVMFAAEGSA 3569 FRLVESWGMRPAALLGHSVGEIAAAHVAGVFSLADAAR 3629 HAFHSAHMDGMLDGFRAVLETVEFRRPSLTVVSNVTGL 3749 APHNAYLDALAARRRATGRSAVSVAWGPWDGGGMAAGD 2729 :||| GAGTDADDDPIAIVAMSCRYPGDIRSPEDLWRMLSEGG 2969 DALGRAYVREGGFLHDAAEFDAEFFGVSPREALAMDPQ 3029 CSSSLTALHLAVRALRSGECTMALAGGVAMMATPHMFV 3149 SREASLPGHLPWVLSAKDEQSLRGQAAALHAWLSEPAA 3449 AAEDEIRVWLETEERYAGRLDVAAVNGPEAAVLSGDAD 3689 ----- 100 100 16 ----- 01MPED----- 91 56 LLSVCGWSQTI

a	3750	AAGPDDLCDPEYWVRHVRGTVRFLDGVRVLRDLGVRTCLELGPDGVLTAWAADGLADTPA	3809
}	,		1
ò	101		100
අ	3810	DSAAGSPVGSPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWH	3869
તે	101		100
a	3870	AWFAGSGAHRVDLPTYSFRRDRYWLDAPAADTAVDTAGLGLGTADHPLLGAVVSLPDRDG	3929
à	101		100
g	3930	LLLTGRLSLRTHPWLADHAVLGSVLLPGAAMVELAAHAAESAGLRDVRELTLLEPLVLPE	3989
ò	101		100
සු	3990	HGGVELRVTVGAPAGEPGGESAGDGARPVSLHSRLADAPAGTAWSCHATGLLATDRPELP	4049
ત્રે	101		100
8	4050	VAPDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATT	4109
à	101		100
8	4110	NATAPATANGGGSAAAAPYGIHPALLDASLHAIAVGGLVDEPELVRVPFHWSGVTVHAAG	4169
à	101		100
a	4170	<b>AAAA</b> RVRLASAGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVGGLMHRVAWRP	4229
ጵ	101		100
q	4230	YALASSGEQDPHATSYGPTAVLGKDELKVAAALESAGVEVGLYPDLAALSQDVAAGAPAP	4289
à	101	VLYITR	106
ą	4290	RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAGTRLLLVTRGAVRDPEGSGA	4349
à	107		106
q	4350	DDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSYRTLPSVLSDAGLRDEPQLALH	4409
à	101		106
ą	4410	DGTIRLARLASVRPETGTAAPALAPEGTVLLTGGTGGLGGLVARHVVGEWGVRRLLLVSR	4469
⋧	101		106
ą	4470	RGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAI PAEHPLTAVVHTAGVLSD	4529
à	101		106
ရ	4530	GTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGGAGQGAYAAA	4589
à	107		106
ą	4590	NATLDALAWRRRAAGLPALSLGWGLWAETSGMTGELGQADLRRMSRAGIGGISDAEGIAL	4649
à	107		106
ą	4650	LDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARPSAASASTTA	4709
à	107		106
ą	4710	GTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHARGHRIDAER	4769
à	107		114
ą	4770 (	GFLDLGFDSLTAVELRNRLNSAGGLALPATLVFDHPSPAALASHLDAELPRGASDQDGAG	4829
ጵ	115		114
ą	4830	NRNGNENGTTASRSTAETDALLAQLTRLEGALVLTGLSDAPGSEEVLEHLRSLRSMVTGE	4889

5969	EAAPVLAALSGAGADPVQLDVSPLGDRQRLAATLGEALAAAGGAVDGVLSLLAWDESAHP	5910	qq
125		126	ò
5909	PTYAFQRRHYWLHDSPAVQGSVQDSWRYRIDWKRLAVADASERAGLSGRWLVVVPEDRSA	5850	g
125		126	ઠે
5849	SAHPVLTMTLPETVTGLGTLRREQGGERLVTSLAEAWTNGLTIDWAPVLPTATGHHPEL	5790	qq
125	VTQLG	121	ò
5789	AGLSPRTPEVPFFSTLEGAWITEPVLDGTYWYRNLRHRVGFAPAVETLATDEGFTHFIEV	5730	QQ
120		121	ò
5729	LSIAAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPVDYASHSAHVETIESELAEVL	5670	QQ
120		121	ò
5669	HSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALSEEATRQRIENLHG	5610	qq
120		121	ò
5609	ECESALSRYVDMSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVG	5550	g
120		121	ò
5549	VLGTGQDDFAQALTAPEGLIRGTPSDVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMA	5490	g
120		121	ò
5489	PSVGAGLVPWLVSAKTPAALDAQIGRLAAFASQGRTDAADPGAVARVLAGGRAEFEHRAV	5430	g
120		121	ò
5429	SAGAVELLTEAMDWPDKGDGGLRRAAVSSFGVSGTNAHVVLEEAPAAEETPASEATPAVE	5370	q
120		121	ò
5369	) TYGQGRDGEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGVLPKTLHVEKPTDQVDW	5310	g
120		121	ò
5309	) AVNQDGASSGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQAVIA	5250	g
120		121	ò
5249	   PSTFVEFSRÖRGLAPDGRSKSFSSTADGTSWSEGVGVLLVERLSDARRKGHRILAVVRGT	5190	g
120		115	ò
5189	) GNSGSVASGRVAYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGEVDMALAGGVTVMST	5130	qq
114		115	ò
5129	) AMDPQQRLLLEASWEAFEHAGIPAATARGTSVGVFTGVMYHDYATRLTDVPEGIEGYLGT	5070	g
114		115	ò
5069	) VAGGEDAISEFPQDRGWDVEGLYDPNPEATGKSYAREAGFLYEAGEFDADFFGISPREAL	5010	g
114		115	ò
5009	) MSTVNEEKYLDYLRRATADLHEARGRLRELEAKAGEPVAIVGMACRLPGGVASPEDLWRL	4950	g
114		115	ò
4949	) TGTGTASGAPDGAGSGAEDRPWAAGDGAGGGSEDGAGVPDFMNASAEELFGLLDQDPSTD	4890	qq
114	***************************************	115	ò

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6690 VMSTPTTFVEFSRQRGLAEDGRSKAFAASADGFGPAEGVGMLLVERLSDARRNGHRVLAV 6749 133	7770 VIRDAVAAKSGDGLKSTGQAAVWGLCKSAQIESFCKFVLLDLAGEAKIAGIALIAUDGLI.
133 132 6750 VRGSAVNQDGASNGLTAPNGPSQQRVIRRALADARLTTADVDVVEAHGTGTRLGDPIEAQ 6809	7830 GDATVGGTSGDAALGSALATALGSGEPQLALRDGALLVPRLARAAAPAAADGLAAADGLA
VDRPSD	Oy 138 137  Db 7890 ALPLPAAPALWRLEPGTDGSLESLTAAPGDAETLAPEPLGPGOVRIAIRATGLNFRDVLI 7949
ALIAI TGGGKU IEQFEKEGSLASNI GHIQAAAGVSGI I KAYQAARKHGV LFTI I TAVIKASU	QY 138 137  Db 7950 ALGMYPDPALMGTEGAGVVTATGPGVTHLAPGDRVMGLLSGAYAPVVVADARTVARMPEG 8009
6870 QIDWSAGTVELLTEAMDWPRKQEGGLRRAAVSSFGISGTNAHIVLEEAPVDEDAPADEPS 6929 133	138
133 132 6990 TGQDDLAAALAAPEGLVRGVASGVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAWAECE 7049 133	OY 138

; SEQ ID NO 5 ; LENGTH: 1690 ; TYPE: PRT ; ORGANISM: human US-09-788-043C-5 Query Match Best Local Similarity 17.9%; Score 231; DB 10; Length 1690; Best Local Similarity 17.9%; Pred. No. 0.071; Matches 60; Conservative 24; Mismatches 63; Indels 188; Gaps	QY         1 AAGGILHLEL	26	OY S6 KMVILTEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGN 115   ::           ::	RESULT 14 US-09-121-1987B-2  Sequence 2, Application US/09121987B  Sequence 2, Application US/09121987B  Patent No. US20020102210A1  GENERAL INFORMATION:  APPLICANT: Kimble, Judith E  APPLICANT: Blelloch, Robert H  TITLE OF INVENTION: Agent and Method for Modulating Cell Migration FILE REFERENCE: 960296.95386  CURRENT APPLICATION NUMBER: US/09/121,987B  CURRENT FILING DATE: 1999-05-29  PRIOR FILING DATE: 1998-05-29  PRIOR FILING DATE: 1998-04-13  PRIOR FILING DATE: 1998-04-13  NUMBER OF SEQ ID NOS: 5  SOFTWARE: Patentin Ver: 2.1  SEQ ID NO SEQ ID NOS: 5  TYPE: PRT  ORGANISM: Caenorhabditis elegans	US-09-321-987B-2
Db         8130 GGRFVEMGKTDVRDAERVAADHPGVGYRAFDLGEAGPERIGEMLAEVIALFEDGVLRHLP 8189           Qy         138	Qy         138	138		OY         145           Db         8670 ASDDDLFSFIDKELGDSDFMANNEDKLRDYLKRVTAELOQNTRLREIEGRTHEPVAIVG 8729           OY         145           Db         8730 MACRLPGGVASPEDLWQLVAGDGDAISEFPQDRGWDVEGLYDPDDDASGRTYCRSGGFLH 8789           OY         145           Db         8790 DAGEFDADFFGISPREALAMDPQQRLSLTTAWEAIESAGIDPTALKGSGLGVFVGGWHTG 8849           QY         145           Db         8850 YTSGQTTAVQSPELEGHLVSGAALGFLSGRIAYVLGTDGPALTVDTACSSSLVALHLAVQ 8909           QY         145           I 145         II 148           Db         8910 ALRKGECDMALAGGVTV 8926	US-09-788-0425-5  Sequence 5, Application US/09788043C  Patent No. US20020107361A1  GENERAL INFORMATION:  APPLICANT: Heller, Renu  APPLICANT: Zuo, Fengrong  APPLICANT: Klonowski, Pau  TITLE OF INVENTION: No. US20020107361A1el Metalloproteases Having  TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions  TITLE OF INVENTION: Encoding the Same  TITLE OF INVENTION: Encoding the Same  TITLE OF INVENTION: Encoding the Same  CURRENT APPLICATION NUMBER: US/09/788,043C  CURRENT FILING DATE: 2001-02-16  PRIOR FILING DATE: 2000-02-18  NUMBER OF SEQ ID NOS: 10  SOFTWARE: FastSEQ for Windows Version 4.0

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11   TINNINGABLIAGOR PHYLYMENTITERGANITYTESSLANDESTITURE 90   1435     11   11   11   11   11   11   11	g	TSVNETETTVATWQDQWEDVIERKARSRRAANSWDHYVEVLVVADTKMYEYHGRSLEDYV	142
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100	ò	LINLNIGAELLEDPSLGAOFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWSOTINPE	2851
DITTO-GRADUAL/LITREDLELPOCKROVEGA,   125   144     14	g	LTLFSTVASIYRHQSLRASINVVVVKLIVLKTENAGPRITQNAQQTLQDFCRWQQYYNDP	000
156   DOSCUMENTIAL PROPERTY SOURCE CONTINUED NOT SAFETY   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126   DOSCUMENT   126	ò	pptdpghaplvly1jrfdlelpdgnrqvrgvtqlg	147
126	g		1445
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136   1365 DIECSED   126   1265 DIECSED   126   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1265 DIECSED   1	g	ELGHVFSI PHDDERKCSTYMPVNKNNFHIMAPTLEYNTHPWSWSPCSAGMLERFLENNRG	
126   1265 DIEGES    126	ò		
126   144   1	윱	OTQCLFDQPVERRYYEDVFVRDEPGKKYDAHQQCKFVFGPASELCPYMPTCRRLWCATFY	
136   GOGYONGCRTQHMPWADGTPCDESRSHYCHGACVRLAPESLTKIDGQWGDNRSWGECSRTC 604   125   GOSTOCTCHHRAPDGTPCDESRSHYCHGACVRLAPESLTKIDGQWGDRSWGENCHGACVRLAPESLTKIDGQWGDNRSWGENCHGGACSTCTC 604   GOSTOCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACRCALROCTCRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACVRCALROCTCHGACRCALROCTCHGACRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCHGACRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCALROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROCTCRCARROC	ò		•
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605 GGCVOXGLRDCDSPKPRNGGKCVCQRERYRSCNTOECPWDTOPYREVOCSEFNNKDIGI 664   15 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17 Sequence 155, 17	ò		RESULT 15
126	qq	GGGVQKGLRDCDSPKPRNGGKYCVGQRERYRSCNTQECPWDTQPYREVQCSEFNNKDIGI	US-09-800-729-155 ; Sequence 155, Applicatio
665 OGVASTNTHWVPKYANVAPNERCKLYCRLSGSAAFYLLRDKVVDGTPCDRNGDDICVGA 724  128 CSP  128 CSP  128 CSP  129 CSP  129 CSP  130 CSP INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF INVERSION OF	ò	¥5	; Patent No. US2002006831; ; GENERAL INFORMATION:
128   CSP	g		; APPLICANT: Ni et al. ; TITLE OF INVENTION: 33
131   132   133   134   134   134   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135	ò	SO	; FILE REFERENCE: P20448; CURRENT APPLICATION NUM
131     130   PRIOR FILING	g	   CMPAGCDHQLHSTLRRDKCGVCGGDDSSCKVVKGTFNEQGTFGYNEVMKIPAGSANIDIR	CURRENT FILING DATE:
131   132   133   134   135   134   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135	ò		; PRIOR FILING DATE: 200
131	a	QKGYNNWKEDDNYLSLRAANGEFLLNGHFQVSLARQQIAFQDTVLEYSGSDAIIERINGT	, PRIOR FILING DATE: 1995 , NUMBER OF SEQ ID NOS:
134   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT   174PE: PRT	ò	SML	; SEC ID NO 155
134	g	:   GPIRSDIYVHVLSVGSHPPDISYEYMTAAVPNAVIRPISSALYLWRVTDTWTECDRACRG	; LENGTH: 2165 ; TYPE: PRT
905 QQSQXLMCLDMSTHRQSHDRNCQNVLKPKQATRMCNIDCSTRW TEDVSSCSAKCGSGQK 964  140	ò	ILED	
140	g		Query Match
965 RQRVSCVKMECDRQTPASEHLCDRNSKPSDIASCYIDCSGRKWNYGEWTSCSETGGSNGK 1024  140	ò		Best Local Similarity Matches 61, Conservati
140	QQ	RQRVSCVKMEGDRQTPASEHLCDRNSKPSDIASCYIDCSGRKWNYGEWTSCSETCGSNGK	m
1025 MHRKSYCVDDSNRRVDESLCGREQKEATERECNRIPCPRWYGHWSECSRSCDGGVKMRH 1084 Qy 9 140	ò		
140       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description       Description <t< td=""><td>g</td><td></td><td>•</td></t<>	g		•
1085 AQCLDAADRETHTSRCGPAOTQEHCNEHACTWWQFGVWSDCSAKCGDGVQYRDANCTDRH 1144 Qy 9  140	ò		
140	a	AQCLDAADRETHTSRCGPAQTQEHCNEHACTWWQFGVWSDCSAKGGDGVQYRDANCTDRH	
1145 RSVLPEHRCLKMEKIITKPCHRESCPKYKLGEWSQCSVSCEDGWSSRRVSCVSGNGTEVD	ò		
140 139 Db 185 1205 MSLCGTASDRPASHQTCNLGTCPFWRNTDWSACSVSCGIGHRERTTECIYREQSVDASFC 1264 Qy 9	සු	RSVLPEHRCLKWEKIITKPCHRESCPKYKLGEWSQCSVSCEDGWSSRRVSCVSGNGTEVD	
1205 MSLCGTASDRPASHQTCNLGTCPFWRNTDWSACSVSCGIGHRERTTECIYREQSVDASFC 1264	ò		
	qq	MSLCGTASDRPASHQTCNLGTCPFWRNTDWSACSVSCGIGHRERTTECIYREQSVDASFC	6 VO

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GPRVLQKLQADVPPIRWATGPWTACSATCGNGTQRRLLKCRDHVR 1384
                                    PCTSWKPSHWSPCSVTCGSGIQTRSVSCTRGSEGTIVDEYFCDRN 1324
                                                                                                                                                                                                         TRNCRLRDCSYWKMAEWEECPATCGTHVQOSRNVTCVSAEDGGRT 1444
                                                                                                                                                                                                                                                                                     ARNCRLEPCPKGEEHIGSWIIGDWSKCSASCGGGWRRRSVSCTSS 1504
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 NGTORRLLKCRDHVRDLPDEYCNHLDKEVSTRNCRLRDCSYWKMAEWEECPATCGTHVQO
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 Qy
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 1445
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 Qy
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 Qy
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 1565
 RKIWCEDVLSGRKQDDIECSEIKPREQRDCEMPPCRSHYHNKTSSASMTSLSSSNSNTTS
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 Qy
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 SASSASSLPILPPVVSWQTSAWSACSAKCGRGTKRRVVECVNPSLNVTV
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Search completed: March 20, 2003, 12:40:57 Job time : 97 secs

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   Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Satoahara, Sa
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US-09-369-364A-13
IS-09-369-364A-13
Sequence 13, Application US/09369364A
Setonce 13, Application US/09369364A
Setonce No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte. Sunce1
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REPERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT PILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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37.5%; Pred. No. 6.5e-18;
ive 22; Mismatches 55
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Patent No. 6391610
GENERAL INFORMATION:
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Best Local Similarity 37.5%
Matches 48; Conservative
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Sequence 11,
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(Ggn2_6/ptodata/2/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                                     GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-369-364A-5
US-09-369-364A-11
US-09-491-522-11
US-09-491-522-17
US-09-369-364A-15
US-09-369-364A-12
US-09-30-972-2
US-09-30-972-2
US-09-30-972-2
US-09-30-972-2
US-09-30-972-2
US-09-369-364A-9
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Sequence 5, Application US/09369364A
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TILE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1994-09-05
EARLIER FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOSE: 16
NUMBER OF SEQ ID NOSE: 16
SOFTWARE: FRIENG DATE: 1997-09-06
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25.7%; "Score 184; DB 4;
Best Local Similarity 29.5%; Pred. No. 6.9e-14;
Matches 38; Conservative 28; Mismatches 55.
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Sequence 2, Application US/09130491
Patent No. 6416974
                                                                                                                         TYPE: PRT
ORGANISM: Homo Bapiens ADAMTS-9
                                                                                                                                                                                                                                                                   LOCATION: (468)
OTHER INFORMATION: %aa = C
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (521)
OTHER INFORMATION: Xaa = Y
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            PatentIn Ver.
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                                                                                                                                                                                                          FEATURE:
NAME/KEY: MOD_RES
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US-09-369-364A-5
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TYPE: PRT
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                                                ID NO 13
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268 RKDIEHYILSVANIVAKLYRDSSLGNVVNIIVARLIVLTEDQ--PNLEINHHADKSLDSF 325
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APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata, Satohata,
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Patent No. 6451575
GENERAL INFORMATION:
APPLICANTION:
APPLICANTION: AGGRECAN DEGRADING METALLO PROTEASES;
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 PTWSCLITEDTGFDLGVTI 136
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (450)
OTHER INFORMATION: Xaa = L
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Best Local Similarity 30.29
Matches 38; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Length 1205; 57; Indela

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RESULT 8
US-09-491-522-7
Sequence 7, Application US/09491522
Sequence 7, Application US/09491522
Sequence 7, Application US/09491522
Sequence 7, Application US/09491522
SEQUENCE 7, COLIGE, Alain
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                 60 NLTSSLLSVCGWSQ-TINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                         268 VDDSVVQFHGTEHVQKYLLTLMNIVNEIYHDESLGAHINVVLVRIILLSYGKSMSLIEIG 327
                                                                                                                                                                                                                                                                                                               2 VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                                                                                              Ouery Match
22.2%; Score 159; DB 4;
Best Local Similarity 33.3%; Pred. No. 5.3e-11;
Matches 44; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows
SOFTWARE: FREEESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
               TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 566 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acidé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TWSCLITEDTGF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 VRSCTLNHEDGF 394
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US-09-491-522-7
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relephone:
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TOPOLOGY:
US-09-491-522-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 DLONHILTLMSVAARIYKHPSIKNSINLMVKVLIVEDEKWGPEVSDNGGLTLRNFCNWQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 DTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWS 72
                                                  Sequence 11, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteages
FILE REPERINCE: 26473/4007/10-30-00
CURRENT APPLICANTE: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEO ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.7%; Score 170; DB 4; Length 245; Best Local Similarity 26.6%; Pred. No. 2e-13; Matches 33; Conservative 28; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketce
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Abrams, Samuel B
REGISTATION NUMBER: 30,605
REFERENCE DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               SEQ ID NO 11
LENGTH: 245
; TYPE: PRT
OCGANISM: Homo sapiens ADAMTS-8
US-09-369-364A-11
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                                         09-369-364A-11
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334 NPSQSLENVCRWAYLQOKPDTGHDEYHDHAIFLTRQDF----GPSGMQGYAPVTGMCHPV 389
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; Patent No. 6391610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09369364A; Patent No. 6391610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: mus musculus ADAMTS-5
US-09-369A-2
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; ORGANISM: Mus musculus ADAMTS-9
US-09-369-364A-15
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                                                         120 WSCLITEDTGF 130
                                                                                             390 RSCTLNHEDGF 400
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                                                                                                                                                      RESULT 10
US-09-369-364A-15
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US-09-369-364A-2
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SEQ ID NO 2
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                                                                                                                                                                      60 NLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPT 119
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                                                         Gaps
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                                                                                               2 VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
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                   Query Match
21.9%; Score 157; DB 4; Length 566;
Best Local Similarity 31.3%; Pred. No. 3.1e-11;
Matches 41; Conservative 24; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8389-0060-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLIANCE DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09491522
Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 31.39
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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390 RSCTLNHEDGF 400
                                                                                                                                                                                                                                                120 WSCLITEDIGE
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208 OWQHSKNYLGGIQHDT-----AVLVTREDICRAQDKCDTLGLAELGTICDPYRSCSIS 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 QHYLLIMASIANRLYSHASIENHIRLAVVKVVVLLTDKOTSLEVSKNAATTLKNFCKWQHQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 HQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVC 69
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APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hicholate, Satoach
TIILE OF INVENTION: Wouled to Acids Encoding Zinc Metalloprotesses
FILE REPERENCE: 26473/4007/10-30-00
CURRENT APPLICATION WIMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohara, Satoshi
TITLE OF INVENTON: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 874;
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20.9%; Score 149.5; DB 4;
Best Local Similarity 28.7%; Pred. No. 5.8e-10;
Matches 35; Conservative 22; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.6%; Score 154.5; DB 4; Best Local Similarity 27.5%; Pred. No. 1.2e-10; Matches 36; Conservative 26; Mismatches 58;
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298 VDKKWMQNHGHENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISHH 357
                                                                                                          358 ADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLDICSWKNEPCD----TLGFAPISGMCSK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 RRFNKPSDRHPEHYDTAILFTRQNFCGKGEQCDTLGMADVGTICDPDKSCSVIKDEGLQA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 QTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDL 132
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                                                              61 LISSLLSVCGWSQTINPEDDTDPGHADLV--LYITRFDLELPDGNRQVRGVTQLGGACSP
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aptro.
APPLICANT: Aptro.
APPLICANT: Hurekainen, Tilna L.
APPLICANT: Hurekainen, Tilna L.
APPLICANT: Hichata, Satoshi
TITLE OF INVENTION: Nucleich Acids Encoding Zinc Metalloproteases
FILE REFERRNCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Patent No. 6451575
GENERAL INFORMATION:
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REPRENCE: DM6909
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 930
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19.8%; Score 141.5; DB 4; Length 9
Best Local Similarity 27.9%; Pred. No. 5.9e-09;
Matches 34; Conservative 22; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.5%; Score 147; DB 4; 24.2%; Pred. No. 1.1e-09; tive 27; Mismatches 67
                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus ADAMTS-8
                                                                                                                                                           119 TWSCLITEDTGFDLGVTI 136
                                                                                                                                                                                                     414 YRŚCTINEDTGLGLAFTI 431
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Best Local Similarity 24.2%,
Matches 30; Conservative
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US-09-122-126B-15
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US-09-122-126B-15
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US-09-369-364A-9
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US-09-930-872-2
Sequence 2, Application US/09930872
; Sequence 2, Application US/09930872
; Sequence 2, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
    APPLICANT: Hilbun:
    TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the FILE REFERENCE: LEX-0219-USA
    CURRENT APPLICATION NUMBER: US/09/930,872
    CURRENT FILING DATE: 2001-08-14
    PRIOR FILING DATE: 2000-08-16
    NUMBER OF SEQ ID NOS: 5
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the :
FILE REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
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      75 INPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGV 134
                                  298 VDKKMMQNHGHENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISHH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LTSSLLSVCGWSQTINPEDDTDPGHADLV--LYITRFDLELPDGNRQVRGVTQLGGACSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 ADHTLSSFCOWOSGLMGKDGTRHDHAILLTGLDICSWKNEPCD----TLGFAPISGMCSK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 491;
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20.6%; Score 147.5; I
Best Local Similarity 31.2%; Pred. No. 4e-10
Matches 43; Conservative 22; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09930872
Patent No. 6448388
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: homo sapiens
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TV 408
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Search completed: March 20, 2003, 12:36:05 Job time : 26.0541 secs

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March 20, 2003, 12:32:34 ; Search time 24.8108 Seconds (without alignments) 526.959 Million cell updates/sec
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716
1 AVGPDVFQAHQEDTERYVLT.....SPTWSCLITEDTGFDLGVTI 136
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                         283224 seqs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		_	z	_	æ	_	_	angiogenesis inhib	beta-1,4-mannosyl-	hypothetical prote	ribulose-phosphate	probable glutamine	hypothetical prote	hypothetical prote	probable monooxyge	probable amidase -		probable translati	conserved hypothet	conserved hypothet	hypothetical prote	peptidyl-prolyl ci	hypothetical prote	conserved hypothet	arsenate reductase	lcohol dehy	opherin	nuclear pore-targe
SUMMARIES		T21371	T00017	T00355	T18517	T16892	T15976	4	T22836	T18856	JN0586	T14765	G82052	H82957	T08769	E71230	T36402	F70972	T42624	T11583	D81196	A81086	G81857	E83541	T22344	D69199	AH3460	G82719	35	6628
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•	Query Match	28	24.8	24	22	15	11	10	20	2	2	2	σ	0	σ	σ	o	σ	σ	6	ο.	6	φ.	σ	<u>ه</u>	9.	6	0	٥.	
	Score	201	177.5	172.5	159	112.5	85	75.5	75.5	73.5	72	71.5	71	7,1	71	70.5	70.5	70.5	70.5	70.5	70	70	70	69.5	69.5	69.5	69	69	69	69
			N	Э	4	ហ	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

gene ADAMTS-1 protein - mouse C;Species: Mus musculus (house mouse) C;Date: 22-Jan.1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000 C;Accession: T00017

beta-1,4-mannosyl- PERA-1,4-mannosyl- PERA-1,0 protein - KAP95 protein - ye ribulose-phoophate homeoitc protein e agrine-tRNA ligase importin beta chai probable RNA helic BIR repeat contain conserved hypothet CT021 hypothetical probable multicopp probable multicopp probable htpG prote two-component sens	ALIGNMENTS rhabditis elegans on 15-Oct-1999 #text_change 29-Oct-1999 February 1996	:CAA93287.1; GSPDB:GN00022; CESP:F25HB.3 ebruary 1996 m GB/EMBL/DDBJ :CAA93288.1; GSPDB:GN00022; CESP:F25HB.3	SP:F25HB.3  SP:F25HB.3  SP:F25HB.3  SP:F25HB.3  11/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744  28.1%; Score 201; DB 2; Length 265;  al Similarity 33.6%; Pred. No. 1.4e-12;  44; Conservative 17; Mismatches 70; Indels 0; Gaps 0;  VFQAHQEDTERYVLTNLNIGAELLERPSLGAOFRVHLVKMVILTEPEGAPNITANLTSSL 65  SINCH
A43415 JC4362 A86350 S51350 A40019 A40019 A70018 B7563 A70118 A70523 A70523 A70523 A70523	0	IDN:C	/3; 216 Score Pred. 7; Mil LRDPSLM         VXYITR ::
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336 336 336 337 337 337 337 337 337 337	3 - 1eg ce_ Lib	936 1115 1318 1818	5/2; 28.1; 33.6; 33.6; 1.1.6; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.1.7.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0.0; 1.0
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procollagen N-endopeptidase (EC 3.4.24.14) I - bovine
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383 VRSCTLNHEDGF 394
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                                                                                                         Accession: T18517
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C,Function:
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R;Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K. Genomics 46, 466-471, 1997

Genomics 46, 466-471, 1997

A;Title: The exonintron organization and chromosomal mapping of the mouse ADAMTS-1 gene A;Reference number: Z14055; MUID:98110583; PMID:9441751

A;Accession: T00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotherical protein KIAA0688 - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Ol-Reb-1999 #sequence_revision Ol-Feb-1999 #text_change 21-Jul-2000 C; Accession: T00355 R; Shikawa, K; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. S, 169-176, 1998 A; Ries. S, 169-176, 1998 A; Reference number: Z14142; MUID:98403880; PMID:9734811
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                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Roaldus: 1-951 <KUN>
A;Roaldus: 1-951 <KUN>
A;Cross-references: EMBL:AB001735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057
A;Experimental source: strain 1298vJ
C;Genetics:
A;Genet ADAMTS-1
A;Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
C;Superfamily: thrombospondin type 1 repeat homology
F;542-598/Domain: thrombospondin,type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AB014588; NID:g3327189; PIDN:BA311663.1; PID:g3327190
A;Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 951;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.8%; Score 177.5; DB 2; Length 9 Best Local Similarity 28.6%; Pred. No. 1.6e-10; Matches 36; Conservative 23; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-837 <ISH>
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nes 38; Conservative
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Ribentley, D.
submitted to the EMBL Data Library, December 1995
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: 218599
A;Recession: T16892
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-860 <BEN>
A;Cross-references: EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CEST
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                                                                                                                       Ricolige, A.; Nusgens, B.V.; Lapiere, C.M.
submitted to the EMBL Data Library, February 1996
A; Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.
A; Reference number: 218941
A; Reference number: 218941
A; Reference number: 218941
A; Reteates preliminary; translated from GB/EMBL/DDBJ
A; Rocession: T18517
A; Molecule type: mRNA
A; Rocessidues: 1.1205 <COL>
A; Residues: 1.1205 <COL>
A; Residues: 1.1205 <COL>
A; Residues: EMBL; X96389; NID:e990769; PID:e228215; PIDN:CAA65253.1
A; Experimental source: skin
Alternate names: procollagen N proteinase
Species: Bos primigenius taurus (cattle)
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Caenorhabditis elegans
Space: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T16892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 VDDSVVQFHGTEHVQKYLLTLMNIVNEIYHDESLGAHINVVLVRIILLSYGKSMSLIEIG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 NLTSSLLSVCGWSQ-TINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAOFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.2%; Score 159; DB 2; Length 12 Best Local Similarity 33.3%; Pred. No. 2e-08; Matches 44; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indela
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15.7%; Score 112.5; DB 2;
Best Local Similarity 26.3%; Pred. No. 0.0012;
Matches 35; Conservative 24; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T19D2.1 - Caenorhabditis elegans
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A; Experimental source: clone T07C5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: CESP: C02B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:F57B7.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Reaidues: 1-957 «BEN»
A;Cross-references: EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721.1; CESP:F08C6.
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Genetica:
Afgene: CESP:F08C6.1
Afintrons: 23/1: 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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hypothetical protein FOBC6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15976
R;Bentley, D. Bentley, D. Babb Data Library, June 1995
A;Description: The sequence of C. elegans cosmid FOBC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 EIHEEEKEQEQDMHIEYGRDQADELSINSEAVNDPSPAA---IHLGEASSDYAQSSVRGV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 YTLTLINNIQIMYYQPTASPPLTFRVIRYEVLTRQPSALAGYLHNHGNAQMYLDRFCRYQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 QAHQEDTE------RYVLTNLNIGAELLRDPSLGAQFRVHLVKM---VILTEPEGA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 YVLTNINIGAELLRDPSLGAQFRVHLVKMVILT-EPE---GAPNITANLTSSLLSVCGWS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 QTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.5%; Score 75.5; DB 2; Length 2;
Best Local Similarity 23.4%; Pred. No. 2.1;
Matches 33; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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A.Status: preliminary
A.Molecule type: DNA
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A;Map position: 2
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RESULT 8

A:Map position: X A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509 ñ ä A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Mesidues: 1-1444 <WIL> A;Cross-references: EMBL:250004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1 A;Experimental source: clone C02B4 A;Residues: 1-1444 <W12> A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB;GN00028; CESP:C02B4.1 A;Cross-references: EMBL:274037; PIDN:CAA98493.1; GSPDB:GN00023; CESP:F57B7.4 A;Experimental source: clone F57B7 hypothetical protein F57B7.4 - Caenorhabditis elegans
hypothetical protein F57B7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C;Accession: T22836
A;Reference number: 219623
A;Accession: T22836
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from CB/EMBL/DDBJ
A;Residues: 1-508 -WIL>
A;Residues: 1-508 -WIL> angiogenesis inhibitor homolog - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000 C;Accession: T18856; T24653 63 SSLLSVCGWSQTINPEDD-TDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWS 121 DALISSDMPKKLRKFVDITLEEMQENNSTEMTLKIDSKKAIDKFTIWLKEQTGLPRHEHA 251 Gaps 31 DPSLGAQPRVHLVKWVILTEPEGAPNITANLTSSLLSVCGWSQ-TINPEDDTD-PGHADL 88 .. 2 DB 2; Length 1444; DB 2; Length 508; 34; Indels š Indels 89 VLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDL 132 294 A;Map position: 5 A;Introns: 45/3; 137/2; 221/2; 256/2; 306/2; 409/3; 451/3 55; A; Status: preliminary; translated from GB/EMBL/DDBJ Query Match 10.5%; Score 75.5; DB Best Local Similarity 29.8%; Pred. No. 5.6; Matches 31; Conservative 15; Mismatches Query March
10.3%; Score 73.5; DB
Best Local Similarity 30.6%; Pred. No. 33;
Matches 22; Conservative 11; Mismatches submitted to the EMBL Data Library, July 1995 A;Reference number: 219917 A;Accession: T24653 submitted to the EMBL Data Library, July 1995 A;Reference number: Z19031 A;Accession: T18856

Thu

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C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: 682052.
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Oin, H.; Dragoi, I.; Se Nature 406, 477-483, 200
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerar A; Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
Modecule type: DNA
A;Modecule type: DNA
A;Cross-references: GB:AE004329; GB:AE003852; NID:g9657211; PIDN:AAP95766.1; GSP!
A;Cross-references: GB:AE004329; GB:AE003852; NID:g9657211; PIDN:AAP95766.1; GSP!
C;Genetics:
A;Gene: VC2625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable glutamine synthetase PASSOB [imported] - Pseudomonas aeruginosa (strain C'Species: Pecudomonas aeruginosa C'Species: Pseudomonas aeruginosa C'Species: Pseudomonas aeruginosa C'Species: Pseudomonas aeruginosa C'Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H82957

R'Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M adman, S.; Yuan, Y.; Brody, L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunisti A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A;Residues: 1-443 acsto-A
ribulose-phosphate 3-epimerase VC2625 [imported] - Vibrio cholerae (strain N1696
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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 VHLVKMVI-----LTEPEGAPNITANLTSSLLSVCGW---SQTINPE---DDTDP--GHA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 GAPNITANLTSS-----LLSVCGWSOTINPEDDTDPGHADLVL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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C;Superfamily: yeast ribulose-5-phosphate-epimerase
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9.9%; Score 71; DB 2;
Best Local Similarity 32.6%; Pred. No. 14;
Matches 30; Conservative 9; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
9.9%; Score 71; DB 2
Best Local Similarity 29.2%; Pred. No. 6.5;
Matches 31; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                 Thata, Y.; Nishikawa A.; Tohma, T.; Soejima, H.; Niikawa, N.; Taniguchi, N.
Blochem. 113, 692-699, 1993
Flick Construction of human N-acetylglucosa
Flick Construction of human N-acetylglucosa
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A;Map position: 22q13.1
C;Superfamily: UDP-N-acetylglucosamine acyltransferase
C;Superfamily: UDP-N-acetylglucosamine acyltransferase
C;Keywords : glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F;6-21/Domain: transmembrane #status predicted <TMM>
F;6-21/Domain: transmembrane factor-like
F;169-180/Region: epidermal growth factor-like
F;139,239,257,395/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;139,239,257,395/Binding site: carbohydrate
                                                                                                                 beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase (EC 2.4.1.144) - H
N/Alternate names: beta-D-mannoside betal,4 N-acetylglucosaminyltransferase III; N-acety
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14765
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999
A;Reference number: 218181
                                                                                                                                                                                                 Species: Homo sapiens (man)
Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LHFFKTLSYVTFPRELASLSPNLVSSFF----WNNAPVTPQASPEPGGPDLLRTPLYSHS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match

10.1%; Score 72; DB 2; Length 531
Best Local Similarity 25.3%; Pred. No. 14;
Matches 25; Conservative 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
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Matches 26; Conservative
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hypothetical protein PH0103 - Pyrococcus horikoshii

C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C; Accession: E71230
R; Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S.; Sekin M; Obluku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A; Accession: E71230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW> A;Residues: 1-266 <KAW A;Residues: 1-266 <KAW A;Residues: 1-266 <KAW A;Residues: 1-266 <KAW A;Residues: 1-266 <KAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues: 1-266 <KWAW A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRF-DLELPDGNRQ------VR 107
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                    R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
A;Reference number: 216468
A;Accession: T08769
A;Molecule type: 1-726 <KOE>
A;Rosiques: 1-726 <KOE>
A;Cross-references: EMBL:AL050134
A;Experimental source: adult uterus; clone DKFZp586K011
C;Genetics:
A;Note: DKFZp586K011.1
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9.8%; Score 70.5; DB 2; Length 266;
Best Local Similarity 25.0%; Pred. No. 8.5;
Matches 24; Conservative 9; Mismatches 26; Indels 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
9.9%; Score 71; DB 2; Length 726;
Best Local Similarity 26.4%; Pred. No. 26;
Matches 37; Conservative 23; Mismatches 50; Indels
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C, Accession: T08769
R, Koehrer, K.; Beyel
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InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep MAZB_propep; 1.
SMART; SM00209; TSP1; 2.
                                                                                                                                                   STANDARD;
534
575
789
859
184
467
1083
451
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ATS7 HUMAN
Q9UKP4;
45567880012844
4556788012884
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O9p214 homo sapien
O9b16 homo sapien
O9uhi8 homo sapien
O9ukp5 homo sapien
O9ukp5 homo sapien
O9up73 homo sapien
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O9up73 homo sapien
O9up73 homo sapien
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O9sep7 rattus norv
O9sep7 rattus norv
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O9sep7 homo sapien
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O9una0 homo sapien
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O910 mus musculu
O9una0 homo sapien
O9110 mus musculu
O91175 schizosacch
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P5226 rattus norv
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                                                               (without alignments)
341.028 Million cell updates/sec
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                                                                                                      1 AVGPDVFQAHQEDTERYVLT.....SPTWSCLITEDTGFDLGVTI 136
                                                      March 20, 2003, 12:32:11 ; Search time 16.5405 Seconds
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         GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                             112892 segs, 41476328 residues
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HUMAN
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ATS3_HUMAN
ATS5_MOUSE
ATS8_MOUSE
ATS5_HUMAN
GSAB_PICPA
GNT3_HUMAN
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CDB8_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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33210987654331098765
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- (- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

- (- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

- (- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (BY similarity).

- (- TISSUE SPECIFITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG, ITSSUE SPECIFICITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG, ITSSUE SPECIFICITY: EXPRESED IN HEART, BRAIN, PLOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

- (- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                     gallus gall
potato leaf
potato leaf
          mus musculu
bacteriopha
rattus norv
caenorhabdi
                                                                                                                                                                                                     Baccharomyc
BchizoBacch
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gallus gall
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 7) (ADAM-TS 7).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Q60750 | P16009 | Q60180 | Q09263 | Q09263 | Q09263 | Q09261 | Q09261 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092192 | Q092
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-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
               EPA1 MOUSE
VG05_BPT4
AD07_EAT
YQD3_CAEEL
YGB8_YEAST
DNPE_SCHPO
CPD9_MOUSE
MAN1_YEAST
WDR_CHICK
RRPO_FLEVU
RRPO_PLRVU
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MIM; 605009; -.
InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_MIZB_propep.
InterPro; IPR001590; Reprolygin.
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HSSP; P15167; 1ATL.
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             PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
FOR A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISTANTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF001090; tsp_1; 611 milreptuse.
Pfam; PF01421; Reprojetin; 1.
Pfam; PF01622; Pep_M12B_propep; 1.
Pfam; PF01652; Pep_M12B_propep; 1.
PR03TTE; PSS00215; ADAM MEPRO; 1.
PROSITE; PSS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS000427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS000427; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILAR!
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILAR!
ZINC (CATALYTIC) (BY SIMILAR!
N-LINKED (GLCNAC...) (POTEN
                                                                                                                 -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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ADAMTS-12.
DISINTEGRIN-LIKE.
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TSP TYPE-1 3.
TSP TYPE-1 3.
SPACER 2.
TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 7.
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CYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001762; Disintegrin.
InterPro: IPR002870; Pep M12B propep.
InterPro: IPR001590; Reprolysin.
InterPro: IPR000884; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                     EMBL; AJ250725; CAC20419.1; -.
                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:14605; ADAMTS12.
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     SIMILARITY)
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CARBOHYD
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TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely
expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           origin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.,
"Identification, characterization, and intracellular processing of
ADAM-TS12, a novel human disintegrin with a complex structural
organization involving multiple thrombospondin-1 repeats.";
J. Biol. Chem. 276:17932-17940(2011)
-:- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPQVESYVLTIMNMVAGLFHDPSIGNPIHITIVRLVLLEDEEEDLKITHHADNTLKSFCK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 WSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITEDT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00427; DISINTEGRIN 1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signāl; Glycoprotein; Zymogen; Repeat; Extracellular matrix. POTENTIAL.
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BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                         29.7%; Score 212.5; DB 1; Length 997; Ilarity 37.5%; Pred. No. 7e-14; Conservative 22; Mismatches 55; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                     7e-14;
-hes 55; Indels
                                                                                                   POTENTIAL.
BY SIMILARITY.
ADAMTS-7.
CYSTEINE SWITCH (POTENTIAL)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-12 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADA
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CYS-RICH.
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TSP TYPE-1
PS00142; ZINC_PROTEASE; 1.
PS50215; ADAM_MEPRO; 1.
PS50092; TSP1; 1.
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MEDLINE-21264577; PubMed=11279086;
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hes 48; Conserv
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P58397;
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CONFLICT
SEQUENCE
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VARSPLIC
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Magage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

Nagage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

Nagage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";

The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";

L. S. 156-73 12000)

C. -I. CORACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

C. -I. CORACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

C. -I. CORACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

C. -I. SUBCELULAR LOCATION: Secreted. Associated with the extracellular matrix (By shillarity).

C. -I. SUBCELULAR EDCATION: Secreted. Associated with the extracellular matrix (By shillarity).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                          325 QKSINPKSDLNPVHHDVAVLLTRKDI-CAGFNRPCETLGLSHLSGMCQPHRSCNINEDSG 383
                                                                                                                                                                       72 SQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITEDTG 129
                                                                               Gaps
                                                                                                                                     12 EDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                         Length 1593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                  Indels
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                         29.5%; Score 211.5; DB 1; 35.4%; Pred. No. 1.6e-13; ive 26; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 67:343-350(2000).
           Ouery Match
Best Local Similarity 35.4%
....hes 45, Conservative
                                                                                                                                                                                                                                                                                                                                                            130 FDLGVTI 136
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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PROSITE; PS00427; DISTRIBERIN_1; FALSE_NEG.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.
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Pred. No. 4.6e-11;
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MISSING (IN SHORT ISOFORM).
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ADAMTS-9.
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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SIMILARITY.
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TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 10.
TSP TYPE-1 11.
POLY-SER.
CYSTEINE SWITCI
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001890; RepFolysin.
InterPro; IPR001890; RepFolysin.
InterPro; IPR001894; TSP1.
InterPro; IPR000180; ZN MTpeptdse.
Pfam; PF00090; tsp_1; 11.
Pfam; PF01421; RepFolysin; 1.
Pfam; PF01562; Pep M128 propep; 1.
SMART; SM00209; TSP1; 12.
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                                                                                    EMBL, AF261918; AAF89106.1; -.
EMBL, AB037733; BAA92550.1; -.
HSSP, P15167; 1ATL.
                                                                                                                                                     MEROPS; M12.021; -.
Genew; HGNC:13202; ADAMTS9.
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Best Local Similarity
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MEDLINE=20289799; PubMed=10830953;
MEDLINE=20289799; PubMed=10830953;
ABCLOTA N. Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
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Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
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                                                                                      ATSI HUMAN STANDARD; PRT; 967 AA.

GOUNIS, GOUNES, COPERC; GONSJB;

JO-MAY-2000 (Rel. 39, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

ADAMTS-1 precursor (EC 3 4.24 - ) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1)

ADAMTSI OR METHI OR KIAA1345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
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The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
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                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20247184; PubMed=10785405; Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B., Rosenthal A., Thicerach K.H.; "Differential gene expression by endothelial cells in distinct
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orthologue of murine Adamcs-1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenic states.";
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99367466; PubMed=10438512;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 418-967 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Endothelial cells;
                                                                                                                                                                                                       (Human)
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128 TGFDLGVTI 136
                        424 SGLSTAFTI 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                        Homo sapiens
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGUYCAN, AND MAY BE INVOLVED IN ITS TURNOVER (BY SIMILARITY). HAS ANGIOGENIC INHIBITOR ACTIVITY. ACTIVITY. ACTIVITY. ACTIVITY. ACTIVITY. ACTIVITY. ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLU-|-LEU-1939 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN.
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                         matrix (By similarity).
-!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R MIM; boll/4; blsintegrin.
R InterPro; IPR001762; Disintegrin.
R InterPro; IPR00180; Pep_M12B_propep.
R InterPro; IPR00180; Reprolyain.
R InterPro; IPR001804; TSP1.
R InterPro; IPR000181; IS — MTDeptdse.
R InterPro; IPR000181; Is — MTDeptdse.
R Eam; PF01562; Pep_M12B_propep; 2.
R Eam; PF01562; Pep_M12B_propep; 2.
R Eam; PF01562; Pep_M12B_propep; 2.
R SWART; SM00209; TSP1; 3.
R ROSITE; PS0002; TSP1; 3.
R ROSITE; PS0002; TSP1; 2.
R ROSITE; PS000142; ZINC_PROTEASE; 1.
R Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRNIA - STRN
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N-LINKED (GLCNAC. ..) (POTENTIAL).
P -> A (IN REF. 4 AND 5).
O -> H (IN REF. 1).
S -> N (IN REF. 1).
MW; C189389324741ED1 CRC64;
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ZINC (CATALYTIC) (BY SIMILARI BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARI ZINC (CATALYTIC) (BY SIMILARI DISINTEGRIN-LIKE.
TSP TYBE-1 1.
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-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
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TSP TYPE-1 3.
POLY-LYS.
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EMBL, AF060152, AAD48080.1; ALT_INIT.
EMBL, AB037767; BAA92584.1; ALT_INIT.
EMBL, AP01697; BAA95502.1; --
EMBL, ALG2080, CAB82413.1; --
MEROPS, MIZ. 222; --
Genew, HGNC: 217; ADAMTS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEDUBNCE OF 18-967 FROM N.A.

STRAINS=20304099; PubMed=10847486;

MEDLINE=20304099; PubMed=10847486;

MEDLINE=20304099; PubMed=10847486;

Medline of the rat ADAMTS-1 gene and its down regulation in endothelial cells in cirrhotic rates.";

Liver 20:165-172(2000)

LIVER 20:165-172(2000)

C -1- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA, MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY)

SIMILARITY)

SIMILARITY)
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).
                                                                                                                                                                                                                                       CATALTATICAL ACTIVITY: CLEAVES AGGRECAN AT THE 1683-CLU-|-LEU-1684 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                              | : |:| :: | :| :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley, TISSUE=Brain,
Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.,
Little S.P.,
"Induction of a disintegrin and metalloprotease with the
thrombospondin type I motif (ADAMTS).",
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              70 GWSQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITED 127
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                  10 HQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVC 69
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2
                                                                60; Indels
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              24.9%; Score 178.5; DB ]
28.9%; Pred. No. 2.1e-10;
ive 26; Mismatches 6(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  967 AA
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                                                                   37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                          Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        391 DGLQAAFT 398
                                                                                                                                                                                                                                                                                                           128 TGFDLGVT 135
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                   Query Match
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PSO0142; ZINC_PROTEASE; 1.
PROSITE; PSO00427; TSP1; 2.
PROSITE; PSO0427; DISINTEGRIN 1; FALSE NEG.
Hydrolase; Metalloprotease; Zinc; Signāl; Glycoprotein; Zymogen;
Repeat; Extracellular matrix; Hepatin-binding.
SIGNAL 1 POPETIAL.
PROPEP 55 252 BY SIMILARITY.
CHAIN 253 967 ADAMTS-1.
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TSP TYPE-1 3.

PULYARG.
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K -> P (IN REF. 2).

K -> P (IN REF. 2).

K -> G (IN REF. 2).

TMLV -> NLLK (IN REF. 2).

TMLV -> NLLK (IN REF. 2).

TMLV -> NLLK (IN REF. 2).

TMLV -> NLLK (IN REF. 2).

TMLV -> NLLK (IN REF. 2).

TMLY -> NLLK (IN REF. 2).

L -> T (IN REF. 2).

L -> T (IN REF. 2).
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001870; Reprolysin.
InterPro; IPR001890; Reprolysin.
InterPro; IPR000180; Zn_MTpeptdse.
Pfam; PF001090; tsp_1; 6.
Pfam; PF01421; Reprolysin; 2.
Pfam; PF01421; Reprolysin; 2.
Pfam; PF01421; Reprolysin; 2.
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967 AA;
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7

FRAMESHIFT IN POSITION 7.

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INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY CELLS GRACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA CELLS OF PREVOVULATORY FOLLICLES.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. FOR A TIGHT INTERACTION BY A FURIN ENDOPEPTIDASE. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 JESTNITGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 STSP TYPE-1 DOMAINS.
CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
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J. Biol. Chem. 272:556-562(1997).
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Proc. Natl. Acad. 521. U.S.A. 97:4689-4694 (2000).
Proc. Natl. Acad. 521. U.S.A. 97:4689-4694 (2000).
INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (8Y SIMILARITY). ACTIVE METALLOPROFERSE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (8Y
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                                                                                                           metalloproteinase
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                                                                                                                                                                                                                                                                                                                                   Kuno K., Lizasa H., Ohno S., Matsushima K.; "The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene encoding an ADAM family protein with TSP motifs."; Genomics 46:466-471(1997).
                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE-20043757; PubMed=10781075;
Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.,
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"ADAMTS-1 is an active metalloproteinase associated with the
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Ohno H., Matsushima K.;
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Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
Matsushima K.;
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PEBS Lett. 478:241-245(2000).
ATSI MOUSE STANDARD; PRT; 968 AA.
P97857; O54768;
30-MAY-2000 (Rel. 39, Created)
16-OT7-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TSI).
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MEDLINE=99303657; PubMed=10373500;
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                                                                                                                                                                                                                                                                                                      STRAIN=129/SvJ;
MEDLINE=98110583; PubMed=9441751;
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EMBL; D67076; BAA11088.1; ALT_FRAME.
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16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-6 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 6) (ADAM-TS 6).
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R InterPro; IPR0012870; Pep_M12B_propep.

R InterPro; IPR0012870; Pep_M12B_propep.

R InterPro; IPR0012890; Reprolysin.

R InterPro; IPR000130; Zn_MTpeptdse.

R InterPro; IPR000130; Zn_MTpeptdse.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01421; Reprolysin; 1.

R PR051TE; PS00192; TSP1; 1.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=99395124; PubMed=10464288;
Hurakainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
Hurakainen T.S., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TSS, ADAM-TS6, and ADAM-TS7, novel members of a new family
zinc Metalloprocesses.";
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-:- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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(BY
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ZINC (CATALYTIC) (
DISINC CATALYTIC) (
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
TSP TYPE-1 2.
TSP TYPE-1 2.
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ADAMTS-6
ZINC (CATALYTIC)
860 AA.
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Genew; HGNC:222; ADAMTS6.
STANDARD;
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860
403
404
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453
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ATS4 HUMAN STANDARD; PRT; 837 AA.
075173; OGUNB3;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
15-UN2002 (Rel. 41, Last annotation update)
MDAMTS-4 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS 4) (ADAM-TS 4)
                                                                                                                                                                                                                                                                                                                                                                                       268 RKDIEHYILSVMNIVAKLYRDSSLGNVVNIIVARLIVLTEDQ--PNLEINHHADKSLDSF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGWSQTI---NPEDDTDP----GHADLVLYITRFDL----ELPDGNRQVRGVTQLGGACS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN--LTSSLLSV 68
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99286303; PubMed=10356395;
MEDLINE=99286303; PubMed=10356395;
Tortorella M.D. Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M.,
Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
Nagase H., Itch Y., Ellis D.M., Rose H., Wiewall B.H., Murphy K.,
Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
Trzaskos J.M., Arner E.C.;
Purification and cloning of aggrecanase-1: a member of the ADAWTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishikawa K.-I., Nagasa N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDLINE=20400518; PubMed=10827174;
Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross H.,
Burn T.C., Arner E.C.;
                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                Length 860;
                                                                                                                                                                                                                                                                                                    51; Indels
                      99 N-LINKED (GLCNAC. . . ) (POTE 172 N-LINKED (GLCNAC. . . ) (POTE 234 N-LINKED (GLCNAC. . . ) (POTE 234 N-LINKED (GLCNAC. . . ) (POTE 676 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-LINKED (GLCNAC. . . ) (POTE 678 N-L
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                                                                                                                                                                                                                                                   Score 176; DB 1;
Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837 AA.
                                                                                                                                                                                                                                                                                                         23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                   24.6%;
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Science 284:1664-1666(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTWSCLITEDTGFDLGVTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 PERSCSINEDIGLGSAFTI 401
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  665
99
172
222
234
676
                                                                                                                                                                                             860 AA;
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TISSUE=Brain;
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CARBOHYD
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SEQUENCE
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"The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";
J. Biol. Chem. 275:25791-25797 (2000).
I. Biol. Chem. 275:25791-25797 (2000).
I. FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTECCLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISBASES. COULD ALSO BE A ONE ALZHEIMER'S DISBASE.
CRITICAL FACTOR IN THE EXACERBATION OF NEURODEGENERATION IN ALZHEIMER'S DISBASE.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                   -1-SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1-SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1-TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED AT VERY LOW LEVEL IN PLACENTA AND SKELETAL MUSCLES.
-1-INDUCTION: BY INTERLEUKTY.
-1-DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-1-STMILARITY: BELONGS TO PEPTIDASE FAMILY MI2B.
-1-SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1-SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1-CAUTION: HAS SOMETIMES BEEN REFERRED TO AS ADAMTS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603376;

R InterPro; IPR001762; Disintegrin.

R InterPro; IPR001890; Reprolygin.

R InterPro; IPR001891; Zn_MTpeptdse.

R Pfam; PF00421; Reprolyain; I.

R Pfam; PF01421; Reprolyain; I.

R PROSITE; PS00142; LINC_PROTEASE; I.

R PROSITE; PS00125; ADAM MERRO; I.

R PROSITE; PS00427; DISINTEGRIN_I; FALSE_NEG.

R PROSITE; PS00427; DISINTEGRIN_I; Signal; Glycoprotein; Zymogen; M Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC)
ZINC (CATALYTIC)
ZINC (CATALYTIC)
TSP TYPE-1.
CYS-RICH.
SPACER.
POLY-ALA.
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAMTS-4.
CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> T (IN REF. 1).
-> Q (IN REF. 3).
-> R (IN REF. 3).
5DF9C9AC137DF41F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB014588, BAA31663.1; --
EMBL, AF148213, AAD41894.1; --
EMBL, AY044847, AAL02262.1; --
GENEW, HZ2.221, --
Genew, HGNC:220, ADAMTS4.
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837 AA;
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                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWTS-10 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombospondin type I repeats."
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: BINDS 1 ZINC IDN (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-!- DOMAIN: THE SPACER DOWAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                               GWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTG 129
                                                                                    Apte S.S.; "ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                   HOEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVC
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTECRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                   PRT; 1077 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep M12B propep.
InterPro; IPR001890; Reprolysin.
InterPro; IPR001894; TSP1.
InterPro; IPR001010; Zn_MTpeptdse.
Pfam; PP00190; tsp_1; 5.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF014522; Pep_M12B_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF163762; AAG35563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.235; -.
Genew; HGNC:13201; ADAMTS10.
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                  130 FDLGVT 135
                                                                                                                                                                    353 LQSAFT 358
                                                                                                                                                                                                                                     AT10_HUMAN
ID AT10_HUMAN
AC Q9H3Z4;
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TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
ADAMYS-8 precursor (EC 3-4,24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS 8) (ADAM-TS 9)
                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES.
-I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                    71 WSQTI-----NPEDDTDPGHADLVLYITRFDL----ELPDGNRQVRGVTQLGGACSPT 119
                                                                                                                                                                                                                                                                                                                                                                                                             291 WOKSIVNHSGHGNAIPENGVANHDTAVLITRYDICIYKNKPCG---TLGLAPVGGMCERE 347
                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Lung;

BELINE-99367466; PubMed-10438512;

Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,

Lombardo M., Iruela-Arispe M.L.;

METH-1. a human ortholog of ADAMTS-1, and METH-2 are members of

family of proteins with anglo-inhibitory activity.";

J. Blol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20079168; PubMed=10610729;
Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;
ADAM-TSS, a novel metalloprotease of the ADAM-TS family located
mouse chromosome 9 and human chromosome 11.";
Genomics 62:312-315 (1999).
                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                          POTENTIAL)
                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                  (POTENTIAL)
  (BY SIMILARITY)
                                                                                                                                                                                                                                                                        Length 1077;
                                                                                                                                                                                                                                                                                                   56; Indels
                                                                                                                                                                                                                                             118072 MW; 3914DE18DCBBF587 CRC64;
                                                                                                                                                                                          (GLCNAC. .)
                          (BY
(BY
                                                               CYS-RICH.
SPACER.
TSP TYPE-1 1.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 5.
N-LINKED (GLCNAC..)
N-LINKED (GLCNAC..)
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BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
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DISINTEGRIN-LIKE.
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                                                                                                                                                                                                                                                                       Score 172;
Pred. No. 1.
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N-LINKED
                                                                                                                                                                                                                                                                   24.0%; Scor
31.4%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                           120 WSCLITEDTGFDLGVTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 RSCSVNEDIGLPOAFTI 364
                                                                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                      976
                                                                                                                                                                                                                                               .077 AA;
                                                                                                                                                                                                                                                                                        Local Similarity
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16-OCT-2001 (Re
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SEQUENCE
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                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 QTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDL 132
EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTERYVLINLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R InterPro; IPR001590; Reprolygin.
R InterPro; IPR001590; Reprolygin.
R InterPro; IPR001590; Reprolygin.
R InterPro; IPR00130; Zn MTpeptdse.
R InterPro; IPR00130; Zn MTpeptdse.
R Pfam; PF01421; Reprolygin; 1.
R Pfam; PF01421; Reprolygin; 1.
R Pfam; PF01562; Pep M12B, Propep; 1.
R SWART; SW00209; TSP1; 2.
R PR051TE; PS501215, ADAM_MEPRO; 1.
R PR051TE; PS50092; TSP1; 1.
R PR051TE; PS00427; DISINTEGRIN 1.; PALSE_NEG.
R PR051TE; PS00427; DISINTEGRIN 1.; PALSE_NEG.
W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; W Repeat; Extracellular_matrix; Heparin; binding.
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N-LINKED (GLCNAC. . ) (POTENTI
E -> R (IN REF. 2)
YLTELLDGGHGDCLLDAPGAALPLPTGL ->
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                                                                          A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%; Score 170; DB 1; Length 89:
26.6%; Pred. No. 1.4e-09;
ive 28; Mismatches 63; Indels
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                                                                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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POLY-PRO.
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EMBL, AF175283; AAF25806.1; -.
HSSP, P34179; 11AG.
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                                                                                   FOR A TIGHT
                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MECTIX (BY SIMILARIEY).
TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
DOMAIN: THE SPACER DOMAIN AND THE TYPE-1 DOMAINS ARE IMPORTANT
FOR A TICHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                      OFESP7: OBESP8: OFESP6:
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
ADAMTS-4 precursor (EC 3 4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                           BΕ
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Brain;
MEDLINE=20415831; PubMed=10961658;
MEDLINE=20415831; N., Yokora H.;
"Abanyrs-4 (a disintegrin and metalloproteinase with thrombospondin motifs) is transcriptionally induced in beta-amyloid treated rat astrocytes.";
                                                                                                                                                                                                                                                                                                                                                                               Neurogci. Lett. 289:177-180(2000).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILLAGE PROTEOGLYCAN, AND MAY INVOLVED IN 1TS THRNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu- |-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSS0215; ADAM_MEPRO; 1.
PROSITE; PSS00125; TSP1; 1.
PROSITE; PSS00142; ZINC_MERSE; 1.
PROSITE; PS00427; DISINTECRIN 1; FALSE_NEG.
Hydrolase; Metalloprotease; ZInc; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
ADAMTS-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB042272; BAB16474.1; --
EMBL; AB042271; BAB16473.1; --
EMBL; AB042273; BAB16473.1; --
Interpro; IPR001762; Disintegrin.
Interpro; IPR001590; Reprolysin.
Interpro; IPR001590; Reprolysin.
Interpro; IPR001390; Zn_MTpeptdse.
Ffam; PF00090; tsp_1; 2.
Ffam; PF001421; Reprolysin; 1.
                                                                                                                                                                                                                        Rattus norvegicus (Rat)
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NON TER 1
PROPEP <1
CHAIN 6 63
                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
              133 GVTI 136
                                       359 AHTL 362
                                                                                                                                                                                                 (Fragment).
ADAMTS4.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
ADAMTS-2 precursor (EC 3-4-24.14) (A disintegrin and metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
N-proceinase) (PC I-NP) (Procollagen N-endopeptidase) (pNPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95348096; PubMed=7622483; Colige A., Beechin A., Samyn B., Goebels Y., Van Beechmen J., Nusgene B.V., Laplere C.M.; Musgene B.V., Laplere C.M.; Individual amino acid sequencing of a 107-kDa procollagen I N-proteinase purified by affinity chromatography on immobilized type XIV collagen. ").

i. a.tol. Chem. 270:16724-16730(1995).

i. FUNCTION: CLEAVES THE PROPEPTIDES OF TYPE I AND II COLLAGEN PRIOR TO FIBRIL ASSEMBLY. DOES NOT ACT ON TYPE III COLLAGEN. MAY ALSO PLAY A ROLE IN DEVELOPMENT THAT IS INDEPENDANT OF ITS ROLE IN COLLAGEN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97225960; PubMed=9122202;
Colige A., Li S.W., Steron A.L., Nusgens B.V., Prockop D.J.,
Laplere C.M.; "CDNA cloning and expression of bovine procollagen I N-proteinase: a
new member of the superfamily of zinc-metalloproteinases with binding
sites for cells and other matrix components.";
Proc. Natl. Acad. Sci. U.S.A. 94:2374-2379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 GWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 HOEDTERYVLTNLNIGAELLRDPSLGAOFRVHLVKMVILTEPEGAPNITANLTSSLLSVC
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H
                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                           SIMILARITY)
SIMILARITY)
     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 630;
                                                                                                                                                                                                                                                                                                                                                                              23.5%; Score 168.5; DB 1; Length 29.4%; Pred. No. 1.3e-09; ive 21; Mismatches 67; Indele
                                                                                                                                                                                                                                                                                                      63A428753167C7EF CRC64;
                                                           (BY
ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
DISINTEGRIN-LIKE.
CYS-RICH.
SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1205 AA
                                                                                                                                                                                                                                                                                                                           68384 MW;
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                                                                                                                                                                                                                                                                                                                        630 AA;
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P79331;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                             -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity)
-!- TISSUE SPECTFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVEL
-!- TISSUE SPECTFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVEL
IN ALL TYPE I COLLAGEN RICH TISSUES SUCH AS SKIN, BONES, TENDONS
AND AORTA AND AT LOW LEVEL IN BRAIN AND THYMUS. THE MRNA LEVELS
WERE DISPROPORTIONATELY HIGH IN HEART, LIVER, RETINA AND MUSCLE.
-!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                              -1- DISEASE: DEFECTS IN ADAMTS2 ARE THE CAUSE OF DERMATOSPARAXIS, A RECESSIVELY INHERITED DISORDER CHARACTERIZED BY SEVERE SKIN FRAGELLITY AND BIOCHEMICALLY BY THE PRESENCE IN SKIN OF PROCLEAGEN INCOMPLETELY PROCEESSED AT THE AMINO TERMINUS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI2B.
-1- SIMILARITY: CONTAINS 1 DISINITINGRININ-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-1- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO
COLLAGEN TYPE XIV.
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(POTENTIAL).
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
CELL ATTACHMENT SITE (POTENTIAL)
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SIMILARITY)
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY
ZINC (CATALYTIC) (BY SIMILARITY
DISINTEGRIN.LIKE.
TSP TYPE-1 1.
CYS-RICH.
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N-LINKED
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687
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DISEASE: DE
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ACT SITE
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CARBOHYD
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-1- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI;
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SIGNIFICANT N- PROCOLLAGEN PEPTIDASE ACTIVITY.
-1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON AND ARAIN.
-1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-1- PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
ADAMTS-2 precursor (EC 3.4-3.4.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I/N-proceinase) (PC I-NP) (Procollagen N-endopeptidase) (pNPI)
N-proceinase) (PC I-NP) (Procollagen N-endopeptidase) (PNPI)
ADAMTS-2 OR PCINP OR PCPNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: Defects in ADAMTS2 are the cause of Ehlers-Danlos syndrome type VIIC (EDS-VIIC), a recessively inherited connective-tissue disorder characterized clinically by severe skin fragility and joint hypermobility and biochemically by the presence in skin of procollagen incompletely processed at the N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99347935; PubMed=10417273;

Colige A., Sieron A.L., Li S.-W., Schwarze U., Petty E.,

Wertelecki W., Wilcox W., Krakww D., Cohn D.H., Reardon W.,

Byers P.H., Lapierc C.M., Prockop D.J., Nusgens B.V.;

"Human Ehlers-Danlos syndrome type VII C and bovine dermatosparaxis

are caused by mutations in the procollagen I N-proteinase gene.";

Am. J. Hum. Genet. 65:308-317(1999).

I. FUNCTION: Cleaves the propeptides of type I and II collagen prior

to fibril assembly. Does not act on type III collagen. May also

play a role in development that is independant of it, role in

collagen biosynthesis.

-:- CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain

alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains
                                                                                                                                                                                                                                             60 NLTSSLLSVCGWSQ-TINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSP 118
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                        VGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNI-TA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL)
1205 Aa; 133887 MW; 7B5B232A45320371 CRC64;
                                                                Length 1205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE
                                                                   Score 159; DB 1; Length 12
Pred. No. 2.7e-08;
3; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1211 AA.
                                                                                                              23; Mismatches
                                                                       22.2%;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                          119 TWSCLITEDIGF 130
                                                                                                                                                                                                                                                                                                                                                                                   383 VRSCTLNHEDGF 394
                                                                       Query Match
Best Local Similarity
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    CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix (By similarity).
--- TISSUE SPECIFICITY: Found in cartilage and skin.
--- TISSUE SPECIFICITY: Found in cartilage and skin.
--- TISSUE SPECIFICITY: Found in cartilage and skin.
--- TIGHT INTERACTION WITH THE EXTRACELLULAR MATRLX.
--- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           015072; 098X28;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-3 precursor (EC 3.4.4.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS3) (Procollagen II
SEQUENCE OF 1-227 FROM N.A.
MEDLINE=21402912; PubMed=11408482;
Fernance R.J., Hirchata S., Engle J.M., Colige A., Cohn D.H.,
Fyre D.R., Apte S.S.;
"Procollagen II amino propeptide processing by ADAMTS-3. Insights on
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
                                                                                                                                                                                         PRT; 1205 AA.
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Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatcopparaxie.";
J. Biol. Chem. 276:31502-31509(2001).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF247668; AAK28400.1; -. EMBL; AB002364; BAA20821.1; -.
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Genew; HGNC:219; ADAMTS3.
                                                                                                                                                                                             STANDARD;
                                                          120 WSCLITEDIGF 130
                                                                                        390 RSCTLNHEDGF 400
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ADAMTS3 OR KIAA0366.
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                         MIM; 604539; -.

R MIM; 604539; -.

R MIM; 225410; -.

R InterPro; IPR001562; Disintegrin.

R InterPro; IPR001590; Reprolysin.

R InterPro; IPR001590; Reprolysin.

R InterPro; IPR000130; Zn MTpeptdse.

R InterPro; IPR000130; Zn MTpeptdse.

R InterPro; IPR000130; Zn MTpeptdse.

R InterPro; IPR000130; Zn MTpeptdse.

R Pfam; PF01421; Peprolysin; 1.

R Pfam; PF01421; Peprolysin; 1.

R Pfam; PF01421; Peprolysin; 1.

R RNSTIF; PS00012; TSP1; 4.

R RNSTIF; PS00012; ZINC_PR0FBASE; FALSE_NEG.

R RNSTIF; PS00012; ZINC_PR0FBASE; FALSE_NEG.

R RNSTIF; PS00012; ZINC_PR0FBASE; FALSE_NEG.

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R RNSTIF; PS00012; ZINC_PR0FBASE; FALS
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TLGGOGRWIA (IN ISOFORM SPNPI).
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1211 AA; 134722 MW; BECEEF25C23CAD2D CRC64;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS. CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3
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ZINC (CATALYTIC) (
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TSP TYPE-1 4.
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MEROPS; M12.301; -..
Genew; HGNC:218; ADAMTS2.
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15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 34.24.-) (A disintegrin and metalloproteinas with thrombospondin motife 5) (ADAM-TS 5) (ADAM-TSS) (Aggrecanase-2) (ADAM-LS) (Implantin).
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MEDLINE=99395124; PubMed=10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TSS, ADAM-TS6, and ADAM-TS7, novel members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. VCBI_TaxID=10090;
                                                                                                                                                                                                                                Glycoprotein; Zymogen;
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(BY
                                    Pfam; PF00000; tap_1; 4.
Pfam; PF01421; Reprolygin; 1.
Pfam; PF01421; Reprolygin; 1.
Pfam; PF01421; Reprolygin; 1.
PROSTTE; PS00020; TSP1; 4.
PROSTTE; PS00012; TSP1; 4.
PROSTTE; PS00042; TSP1; ADAM MEPRO; 1.
PROSTTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTE; PS00427; DISINTEGRIN 1; FALSE NEG. PROSTER; PS00427; DISINTEGRIN 1; FALSE NEG. PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS00427; PS004
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TSP TYPE-1 3.
TSP TYPE-1 3.
POLY-ARG.
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*ZINC (CATALYTIC) (FOR SIMULANTY (CATALYTIC) (FOR SINC (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATALYTIC) (FOR SINCE (CATACYTIC) (FOR SINCE (C
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; Pred. No. 1.1e-07;
21; Mismatches 63
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                                                                                                                                                                                                                                                                                                    SIMILARITY.
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InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135570 MW;
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31.3%;
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Matches 41; Conservative
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16-OCT-2001
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ATS5 MOUSE
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                                                                                                                                                                                                                                                                                                                                         COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (BY similarity).

DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR UNDECTABLE LEVEL THEREAPTER.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT POR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
zinc metalloproteases.";
J. Biol. Chem. 274:25555-25563(1999).
J. Biol. Chem. 274:25555-25563(1999).
J. Biol. Chem. 274:25555-25563(1999).
J. Biol. Chem. 274:25555-25563(1999).
INVOLVED IN ITS TURNOVER. MAPPLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARPHRITIC DISBASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANTATION PERIOD.
-:- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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(BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC.
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ZINC (CATALYTIC) (
DISINTEGRIN-LIKE,
TSP TYPE-1 1.
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CYSTEINE SWITCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP TYPE-1 2.
POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; M12.225; -.
MGD; MG1:1346321; Adamts5.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001509; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001890; Reprolysin.
InterPro; IPR00130; Zn_MTpeptdse.
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 AA;
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CARBOHYD
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METAL
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SEQUENCE
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March 20, 2003, 12:34:44 ; Search time 22.0541 Seconds (without alignments) 329.684 Million cell updates/sec
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1 AVGPDVFQAHQEDTERYVLT.....SPTWSCLITEDTGFDLGVTI 136
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.4 p5_4578
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	-15 Sequence 15, App	-4 Sequence 4, App.	Sequence 6,	-1 Sequence 1, Appl	Sequence 2,	B-2 Seguence 2, Appl	B-11 Sequence 11, Ap	Sequence 2,	Sequence 7,		Seguence 16,					A-13 Sequence 13, Ap	2 Sequence 2, Appl	1 Sequence 1, Appl	1 Seguence 1. Appl
ID	US-09-833-328-15	US-09-833-328	US-09-833-328-6	US-09-978-979	US-09-836-712	US-09-781-080B-2	US-09-781-080	US-09-833-328-2	US-09-918-171	US-09-788-043	US-10-163-547-	US-09-321-987	US-09-800-729	US-09-788-043C-7	US-09-972-467-2	US-09-918-171A-1	US-09-912-788-	US-10-097-597-1	115-10-097-580-
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1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAOFRVHLVYMVILTEPEGAPNITAN

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••	APPLIC	ANT	Ke	rschl	APPLICANT: Kerschbaumer, Randolf	Ran	dol f									
•	APPLIC	ANT	Ta	glia	vacca,	Luig.	ına									
••	APPLIC	ANT	: 21	mmeri	mann, K	Tane										
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•••	PRIOR	APPI	LICAT	NOI	NUMBER:	/60	721,:	254								
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	Ouery P	√atc]	æ		10	0.0		Score	716;	DB 10;	Length	-	36;			
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                                                                                                                                                                                                                                                                                   Length 150;
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COMPUTER: TATOPY ALEN
COMPUTER: TATOPY ALEN
COMPUTER: TATOPY ALEN
CORRESTING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30.
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/978,979
FILING DATE: 16-OCC-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/60/241,469
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                100.0%; Score 716; DB 10;
100.0%; Pred. No. 2.3e-73;
ive 0; Mismatches 0;
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TITLE OF INVENTION: Aggrecanase Molecules
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,345
REGISTRATION INMBER: 32,345
TELECOMMUNICATION INFORMATION:
TELEBHONE: (973) 660-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-978-979-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Racie, Lisa, A.
Twins, Natalis, C.
Agostino, Michael, J.
Wolfman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Campus Drive CITY: Parsippany STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09978979 Patent No. US20020151702A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 136; Conservative
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ORGANISM: human
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                                                                                                                            LENGTH: 150
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US-09-978-979-1
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APPLICANT: Schwarz, Hans-Peter
APPLICANT: Antoine, Gerhard
APPLICANT: Tagliavacca, Luigina
APPLICANT: Tagliavacca, Luigina
APPLICANT: Tarecek, Peter
APPLICANT: Furlan, Miha
APPLICANT: Gerrisean, Helena E.
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APPLICANT: Gerrisean, Helena E.
APPLICANT: Gerrisean,
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APPLICANT: Turecek, Perer
APPLICANT: Geritten, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence AAGG
FILE REFERENCE: 247.00CIP
CURRENT APPLICATION NUMBER: US/09/833,328
CURRENT FILING DATE: 2001-04-12
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                                                                                                                                                                                                                                                                                                                                              Schwarz, Hans-Peter
Schoiflinger, Friedrich
Antoine, Gerhard
Kerschbaumer, Randolf
Tagliavacca, Luigina
Zimmermann, Klaus
Furlan, Miha
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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Patent No. US20020136713A1
GENERAL INFORMATION:
APPLICANT: Laemmle, Bernhard
                                                                                                                                                                                                                     Sequence 4, Application US/09833328 Patent No. US20020136713A1 GENERAL INFORMATION:
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                                             121 SCLITEDTGFDLGVTI 136
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         SCLITEDTGFDLGVTI 136
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 148
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US-09-833-328-6
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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Length 203;

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61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
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                                                                                                                                                                                                       1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
                                                                                                       1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
                                                                                                                             14 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAGFRVHLVKMVILTEPQGAPNITAN 73
                                                                                                                                                                                                                                                                                                                                                                                   Security Application US/09781080B
Security Application US/09781080B
Patent No. US20020142439A1
GENERAL INFORMATION:
APPLICANT: HOLLOWAY, JIM
APPLICANT: SHEPPARD, PAUL
APPLICANT: YAMAOTO, GAYLE
TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides,
TITLE OF INVENTION: Adint5
FILE REFERENCE: 99-82
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%; Score 713; DB 10;
99.3%; Pred. No. 7.4e-72;
iive 1; Mismatches 0;
                               Query Match
99.6%; Score 713; DB 10;
Best Local Similarity 99.3%; Pred. No. 7.5e-73;
Matches 135; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09833328; Patent No. US20020136713A1; APPLICANT: Laemmle, Bernhard; APPLICANT: Schwarz, Hans-Peter; APPLICANT: Antoine, Gerhard; APPLICANT: Antoine, Gerhard; APPLICANT: Antoine, Gerhard; APPLICANT: Tagliavacca, Luigina; APPLICANT: Zimmermann, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.61
Best Local Similarity 99.31
Matches 135; Conservative
                                                                                                                                                                                                                                                                                         134 SCLITEDTGFDLGVTI 149
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ORGANISM: Homo sapiens
US-09-781-080B-2
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US-09-833-328-2
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TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC10851A
CURRENT APPLICATION NUMBER: US/09/836,712
CURRENT APPLICATION NUMBER: 2001-04-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTW 120
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                                                             0; Gaps
                                                                                                 1 AVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITAN 60
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100.0%; Score 716; DB 10; Length 1416;
Best Local Similarity 100.0%; Pred. No. 4.6e-72;
Matches 136; Conservative 0; Mismatches 0; Indels 0;
                     Query Match
100.0%; Score 716; DB 10; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.4e-73;
Matches 136; Conservative 0; Mismatches 0; Indels 0
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Patent No. US20020142439A1
GENERAL INFORMATION:
APPLICANT: SHEPPARD, PAUL
APPLICANT: SHEPPARD, PAUL
TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides,
TITLE OF INVENTION: Actint5
FILE REFERENCE: 99-82
CURRENT APPLICATION NUMBER: US/09/781,080B
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09836712; Parent No. US20010049106A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               174 SCLITEDIGFDLGVTI 189
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT CRGANISM: Human US-09-836-712-2
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WENDLY 15.147-16

Sequence 16, Application US/10163547

Sequence 16, Application US/10163547

Sequence 16, Application US/10163547

Sequence 16, Application On . US20030037350A1

APPLICANT: Repeller-Libermann, Maria A. APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . APPLICANT: Myers, Rachel . TITLE OF INVENTION: Unman ubiquitin protease, lipase, dynamin, short chain . TITLE OF INVENTION: therefore . US/10/163,547

TITLE OF INVENTION: therefore . US/10/163,547

CURRENT APPLICATION NUMBER: US/10/163,547

CURRENT FILING DATE: 2000-10-2

PRIOR APPLICATION NUMBER: 09/704,918

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 2000-10-2

PRIOR APPLICATION NUMBER: 09/704,000

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-18

PRIOR FILING DATE: 2001-02-18

PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: 09/704,500

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11
                                                           Sequence 5, Application US/09788043C

Sequence 5, Application US/09788043C

Ratent No. USZ0020107361A1

GENERAL INFORMATION:

APPLICANT: Lau, Fengrong

APPLICANT: Klonowski, Paul

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: ROCH-004

CURRENT APPLICATION NUMBER: US/09/788, 043C

CURRENT FILING DATE: 2000-02-18

NUMBER OF SEO ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO S.
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1 Similarity 36.7%; Pred. No. 1.9e-14;
47; Conservative 22; Mismatches 56; Indels
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Best Local Similarity
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ORGANISM: human
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APPLICANT: Turecek, Peter
APPLICANT: Turecek, Peter
APPLICANT: Turecek, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a Polypeptide Chain with the Amino Acid Sequence AAGG
FILE REFERENCE: 247.00CIP
CURRENT APPLICATION NUMBER: US/09/833,328
CURRENT FILING DATE: 2000-104-12
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 15
SEQ ID NOS 25
SOFTWARE: PatentIn version 3.1
LENGTH: 133
TYPE: PRT
CORGANISM: human
US-09-833-328-2
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Patent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. US2020110894A1
Fatent No. INVENTION: US2020
FATENT FATENT NO. NUMBER: US/09/918,171A
CURRENT APPLICATION NUMBER: US/09/918,171A
FATENT FATENT NUMBER: 09/369,364
FATENT FATENT NUMBER: 09/369,364
FATENT FATENT NO. USC: 21
FATENT FATENT NO. USC: 21
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100.0%; Pred. No. 7.5e-72;
iive 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-7
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Matches 133; Conservative
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Patent No. US20020068319A1
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                                                                                                                                                                                                                                                                                                                                                                                72 SQTINPEDDTDPGHADLVLYITRFDLELPDGNR--QVRGVTQLGGACSPTWSCLITEDTG 129
                                                                                                                                                                                                                                                                                                                                                                                                        6 VFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLISSL 65
                                                                                                                                                                                                                                                                                                                                         12 EDTERYVLTNINIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGW 71
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kimble, Judith E
APPLICANT: Kimble, Judith E
APPLICANT: Manaloch, Robert H
TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386
CURRENT APPLICATION NUMBER: US/09/321,987B
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR APPLICATION NUMBER: 60/129,023
PRIOR APPLICATION NUMBER: 60/129,023
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 5.
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                                                                                                                                                                                                                                      Query Match
28.6%; Score 204.5; DB 9;
Best Local Similarity 34.6%; Pred. No. 1e-14;
Matches 44; Conservative 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%; Score 201; DB 10; 33.6%; Pred. No. 1.1e-13; tive 17; Mismatches 70;
   PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,408
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 16
LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 155, Application US/09800729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09321987B Patent No. US20020102210Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Caenorhabditis elegans US-09-321-9878-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.1%
Begt Local Similarity 33.6%
Matches 44; Conservative
                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo Bapiens
US-10-163-547-16
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US-09-800-729-155
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LENGTH: 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-321-987B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Sequence 7, Application US/09788043C

Sequence 7, Application US/09788043C

Parent No. US20020107361A1

GENERAL INFORMATION:

APPLICANT: Heller, Renu

APPLICANT: Klonowski, Paul

TITLE OF INVENTION: No. US2002107361A1el Metalloproteases Having

TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: ROCH-004

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/184,152

PRIOR APPLICATION NUMBER: 60/184,152

PRIOR APPLICATION NUMBER: 60/184,152

PRIOR FILING DATE: 2000-02-18

NUMBER OF SEO ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEC ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : : | : | | : : | | : : | | : : | 309 HGENLQHYELTHASIVASIYKDPSIGNLINIVIVNLIVIHNEQDGPSISFNAQTTLKNFC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 GWSQTINPEDDTDPG--HADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITED 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 ODFCRWQQYYNDPDDSSVQHHDVAILLTRKDICRSOGKCDTLGLABLGTMCDMQKSCAII 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2165;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
TITLE OF INVENTION: 32 Human secreted proteins
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PARENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%; Score 201; DB 10; 33.6%; Pred, No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.1%; Score 201; DB
Best Local Similarity 33.6%; Pred. No. 1.1e-
Matches 44; Conservative 17; Mismatches
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Best Local Similarity 30.2%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-800-729-155
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ORGANISM: human
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US-09-788-043C-7
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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: | | | | 424 SGLSTAFTI 432

20

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RESULT 15

US-09-972-467-2

Sequence 2, Application US/09972467

Patent No. US2020209373A1

GENERAL INFORMATION:

TELE CANT: PFIZER INC.

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/09/972,467

CURRENT PILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 2

LENGTH: 1629

TYPE: PRT

CORGANISM: Human

US-09-972-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 QWQHSKN----SPGGIHHDTAVLLTRQDICRAHDKCDTLGLAELGTICDPYRSCSISED 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 HOEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

26.2%; Score 187.5; DB 10; Length 1629;
Best Local Similarity 30.2%; Pred. No. 2.5e-12;
Matches 39; Conservative 28; Mismatches 55; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 20, 2003, 12:36:38 Job time : 26.0541 secs
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seqid\_1.rpr

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March 20, 2003, 12:32:34 ; Search time 2.18919 Seconds (without alignments) 526.959 Million cell updates/sec
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                           OM protein - protein search, using sw model
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57
1 AAGGILHLELLV 12
                                                                                                                                                                                           Title:
Perfect score:
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283224 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

283224 segs, 96134422 residues

Searched:

BLOSUM62 ...Gapext 0.5

Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hypothetical prote mobb protein - Thi hypothetical prote aminomethyltransfe ubiquinol-cytochro hypothetical prote hypothetical prote pullulanase (EC 3. phytochrome 1b - M cell adhesion 80K cell adhesion mole YCR37C homolog K08 protein K08E5.2 [i two-component hybr sodium/alanine sym translation elonga translation elonga prote 22K p prote RW1 protein - mous urotensin I precur ubiquinol-cytochro mitochondrial proc mitochondrial proc hypothetical hypothetical hypothetical Description \$62714 \$57535 T14280 \$36390 708807 A31643 A44100 \$43561 G88575 T31094 A72502 B97367 B71094 T35594 A44167 A48043 C98300 AD2983 A26879 G90142 A32840 T19710 ZPBOC1 AH2200 H82200 S75863 AC2348 UOCA1 Query Match Length DB 1142 1178 1829 Score Regult No.

RESULT 2 T08807

mitochondrial processing peptidase (EC 3.4.24.64) beta chain [similarity] - human mitochondrial processing peptidase (EC 3.4.24.64) beta chain [similarity] - human C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: T08807
R.Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
A.Reference number: 216472
A.Residues: 1.316 < ANS>
A.Residues: 1.316 < ANS>
A.Residues: 1.316 < ANS>
A.Residues: 1.316 < ANS>
A.Residues: 1.316 < ANS>
C.Constinental source: adult uterus; clone DKFZpS8611223
C.Genetics:

translation elonga	translation elongs	translation elonga	transducer protein	F7H2.22 protein -	pullulanase (EC 3.	pullulanase (EC 3.	hypothetical prote	ď	fixZ protein - Rhi	aspartate-semialde	hypothetical prote	alanine racemase (	NADH dehydrogenase	hypothetical prote	hypothetical prote
804429	804390	E75536	T48840	D86293	S38801	S11823	A71368	G83882	A22891	F96902	T20655	AE3556	A75388	D87597	T35924
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69	697	9	ã	6	10	2	Ñ	77	35	36	382	39	40	403	424
61.4 69	61.4 69		61.4 8	61.4 9		61.4 10									
61.4	61.4	61.4			61.4	61.4	59.6			59.6	59.6	59.6	59.6		59.6

ALIGNMENTS

RESULT 1
SJ6J6J6 pet a processing peptidase (EC 3.4.24.64) beta chain precursor (validated) N;Alternate names: beta-MPP; mitochondrial processing proteinase chain P52
C;Species: Kattus norvegicus (Norway rat) C;Date: 09-Dec-1993 #sequence_revision 14-Jul-1994 #text_change 31-Dec-2000 C:Accession: S;5390: S36391: PC1229
R.Paces, V.; Rosenberg, L.E.; Fenton, W.A.; Kalousek, F. Proc. Natl. Acad. Sci. U.S.A. 90, 5355-5358, 1993
A,Title: The beta subunit of the mitochondrial processing peptidase from rat liver b.beference number: 834390. MIID:93281757; PMID:8506385
A; Accession: S36390 A: Modernia type: m8NA
A.Residues: 1-489 <pac> A.Cross-references: GB:L12965; NID:q294588; PIDN:AAA41633.1; PID:g294589</pac>
A Accession: S36391
A;Molecule type: protein A;Residues: 46-67;92-104;116-125;409-423;432-441 <pa2></pa2>
C,Genetics:
A;Genome: nuclear C;Superfamily: mitochondrial processing peptidase alpha chain C;Revwords: hererodimer: hydrolase; metalloproteinase; mitochondrial matrix; mitoc
F)1-45/Domain: transit peptide (mitochondrion) #status predicted <tnp> F;46-489/Product: mitochondrial processing peptidase beta chain #status experiment F;101,105/Binding site: zinc (His) #status predicted</tnp>
F,104/Active site: Glu #status predicted
Query Match 70.2%; Score 40; DB 1; Length 489; Best Local Similarity 72.7%; Pred. No. 9.7; Watches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AAGGILHLELL 11  Db 243 AAGGVCHNELL 253

Gaps

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A;Note: no phosphoserine was detected but phosphoinositol and ceramide were A;Note: the N-linked carbohydrates are sulfated type I oligosaccharides C;Comment: This protein is involved in the formation of intercellular contacts upon C;Genetics:
A;Gene: csA
C;Reywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprotein; membra F;1-19/Domain: signal sequence #status predicted <SIG>F;20-514/Product: cell adhesion #8tatus predicted
F;20-514/Product: cell adhesion #status predicted
F;40-479/Region: cell adhesion #status predicted
F;40-479/Region: carboxyl-terminal propeptide #status predicted <CTP>F;132-139,294,399/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;492/Modified site: GSI-anchor ethanolamine amidated carboxyl end (Ser) (in matur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A44100
cell adhesion molecule gp80 - slime mold (Dictyostelium discoideum)
cell adhesion molecule gp80 - slime mold (Dictyostelium discoideum)
c;Species: Dictyostelium discoideum
c;Species: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: A44100
R;Desbarats, L; Lam, T;; Wong, L.M.; Siu, C.H.
J Biol. Chem. 267, 19655-19664, 1992
A;Title: Identification of a unique cAMP-response element in the gene encoding the A;Reference number: A44100; MUID:92406924; PMID:1326559
A;Contents: AX.
A;Accession: A44100
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-514 < DES-
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:113993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCR37C homolog KO8ES.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: S43561
R;Kershaw, J.
submitted to the EMBL Data Library, March 1994
A;Reference number: S43561
A;Accession: S43561
A;Accession: S43561
A;Accession: S43561
A;Residues: 1-526 KER>
A;Ross-references: EMBL: Z30974
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 38; DB 2; Length 514; 70.0%; Pred. No. 25; ive 3; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 38; DB 2;
70.0%; Pred. No. 25;
iive 3; Mismatches
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C, Superfamily: sodium/sulfate cotransporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 38; DB
80.0%; Pred. No. 26;
ive 1; Mismatches
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Matches 7; Conserv
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165 AGGLLNLELI 174
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Cell Biol. 107, 1832-1843, 1988
Title: Mapping of a cell-binding domain in the cell adhesion molecule gp80 of Dictyost; Reference number: A31643; MUID:89034443; PMID:3182938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Molecule type: mRNA
;Residues: 1-514 «KAM»
;Cross-references: GB136545; NID:g167803; PIDN:AAA33212.1; PID:g167804
;Noegel, A; Gerlsch, G.; Stadler, J.; Westphal, M.
MBO J. 5, 1473-1476, 1986
Tiltler Complete sequence and transcript regulation of a cell adhesion protein from agg
;Reference number: A26310
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A;Residues: 20-49 <WON>
A;Cross-references: GB:M13546; NID:g167699; PIDN:AAA33181.1; PID:g167700
R;Kamboj, R.K.; Gartepy, J.; Slu, C.H.
Cell 59, 615-625, 1989
A;Title: Identification of an octapeptide involved in homophilic interaction of the cell
A;Reference number: A33463; MUID:90058644; PMID:2582489
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Readduss: 1-215, G'. 217-514 <NOE>
Gross-references: EMBL:X04004; NID:g7246; PIDN:CAA27634.1; PID:g671860
Hong, L.M.; Siu, C.H.
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A; Reference number: A56857; MUID:89251561; PMID:2721485
A; Contents: annotation; detection of glycosphingolipidinositol anchor
                     A,Note: DKFZp58611223.1
C,Superfamily: mitochondrial processing peptidase alpha chain
C,Keywords: hydrolase; metalloproteinase; mitochondrion; oxidative phosphorylation; oxid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: cell adhesion molecule csA; cell surface glycoprotein, 80K C; Species: Dictyostelium discoideum)
NiAlternate names: cell adhesion molecule csA; cell surface glycoprotein, 80K C; Species: Dictyostelium discoideum
A; Variety: strain AX-2
C; Date: 31.Mar-1990 #sequence revision 31-Mar-1990 #text_change 01-Dec-2000
C; Accession: $22066; A31643; A23951; A33463; $01473
E; Debbarate, L.; Lam, T.Y.; Wong, L.M.; Siu, C.H.
submitted to the EMBL Date Library, June 1992
A; Description: Identification of a unique camp-responsive element in the gene encodidg
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Hoppe-Seyler's Z. Physiol. Chem. 363, 771-776, 1982
A;Title: Improved purification and N-terminal amino acid sequence determination of the A;Reference number: S01473; MUID:83005404; PMID:7118072
A;Reference Navession: S01473
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Pred. No. 15;
1; Mismatches 2; Indels
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;Reaidues: 20-37,'X',39-41,'X',43-46 <STA>
;Stadler, J.; Keenan, T.W.; Bauer, G.; Gerisch,
MBO J. 8, 371-377, 1989
                                                                                                                                                         Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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Residues: 132-139 <KA2>
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Residues: 1-514 <DES>
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A, Accession: A72502
A, Status: preliminary
A, Molecule type: DNA
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A, Residues: 1-116 «KAW>
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R.She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Red arrett, RA.; Ragam, M.A.; Sensen, C.W.; Van der Oost, J. A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A99139  
A;Accession: B90387  
A;Status: preliminary A;Molecule type: DNA
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C.Species: Thiobacillus ferrooxidans
C.Species: Thiobacillus ferrooxidans
C.Species: Thiobacillus ferrooxidans
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C.Accession: S12190
A.Fitle: The mobilization and origin of transfer regions of a Thiobacillus ferroox A.Faccession: S12180
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C;Genetics:
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66.7%; Pred. No. 26;
cive 1; Mismatches 3; Indels
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ive 3; Mismatches 1; Indels
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Matches 8; Conservative
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44 AAGGLQHLE 52
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                                                                                                                                                                                                                                                                                   protein KOBES.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: G88575
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared* in Science 283, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurface antigen BapA - Bacteroides forsythus
Cispecies: Bacteroides forsythus
Cispecies: Date: Oc.Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
Cispecies: Tal094
RiSharma, A.; Sojar, H.T.; Glurich, I.; Honma, K.; Kuramitsu, H.K.; Genco, R.J.
Aificle: Immun. 66, 5703-5710, 1998
Aificle: Cloning, expression, and sequencing of a cell surface antigen containing a leuch Aireference number: 220977; MUID:99043895; PMID:9826345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE1991 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: A72502
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jan-aki, J.; K bNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:chr_III; PIDN:CAA83225.1; PID:g3878357; GSPDB:GN00021; CESP:K08E5
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Molecule type: DNA
Residues: 1-1081 <SHA>
Cross-references: EMBL:AF054892; NID:g3005672; PID:g3005673; PIDN:AAC82625.1
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Pred. No. 58;
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A,Cross-references: GB:chr_III, PIDN:CAA83322
A,Genetics: A,Gene: K085.2
A,Map position: 3
C,Superfamily: sodium/sulfate cotransporter
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Best Local Similarity 80.v.
-Lag 8; Conservative
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              485 GGIISLELLV 494
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Best Local Similarity
Matches 8; Conserv
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Molecule type: DNA
Residues: 1-534 <STO>
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A,Residues: 1-
A,Cross-refere
C,Genetics:
A,Gene: bspA
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A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-392 CASA>
A/Residues: 1-392 CASA>
A/Cross-references: GB:D1162; NID:g222867; PIDN:BAA01937.1; PID:g222868
A/Cross-references: GB:D1162; NID:g222867; PIDN:BAA01937.1; PID:g222868
A/Experimental source: liver
A/Note: sequence extracted from NCBI backbone (NCBIN:113296, NCBIP:113297)
A/Note: parts of this sequence, including the amino end of the mature protein, wer
R/Okamura-Ikeda, K.; Fujiwara, K.; Yamamoto, M.; Hiraga, K.; Motokawa, Y.
J. Biol. Chem. 266, 4917-4921, 1991
A/FILE: Isolation and sequence determination of CDNA encoding T-protein of the gl
A/Reference number: A23707; MID:91161577; PMID:2002038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 179-392 < OK2>
A; Molecule type: mRNA
A; Residues: 179-392 < OK2>
A; Mote: part of this sequence was confirmed by protein sequencing
C; Comment: A mutation of the T-protein in humans leads to nonketotic hyperglycines
C; Comment: A mutation of the T-protein in humans leads to nonketotic hyperglycines
C; Superfamily: aminomethyltransferase
C; Keywords: mitochondrion; transferase
C; Keywords: mitochondrion; transferase
F:1-16/Domain: transit peptide (mitochondrion) #status predicted <MAT>
F:17-392/Product: aminomethyltransferase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein I - human N.Alternate names: cytochrome bcl core I protein CSpecies: Homo sapiens (man) CSpecies: Homo sapiens (man) C.Date: 02-Jun-1995 #text_change 03-Jun-2002 CAccession: A48043; IS2367 C.Accession: A48043; IS2367 C.Atritiano, A.M.; Chung-Honet, L.C.; Cheng, W.; Katchmai J. Biol. Chem. 268, 21113-21119, 1993 A.Fitle: Complete coding sequence, intron/exon organization, and chromosomal local A.Feference number: A48043; MUID:94012661; PMID:8407948
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A, Molecule type: DNA
A, Residues: 1-480 < +40F>
A, Residues: 1-480 < +40F>
A, Residues: 1-480 < +40F>
A, Cross references: GBLL16842; NID: 9349472; PIDN: AAA20046.1; PID: 9515634
R, Islam, M.M., Tanaka, M.; Suzuki, H.; Torii, K.; Hattori, Ma; Ozawa, T.
Biochem Mol. Biol. Int. 32, 797-805, 1994
A, Title: A complete cDNA sequence for core I protein subunit of human ubiquinol-c; A, Reference number: I52367; MUID: 94348430; PMID: 8069229
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A;Molecule type: mRNA
A;Residues: 1-300,'N',302-480 <1SL>
A;Residues: 1-300,'N',302-480 <1SL>
C;Coss-references: GB:DZ6485; NID:g468934; PIDN:BAA05495.1; PID:g468935
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C;Superfamily: mitochondrial processing peptidase alpha chain
C;Keywords: oxidoreductase
translational initiation region on expression.
A;Reference number: A44167; MUID:92406724; PMID:1526969
A;Accession: A44167
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C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1991 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A4167; B23707
R;Okamrainea, K.; Fujiwara, K.; Motokawa, Y.
J. Biol. Chem. 267, 18284-18290, 1992
A;Title: Molecular cloning of a cDNA encoding chicken T-protein of the glycine cleavage
                                                                                                                                                                                                                                    hypothetical protein Rv3365c - Mycobacterium tuberculosis (strain H37RV)

(Species: Mycobacterium tuberculosis

(Species: Mycobacterium tuberculosis

(Species: Mycobacterium tuberculosis

(Spacesion: D70971

R)Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998

Nature 393, 537-544, 1998

A; Atthore Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Reference number: A70500; MUID: 98295987; PMID: 9634230
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-233 NAM-
A;Residus: 1-233 NAM-
A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SC6G4.43c
A;Experimental source: strain A3(2)
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Pygothetical protein AGR L 2721 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium_tumefaciens
C; Species: Agrobacterium_tumefaciens
C; Species: Agrobacterium_tumefaciens
C; Species: Agrobacterium_tumefaciens
C; Squees: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C; Accession: C98300
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Reference number: A97359; PMID:11743194
A; Recession: C98300
A; Status: preliminary
A; Accession: C98300
A; Status: preliminary
A; Residues: 1-505 *KUR>
C; Geneciue type: DNA
A; Residues: 1-505 *KUR>
C; Geneciue type: DNA
A; Residues: 1-505 *KUR>
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107 AAGGVAHLMCVV 118
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Q8xvIO raletonia a 206457 klebsiella 20458 caenorhabdi p08443 synechococc 09qyb9 mus musculu 043557 home saplen P29541 streptomyce p30844 escherichia p08412 synechococc p76198 escherichia 09c124 pasteurella

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAWARI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa T., Bhinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Anatawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Anatawa T., Saito R., Satto T., Saito T., Saito R., Sadto T., Matsuda H., Ashburner M., Batalov S., Casavant T., Saito R., Redota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Satto R., Kadota K., Matsuda H., Risaito I., Pesole G., Quackenbush J., Rochim L.M., Staubli F., Suzuki R., Tomita M., Wagnar L., Washio T., Ra Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., R. Bata J., Boffelli D., Hofmann M., Carninci P., de Bonaldo M.F., Bulta V., Bult C., Flutta M., Gariboldi M., A Brownstein M.J., Bult C., Flutcher C., Fulita M., Gariboldi M., A Brownstein M.J., Bult C., Flutcher C., Fulita M., Gariboldi M., A Brownstein M.J., Bult C., Flutcher C., Fulita M., Ramaya M., Lee N.H., A Marchime P., Ringwald M., Rodriguez I., Sakamoco N., A Saaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stořch K.-F., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A Hayashizaki Y., Kawaji H., Kohtsuki S., Marchimal annoteation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
-- CATALYTIC ACTIVITY: Release of N-terminal transit peptides from precursor proteins imported into the mitochondrion, typically with Arg in position P2.
-- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Mitochondrial matrix (BY similarity).
-- SUBCELLULAR LOCATION: Mitochondrial matrix (BY similarity).
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitochondrial processing peptidase beta subunit, mitochondrial precursor (EC 3.4.24.64) (Beta-MPP) (P-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: THE MITOCHONDRIAL PROCESSING PROTEASE CLEAVES PRESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS (BY
                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Embryonic head;
MEDLINE=21085660; PubMed=11217851;
                          NASA_KLEPN
YNXS_CAEEL
ATPZ_SYNP6
TN14_MOUSE
TN14_HUMAN
EFG_STRRA
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RESULT 1
MPPB_MOUSE
ID _MPPB_MOUSE
AC Q9CXT8;
 4444MMMMMMMM
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rhizobium s
homo sapien
homo sapien
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                                                                                                         March 20, 2003, 12:32:11 ; Search time 1.45946 Seconds (without alignments) 341.028 Million cell updates/sec
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P07206
O9vaf0
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O8yd03
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P20464
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Q8xrm7
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                 GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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PULA_KLEAE
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URI_CYPCA
YTRE_LEPBI
UCRI_BOVIN
EFG2_SYNY3
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MPPB_RAT
MPPB_RAT
WAZZ_CAEEL
CSA_DICDI
MOBL_THIPE
GCST_CHICK
FIXC_RHISN
UNRI_HUMAN
UCRI_MOUSE
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HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                                                                              - protein search, using sw model
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57
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Result

seqid 1.rsp

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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a
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Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THE MITOCHONDRIAL PROCESSING PROTEASE CLEAVES
PRESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS.

-!- CATALYTIC ACTIVITY: Release of N-terminal transit peptides from precursor procesins imported into the mitochondrion, typically wider in position P2.

-!- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY.

-!- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.

-!- SUBCELLUMAR LOCATION: MILOCHONDRIAL MATTIX.
                                        InterPro; IPR00143; Peptidase M16.
Pfam; PF00675; Peptidase M16; 1.
PROSITE; PS00143; INSULINASE; 1.
Hydrolase; Metalloprotease; Mitochondrion; Transit peptide.
TRANSIT 46 M19 MITOCHONDRION (POTENTIAL).
CHAIN 46 MITOCHONDRIAL PROCESSING PEPTIDASE
                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN. 1994 (Rel. 29, Created)
01-JUN-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitochondrial processing peptidase beta subunit, mitochondrial
precursor (EC 3.4.24.64) (Beta-MPP) (P-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley, TISSUE=Liver;
MEDLINE=93281757; PubMed=8506385;
MEDLINE=93281757; PubMed=8506385;
Paces V., Rosenberg L.E., Fenton W.A., Kalousek F.;
"The beta subunit of the mitochondrial processing peptidase liver: cloning and sequencing of a cDNA and comparison with proposed family of metallopeptidases.";
Proc. Natl. Acad. Sci. U.S.A. 90:5355-5358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE=93135783; PubMed=8422255;
Kitada S., Niidome T., Nagano T., Ogishima T., Ito A.;
"Molecular cloning of the smaller subunit (F52) of rat liver
                                                                                                                                                                                                                                                    Score 40; DB 1; Length 489;
                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                ZINC (BY SIMILARITY).
BY SIMILARITY.
ZINC (BY SIMILARITY).
1B594EE086FE34A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial processing protease.";
Biochem. Biophys. Res. Commun. 190:289-293(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16
                                                                                                                                                                                                                                            70.2%; Score 40, 72.7%; Pred. No. 4.6;
                                                                                                                                                  BETA SUBUNIT.
ZINC (BY SIMI)
                               MGD; MGI:1920328; 3110004018Rik.
                                                                                                                                                                                                                     54614 MW;
               EMBL; AK013995; BAB29105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 3-489 FROM N.A.
                                                                                                                                                                                                                                                                      Local Similarity 72.7
1es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                       243 ÁÁGGVCHNELL 253
                                                                                                                                                                  101
104
105
189 AA;
                                                                                                                                                                                                                                                                                                                       1 AAGGILHLELL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                        MPPB_RAT
ID MPPB_RAT
AC Q03346;
                                                                                                                                                                  METAL
ACT SITE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98318631; PubMed=9653160;
MEDLINE=98318631; PubMed=9653160;
MEDLINE=98318631; PubMed=9653160;
MEDLINE=98318631; PubMed=9653160;
MEDLINE: G. G. Men Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Chen Z.-J. Che
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      | METAL | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 10
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitochondrial processing peptidase beta subunit, mitochondrial
precursor (EC 3.4.24.64) (Beta-MPP) (P-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1; Length 489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98B56A8C6289F852 CRC64;
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-i- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
-i- SUBCELLULAR LOCATION: Mitochondrial matrix.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                           EMBL; L12965; AAA41633.1; -. EMBL; D13907; BAA03007.1; -. PIR; PC1229; PC1229. MEROPS; M16.003; -.
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243 AAGGVCHNELL 253
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489 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Durbin R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE NADC/P/PHOB7 FAMILY OF TRANSFORTERS.
                                                      InterPro; IPR001431; Peptidase_M16.
Pfam; PF00675; Peptidase_M16; 1.
PROSITE; PS00143; INSULINASE; 1.
Hydrolase; Metalloprocease; Mitochondrion; Transit peptide.
TRANSIT 46 489 MITOCHONDRIAL PROCESSING PEPTIDASE
METAL 101 101 ZINC (BY SIMILARITY).
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                                                                                                                                                                                       h Similarity 72.7%; Score 38; DB 1; Length 489; Similarity 72.7%; Pred. No. 11; 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kershaw J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            BY SIMILARITY.
ZINC (BY SIMILARITY).
440A25A3E4486D64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 230974; CAA89225.2; ---
WormPep; K08E5.2; CE28598.
InterPro; IPR001898; Na/Bulf symp.
Pfam; PF00393; Na sulph.symp; 1.
TIGRFAMS, TIGRO0785; dass; 1.
PROSITE; PS01271; Na SULFATE; 1.
FRANSMEM 94 114 POTENTIAL.
TRANSMEM 151 171 POTENTIAL.
TRANSMEM 200 220 POTENTIAL.
TRANSMEM 201 220 POTENTIAL.
TRANSMEM 201 220 POTENTIAL.
TRANSMEM 201 220 POTENTIAL.
TRANSMEM 201 2304 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein K08E5.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                  498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                    489 AA; 54167 MW;
               EMBL; AF054182; AAC39915.1;
                                                                                                                                                                                                                                                                                                                   STANDARD;
                         MEROPS; M16.003; -.
Genew; HGNC:9119; PMPCB.
                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                    101
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243 AAGGVSHDELL 253
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                                                                                                                                                                                                                                     1 AAGGILHLELL 11
                                                                                                                                                                                                     Local Similarity
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                                                603131;
                                                                                                                                                                                                                                                                                                                   CAEEL
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ACT SITE
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                                                                                                                                                                                          Query Match
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Wong L.M., Siu C.-H.;
Wong L.M., Siu C.-H.;
"Cloning of cDNA for the contact site A glycoprotein of Dictyostellium discoideum.";
Proc. Natl. Acad. Sci. U.S.A. 83:4248-4252(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPI-ANCHOR.

MEDLINE-89251561; PubMede-2721485;
Stadler J., Keenan T.W., Bquer G., Geriach G.;
Stadler J., Keenan T.W., Bquer G., Geriach G.;
The contact site A glycoprotein of Dictyostelium discoideum carries a phospholipid anchor of a novel type.";
EMBO J. 8:371-377(1989).
-!- FUNCTION: THIS CELL-SURFACE GLYCOPROTEIN MEDIATES CELL-CELL BINDING VIA HOMOPHILIC INTERACTION.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR THAT CONTAINS A PHOSPHOCERAMIDE MOIETY. SUCH ANCHOR MEDIATES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL-BINDING DOWAIN.
MEDLINE=89034443; PubMed=3182938;
Kamboj R.K., Wong L.M., Lam T.Y., Siu C.H.;
"Mapping of a cell binding domain in the cell adhesion molecule gp80
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noegel A., Gerisch G., Stadler J., Westphal M.; "Complete sequence and transcript regulation of a cell adhesion protein from aggregating Dictyostelium cells."; EMBO J. 5:1473-1476(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINES9163296; MEDLINES9105326; PubMed=1063296; Siu C.-H., Wong L.M., Lam T.Y., Kamboj R.K., Choi A., Cho A.; Molecular mechanisms of cell-cell interaction in Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSA DICDI STANDARD; PRT; 514 AA.
P08756; P19408;
01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Contact site A protein precursor (CSA) (Membrane-associated glycoprotein GP80) (Cell adhesion molecule GP80).
                                                                                                                                         Score 38; DB 1; Length 498; Pred. No. 11;
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                     POTENTIAL.
POTENTIAL.
FAEDB2FAA694BCB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                         Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Cell Biol. 66:1089-1099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 267:19655-19664(1992).
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J. Cell Biol. 107:1835-1843(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92406924; PubMed=1326559;
332 352 PO
371 391 PO
428 448 PO
498 AA; 54517 MW;
                                                                                                                                            66.7%;
                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                         457 GGIISLELLV 466
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FAST AND LONG PERSISTENCE CELL ADHESION OF THE PROTEIN.
DEVELOPMENTAL STAGE: RESTRICTED TO THE AGGREGATION STAGE OF
DEVELOPMENT OF D.DISCOIDEUM.
PTW. ACYLATED, PHOSPHORYLATED ON SERINE AND N-GLYCOSYLATED WITH
TWO TYPES OF OLIGOSACCHARIDE CHAINS.
MISCELLANGOUS: THE EXPRESSION OF THIS STRINGENTLY REQULATED
PROTEIN DURING CELL DEVELOPMENT IS MEDIATED THROUGH CELL-SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                       CAMPA RECEFLORS.
SIMILARITY: THE G-TERMINAL REGION CONTAINS CLUSTERS OF PROLINE REGULARLY ALTERNATING WITH A HYDROXYAMINO ACID AND SHOWS SIMILARITY TO THE HINGE REGION OF IMMUNOCLOBULINS. THIS DOMAIN MIGHT ACT AS A SPACER TO ELEVATE SITES ACTIVE IN CELL CONTACT INTO THE EXTRACELLULAR SPACE.
                                                                                                                                                                                                                                                                                                                                             PIR; A23951; A23951.
PIR; A26310; A26310.
PIR; A26410; A26110.
PIR; A44100; A44100.
DictyDb; D0202005; csaA.
InterPro; IPR002099; IPT_IG.
Pfam; PF01833; TIG; 3
Cell adhesion; Glycopic. cia...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTACT SITE A PROTEIN.
REMOVED IN MATURE FORM (FOTENTIAL)
GROBULAR (POTENTIAL).
PRO-RICH (HINGE STRUCTURE).
2 X 8 AA REPEATS, PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thiobacillus ferrooxidans.
Plasmid pTF1.
Bacteria, Proteobacteria, gamma subdivision, Acidithiobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 38; DB 1; Length 514; 70.0%; Pred. No. 12; Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96A1C7CF42FEC096 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI-ANCHOR (POTENTIAL).
V -> G (IN REF. 1).
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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N-LINKED (GLCNAC.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Mobilization protein mobb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53696 MW;
                                                                                                                                                                                                                                                                                                         EMBL; X04004; CAA27634.1; -. EMBL; M36545; AAA33212.1; -. EMBL; X66483; CAA47110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AGGLLNLELI 174
                                                                                                  CAMP RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPI-anchor, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THIFE
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CARBOHYD
CARBOHYD
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CARBOHYD
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REPEAT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine
                                         J. Bioi. Chem. 266:4917-4921(1991).
-!- FUNCTION: The glycine cleavage system catalyzes the degradation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-32406724; PubMed=1526969;
MEDLINE-32406724; PubMed=1526969;
MOSTALINE-32406724; PubMed=1526969;
MOSTALINE-324063 K., Fujiwara K., Moctokawa Y.,
"Molecular cloning of a cDNA encoding chicken T-protein of the
glycine cleavage system and expression of the functional protein in
Escherichia coli. Effect of mRNA secondary structure in the
translational initiation region on expression.";
J. Biol. Chem. 267:18284-18290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE=91161577; PubMed=2002038;
Okamura-Ikeda K., Fujiwara K., Yanamoto M., Hiraga K., Motokawa Y.;
"Isolation and sequence determination of cDNA encoding T-protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005053; MobA_MobL.
Pfam; PF03389; MobA MobL; 1.
Mobility protein; Plasmid; Trans-acting factor; Conjugation.
SEQUENCE 378 AA; 42636 MW; 4ARE915308C0C194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.9%; Score 37; DB 1; Length 378; 60.0%; Pred. No. 13; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aminomethyltransferase, mitochond
cleavage system T protein) (GCVT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the glycine cleavage system.";
                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52699; CAA36927.1; -. PIR; S12190; S12190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 179-392 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGILHLELLV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GGVLHSELIL 55
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P28337;
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GCST_CHICK
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glycine.

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Genome Res. 6:590-600(1996).

--- PUNCTION: COULD BE REQUIRED FOR THE FORMATION OF A FUNCTIONAL NITROGRNASE FE PROTEIN. PROBABLY ACCEPTS ELECTRONS FROM FIXA/FIXB AND REDUCES A QUINONE.
--- COFACTOR: FAD (POTENTIAL).
--- SIMILARITY: BELONGS TO THE ETF-QO / FIXC FAMILY.

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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: (6S)-tetrahydrofolate + S-
mainomethyldhydrolipoylprotein = (6R)-5.10-
methylenetetrahydrofolate + NH(3) + dihydrolipoylprotein.
SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:
B, T, L, AND H.
SUBCELLULAR LOCATION: Mitochondrial.
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE GCUT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
"Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid sym pNGR234a.
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=96389014; PubMed=8796346;
Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium NGR234 using the 500-kb GC-rich symbiotic replicon of Rhizobium NGR234 using dye terminators and a thermostable 'sequenase': a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                       Transferase, Aminotransferase, Mitochondrion, Transit peptide TRANSIT 1 16 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 392;
Pred. No. 22;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINOMETHYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                      PIR: B23707; B23707.

PIR: A44167; A44167.

PINCERPRO: IPRO02536; GCV_T.

FERM: PF01571; GCV_T, 1.

TIGREAMS; TIGR00528; GCV_T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%;
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 . AA;
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FIXC OR Y4UP.
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A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

A Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,

A Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,

A Chki M., Takagi T., Sakaki Y., Taudian S., Blechschmidg K., Polley A.,

A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

A Rosenthal A., Kudoh J., Shibuya M., Schudy A., Zimmermann W.,

A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,

A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,

A Mamser J., Beck A., Klagse S., Hennig S., Riesselmann L., Dagand E.,

A Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

Lehrach H., Reinhardt R., Yaspo M.-L.;

When A sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P56182; 09NST5;
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NNNP-1 procesin (Novel nuclear protesin 1) (Nucleolar protesin Nop52)
NNP-2008 (D2182056E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                        Nitrogen fixation; Oxidoreductase; FAD; Flavoprotein; Plasmid.
NP BIND 8 22 FAD (ADP PART) (POTENTIAL).
SEQUENCE 415 AA; 47536 MW; 5C4113C66F84BA61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemar
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                       08 1;
                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 36; DB 45.5%; Pred. No. 24; tive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97336061; PubMed=9192856;
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                                                                                                                                                                                                               EMBL; Z68203; CAA92415.1; -.
                                                                                                                                                                                                                                               EMBL; AE000100; AAB91888.1;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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150 AGGVIHADVVV 160
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CHARACTERIZATION
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Duesterhoeft A.
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Mol. Biol. Int. 33:410-410(1994).
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial
UQCRC1.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta;
MEDLINE-94012661; PubMed-8407948;
Hoffman G. Lee S., Christiano A.M., Chung-Honet L.C., Cheng W.,
Katchman G., Lee S., Christiano D.S.;
"Complete coding sequence, intron/exon organization, and chromosomal
location of the gene for the core I protein of human ubiquinol-
cytochrome c reductase.";
                                                          J. Cell Sci. 112:1889-1900(1999).
-!- FUNCTION: PLAYS A CRITICAL ROLE IN THE GENERATION OF 28S RRNA.
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN FETAL AND ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiena (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fibroblast;
MEDLINE=94348430; PubMed=8069229;
MIDAINE=94348430; PubMed=8069229;
MEDLINE=94348430; PubMed=8069229;
"A complete cDNA sequence for core I protein subunit of human ubiquinol-cytochrome c reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95038519; PubMed-7951059;
Islam M.M., Tanaka M., Suzuki H., Torii K., Hattori N., Ozawa T.;
MEDLINE=99276573; PubMed=10341208; Savino T.M., Bastos R., Jansen E., Hernandez-Verdun D.; "The nucleolar antigen Nop52; the human homologue of the yeast ribosomal RNA processing RRP1, is recruited at late stages of
                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                    63.2%; Score 36; DB 1; Length 461; 72.7%; Pred. No. 26; 1.0e 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                 126 K -> R (IN REF. 4). . . 52819 MW; C6F204EF4161AEAE CRC64;
                                                                                                                         -!- SIMILARITY: BELONGS TO THE NNP-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Mol. Biol. Int. 32:797-805(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT ASN-301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :ochrome c reductase.";
Biol. Chem. 268:21113-21119(1993).
                                                                                                                                                                                                                                                 EMBL, U79775; AACS1625.1; -.
EMBL, BR001752; BAA95542.1; -.
EMBL, BC000380; AAH00380.1; -.
EMBL, AL137757; CAB70909.1; -.
CONFLCT 326
SEQUENCE 461 AA, 52839 MW; CC
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 72.7
ses 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       43 AAGGFTHDELL 53
                                                                                                                                                                                                                                                                                                                                                                                                       1 AAGGILHLELL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                   nucleologenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                       Query Match
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P31930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Genet. 104:460-466(1999).

-!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III OR CYTOCHROME B-I COMPLEX), WHICH IS PART OF THE MITOCHOMBIAL RESPIRATORY CHAIN. THIS PROTEIN MAY MEDIATE FORMATION OF THE COMPLEX BETWEEN CYTOCHROMES C AND CI.

-!- CATALYTIC ACTIVITY: OH(2) + 2 ferricytochrome c = 0 + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001431; Peptidase M16.
Pfam; PF00675; Peptidase M16; I.
PROSITE; PS00143; INSULINAE; FALSE NEG.
Mitochondrion; Inner membrane; Electron transport; Respiratory chain; Oxidoreductase; Transit peptide; Polymorphism.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10453733;
Valnot I., Kassis J., Chretien D., de Lonlay P., Parfait B.,
Munnich A., Kachaner J., Rustin P., Roetig A.;
Mairochondrial cyrochrome b mutation but no mutations of nuclearly
encoded subunits in ubiquinol cytochrome c reductase (complex III)
deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN I.
S -> N.
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                                  K., Hattori N., Ozawa T.;
                                                                                                                                                                                                       Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C., Tissoc J.-D., Bairoch A., Appel R.D., Hochstrasser D.F., "Human liver protein map: update 1993."; Electrophoresis 14:1216-1222(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 013629
MEDLINE-9507255; PubMed=7981668;
Islam M.M., Tanaka M., Suzuki H.; Torii K.,
Biochem. Mol. Biol. Int. 33:815-815(1994).
                                                                                                                                                                           MEDLINE=94147969; PubMed=8313870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L16842; AAA20046.1; --
EMBL; D26485; BAA05495.1; --
HSSP; P31800; 1BE3.
MEROPS; M16.973; --
SWISS-2DPAGE; P31930; HUMAN.
PHCI-2DPAGE; P31930; --
HSC-2DPAGE; P31930; --
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Genew; HGNC:12585; UQCRC1.
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480
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                                                                                                                   SEQUENCE OF 35-45.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                             VARIANT ASN-301.
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233 AAGGVEHQQLL 243
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                                                                                                                                                                                                                                                                                                                                                                                                             RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Masuda H.A., Ashburnar M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
RA Felschmann W., Gaasterland T., Glssi C., King B., Kochiwa H.,
RA Kedota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
RA Felschmann W., Gaasterland T., Glssi C., King B., Kochiwa H.,
RA Kedota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
Raka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rousincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Rilngwald M., Rodriguez I., Sakamoto N.,
Nordone P., Ring B., Rilngwald M., Rodriguez I., Sakamoto N.,
Nordone P., Ring B., Rilngwald M., Rodriguez I., Sakamoto N.,
Nynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki V.,
                                         UCRI MOUSE STANDARD;
096213; 095WL6;
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ferrocytochrome c.
-!-SUBUNIT: BC1 COMPLEX CONTAINS 11 SUBUNITS; 3 RESPIRATORY SUBUNITS (CYTOCHROME B, CYTOCHROME C1, RIESKE PROTEIN), 2 CORE PROTEINS AND 6 LOW-MOLECULAR WEIGHT PROTEINS (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX), WHICH IS PART OF THE MITOCHONBIAL RESPIRATORY CHAIN. THIS PROTEIN MAY MEDIATE FORMATION OF THE COMPLEX BETWEEN CYTOCHROMES C AND C1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CAUTION: DOES NOT SEEM TO HAVE A PROTEASE ACTIVITY AS IT LACK THE ZINC-BINDING SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00675; Peptidase M16; Ī.
PROSITE; PS00143; INSULIÑASE; FALSE NEG.
Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptidase M16.
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK013128; BAB28666.1; -. EMBL; AK010553; BAB27022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:107876; Ugcrc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P31800; 1BE3
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
RESULT 11
UCRI_MOUSE
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                                                                                                                                                            ö
           MITOCHONDRION (BY SIMILARITY).
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX
CORE PROTEIN I.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aerogenes W70.";

J. Bacteriol. 169:2301-2306(1987).

-1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
-1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
-1 inkages in pullulan and in amylopectin and glycogen, and the alpha- and beta-limit dextrins of amylopectin and glycogen.
-1- SUBUNIT: HOWOTRIMER.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUN-2002 (Rel. 41, Last annocation update)
Pullulanase precursor (EC 3.2.1.41) (Alpha-daxtrin endo-1,6-alpha-
glucosidase) (Pullulan 6-glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Probable).
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87194626; PubMed=3155373;
Katsuragi N., Takizawa N., Murooka Y.;
"Entire nucleotide sequence of the pullulanase gene of Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                            ..
                                                                                                                          63.2%; Score 36; DB 1; Length 480;
63.6%; Pred. No. 27;
tive 2; Mismatches 2; Indels
                                                         N -> H (IN REF. 1; BAB27022)
C -> Y (IN REF. 1; BAB27022)
9C6D480DC9D5E429 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
WHY FE7D9167CDACFD79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Hydrolase; Glycosidase; Membrane; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                             PRT; 1096 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000461; Alpha amylase.
InterPro; IPR004193; Isoamylase N.
InterPro; IPR005323; PUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M16187; AAA25124.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase N; 1.
Pfam; PF03714; PUD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119335 MW;
Oxidoreductase; Transit peptide.
                                                             223 223 N
318 318 C
480 AA; 52768 MW;
                                                                                                                                           Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
                              480
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233 AAGGVEHQOLL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella aerogenes
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                                                                                                                                                                                              1 AAGGILHLELL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=28451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A26879
                                                                                                                                                                                                                                                                                                                PULA KLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella.
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ACT_SITE
ACT_SITE
SEQUENCE
                                                             CONFLICT
CONFLICT
SEQUENCE
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                 TRANSIT
                                                                                                                                                                                                                                                                                RESULT 12
PULA_KLEAE
                              CHAIN
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RW1 MOUSE
070472;
  HUMAN
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RW1 MOUSE
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X89016; CAA61423.1; -.
EMBL; Z71363; CAA5963.1; -.
HSSP, P21707; 1BTN.
HSSP, S0005031; YNLO87W.
InterPro; IPR000008; C2.
Pfam; PF00168; C2; 3.
SMART; SM0039; C2; 4.
PROSITE; PS50004; C2 DOMAIN 2; 3.
Hypothetical protein; Transmembrane; Repeat.
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                                                  Gaps
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MEDLINE-96310628; PubMed-8740422;
Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M.;
Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M.;
The sequence of a 17,933 bp segment of Saccharomyces cerevisiae chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and fnew open reading frames.";
The sequence of a 17,933 bp segment of Saccharomyces cerevisiae chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and fnew open reading frames.";
The STREELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 132.5 kDa protein in TOP2-MKT1 intergenic region.
YNLO87W OR N2250.
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Score 36; DB 1; Length 1096; Pred. No. 63; 2; Indels 3; Mismatches 2; Indels
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Matches 6; Conservative
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Matches 6; Conserv
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YNI7_YEAST
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AC P48231;
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RESULT 14

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TISSUB-Bone marrow;

MEDILE=97191544; PubMed=9039502;

MEDILE=97191544; PubMed=9039502;

MAGABE T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

"Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";

DNA Res. 3:321-329(1996).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RWI Drotein (Fragment).
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169 SSGGDLHLEL 178
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                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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EMBL; AF060565; AAC15232.1; -.
MGD; MGI:1927110; Rwl.
SEQUENCE 1829 AA; 200508 MW; D0B3E209257AFAE9 CRC64;
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197 SSGGDLHLEL 206
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380, App 380, App 380, App 378, App 378, App 27, Appl 2, Appl

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US-09-605-785-380 US-09-439-313-380 US-09-505-313-380 US-09-605-785-378 US-09-352-616A-378 US-09-314-601-27 US-09-334-601-27 US-09-334-601-27 US-08-484-635-118 US-08-827-570-118 US-09-134-001C-4740 US-09-153-336-6

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US-09-389-705-6 US-09-357-905-9 PCT-US94-00666-6

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Corley, Noil C.
TITLE OF INVENTION: WITCHONDRIAL PROCESSING PEPTIDASE
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.2%; Score 40;
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ATTORNEY/AERT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08895521
Patent No. 5869311
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SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 TOPOLOGY: Inear
IMMEDIATE SOURCE:
ILBRARY: GenBank
CLONE: 294589
US-08-895-51-3
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STATE: C
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                                                                                                     March 20, 2003, 12:33:39 ; Search time 1.94595 Seconds (without alignments) 181.441 Million cell updates/sec
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Seguence 12
Seguence 5,
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Sequence 4,
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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-235-218-3
US-09-235-218-1
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US-08-904-871-4
US-08-904-871-12
US-08-913-014A-2
US-08-913-014A-3
US-08-913-014A-3
US-08-913-014A-3
US-08-913-014A-3
US-08-913-014A-3
US-08-913-014A-3
US-09-072-993C-4
US-09-072-993C-4
US-09-073-08-2
US-09-130-663-2
US-09-413-814-99
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US-09-413-814-99
US-09-911-882-29
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US-09-439-313-379
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Maximum Match 100%
Listing first 45 summaries
                                                                                protein search, using sw model
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Match Length DB
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Length 489;

DB 2;

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PF-0343

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Score 38; DB 2; Length 489;
Pred. No. 37;
1; Mismatches 2; Indels
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Patent No. 6001629
GENERAL INFORMATION:
APPLICANT: Shah, Purvi
APPLICANT: Corlab, Purvi
APPLICANT: Corlab, Nail C.
TITLE OF INVENTION: SUBUNIT
TITLE OF INVENTION: SUBUNIT
  APPLICANT: Corley, Neil C.
TITLE OF INVENTION: MITOCHONDRIAL PROCESSING PEPTIDASE
TITLE OF INVENTION: MUDORIT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyce Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CARE
                                                                                                                                                                                                  COUNTY ON THE STANDARD FORM:

MEDIUM TYPE: Diskette COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: DISKETTE COMPUTER: DOS SOFTWARE: FASTEN: DOS SOFTWARE: FASTEN: DOS CURRENT PEDLICATION DATA: APPLICATION NUMBER: US/08/895,521

FILING DATE: Herewith CLASSIFICATION NUMBER: US/08/895,521

FILING DATE: HEREWITH SPRING APPLICATION NUMBER: FILING DATE: ATTOMNEY AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

RECIETRATION NUMBER: BILLINGS ATTOMNEY AGENT NUMBER: BILLING ATTOMNEY AGENT NUMBER: SETERENCE/DOCKET NUMBER: PF-0343 US

TELEPHONE: 415-855-0555
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CORESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
STRANDEDDESS: single
STRANDEDDESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT14
CLONE: 1593490
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Best Local Similarity 72.7%;
Matches 8; Conservative
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TELEFAX: 415-845-4166
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USCO9-235-218-3

Sequence 3, Application US/09235218

Patent No. 6001629

GENERAL INFORMATION:
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C. '
TITLE OF INVENTION: WITOCHONDRIAL PROCESSING PEPTIDASE
ITILE OF INVENTION: WITOCHONDRIAL PROCESSING PEPTIDASE

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTE: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastesG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,218
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Pred. No. 16;
1; Mismatches
  72.7%; Pred. No. 16; tive 1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,521
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Patent No. 5869311
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
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SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 72.7-
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: 294589
US-09-235-218-3
                                                                                        243 AAGGVCHNELL 253
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243 AAGGVCHNELL 253
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STATE: C/
COUNTRY:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                       APPLICATION NUMBER: US/08/895,521
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corley, Neil C.

TITLE OF INVENTION: MITOCHONDRIAL PROCESSING PEPTIDASE

TITLE OF INVENTION: SUBUNIT
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APPLICATION NUMBER: US/09/235,218
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                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                       APPLICATION NUMBER:
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Pred. No. 37;
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Patent No. (
                         Query Match
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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LIBRARY: GenBa
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TITLE OF INVENTION: MITOCH
TITLE OF INVENTION: SUBUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                   CLONE: 1082896
                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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198: 36,749
            63.2%;
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                                                                                                                                                                                                                                                                                                           08/895,521
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Score 36; DB 3; Pred. No. 82; 2; Mismatches
                                                                                                                                                                                                                                           PF-0343 US
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                          Length 480
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Best Local Similarity 63.4 Matches 7; Conservative

<u>ب</u>

Indels

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AAGGILHLELL

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APPLICANT: Lagarias, John C
APPLICANT: Murphy, John T
TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER: 0F SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                  á
                                                                                                                                                  ; FEATURE:
, NAME/KEY: PEPTIDE
; LOCATION: (1)..(1096)
; OTHER INFORMATION: Pullulanase
US-09-346-237-6
    8
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendeen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629.200-US
CURRENT APPLICATION UNMBER: US/09/346,237A
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 60/094,353
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEO ID NOS: 14
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                                                                                                               Query Match
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                               LENGTH: 1096
TYPE: PRT
ORGANISM: Klebsiella aerogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:: OTHER INFORMATION: alignment Fig. 6 Mcphylb
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  484
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                                                                                             Local
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SASGVTHIELL 494
                                    AAGGILHLELL 11
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                                                                         Similarity 54. 6; Conservative
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                                                                                           63.2%;
54.5%;
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100.0%; Pred. No. 1.1e+02;
                                                                       Score 36; DB 4; Length 1096; Pred. No. 2e+02; 3; Mismatches 2; Indels
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Query Match
Best Local Similarity
Marches 6; Conserve
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                                                                                                                                         ; LOCATION: (1)..(1090)
; OTHER INFORMATION: pullulanase
US-09-346-237-5
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; SEQ ID NO 12
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Alga (Mesotaeinum)
US-08-904-871-12
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US-09-346-237-5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/346,237A CURRENT FILING DATE: 1999-07-01 EARLIER APPLICATION NUMBER: PA 1998 00868 EARLIER FILING DATE: 1998-07-02 EARLIER APPLICATION NUMBER: 60/094,353 EARLIER FILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lagarias, John C
APPLICANT: Murphy, John T
ITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 5629.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae FEATURE:
                                                                                                                                                                                           NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                     ENGTH:
474 SASGVTHVELL 484
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                                   1 AAGGILHLELL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08904871
                                                                      Conservative
                                                                                     54.5%;
                                                                                     Score 35;
Pred. No.
                                                                  Mismatches
                                                                                     3e+02;
                                                                                                   DB 4;
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US-08-913-014A-2

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Sequence 2, Application US/08913014A Patent No. 6235878

GENERAL INFORMATION:

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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 239
ITYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-08-913-014A-2
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08913014A Patent No. 6235878
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COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASUSEQ for Windows Version 2.0
SOFTWARE: FASUSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,014A
FILING DATE: 04-5EP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/02480
FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVId G. Conlin
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/47694
TELECHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin, E
ADDRESSEE: DIKE, BRONSTEIN, R
STREET: 130 Water Street
CITY: Boston,
STATE: MA
                                                                                                                                                               APPLICANT: Nishi, Kazunori
APPLICANT: Hikichi, Yukiko
APPLICANT: Shintani, Yasushi
TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                              ADDRESSEE: David G. Conlin, Esq.
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN,
STREET: 130 Water Street
                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
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                                                                             Boston,
                                                                                                            130 Water Street
                                                           USA
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Hikichi, Yukiko
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Pred. No. 1.3e+02;
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ROBERTS & USHMAN, LLP
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Best Local Similarity
Matches 5; Conserv
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/
FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David G. Conlin
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/JE
FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David G. Conlin
REGISTRATION NUMBER: 27,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 04-SEP-199:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, TITLE OF INVENTION: PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nishi, Kazunori
APPLICANT: Hikichi, Yukiko
APPLICANT: Shintani, Yasushi
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                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David G. Conlin, Esq.
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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)GY: Linear
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                                                                                                                               PCT/JP97/02480
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Pred. No.
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1.3e+02;
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-4
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Best Local Similarity 71.4%;
Matches 5; Conservative
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SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       18-913-014A-25
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COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                          ENERAL INFORMATION:
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APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANYAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ent No.
                                                                                                                                                                APPLICANT: Nishi, Kazunori
APPLICANT: Hikichi, Yukiko
APPLICANT: Shintani, Yasushi
TITLE OF INVENTION: PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILE REFERENCE: GH-50030
URRENT APPLICATION NUMBER: US/09/072,993C
URRENT FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                      204 GGVVHLE 210
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                                                                                                       ADDRESSEE: David G. Conlin, Esq.
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
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71.4%;
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Pred. No. 1
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Pred. No. 1
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Search completed: March 20, 2003, 12:36:01 Job time : 3.94595 secs
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97.
FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David G. Conlin
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   TOPOLOGY: Li
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LENGTH: 242
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REFERENCE/DOCKET NUMBER: 34,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                              206 GGVVHLE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUFTWARE: FASTSEQ FOR WINDOWS Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,014A
FILING DATE: 04-SEP-1997
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Pred. No.
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(without alignments)
329.684 Million cell updates/sec
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Sequence 1, Appli
Sequence 2, Appli
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Sequence 6, Appli
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AT.T GUMENTO	US-10-140-470-242	00-10-123-904-242	٠,	US-10-121-049-242	IIS-10-028-022-242	US-09-951-845-2	US-09-099-823-22	US-10-006-856A-162	US-09-864-761-45340	US-09-864-761-36574	US-09-836-613-2	-132-	US-09-841-132-495	-143.	US-10-066-209-4	US-09-252-656B-2	US-09-027-287-2	US-09-252-656B-39	US-09-027-287-39	US-09-731-872-402	US-09-764-868-1214	US-09-764-868-906	US-09-864-761-35584	US-10-101-464A-957	US-10-101-464A-928	10-11	US-10-117-417-6
	Sequence 242, App	sequence 242, App	742,		, ,	۽ د		Sequence 162. App	Sequence 45340. A	ب سا		565	4	21		N.	N		39.	e 402	1214	906. App	e 355	957	· n	16.	Sequence 6, Appli

## ALIGNMENTS

US-09-833-328-1

1, Application US/09833328 5. US2002013671781

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GENERAL INFORMATION:

APPLICANT: Laemmle, Bernhard

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Hans-Peter

APPLICANT: Schwarz, Randolf

APPLICANT: Antoine, Gerhard

APPLICANT: Tagllavacca, Luigina

APPLICANT: Tagllavacca, Luigina

APPLICANT: Turceck, Peter

APPLICANT: Turceck, Peter

APPLICANT: Turceck, Peter

APPLICANT: Gerritsen, Helena E.

TITLE OF INVENTION: Composition a von Willebrand Factor (vWF) Protea

FILE REFERENCE: 247.00CIP

CURRENT APPLICATION NUMBER: US/09/833,328

CURRENT APPLICATION NUMBER: US/09/833,328

CURRENT APPLICATION NUMBER: 09/721,254

PRIOR APPLICATION NUMBER: 09/721,254

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEG ID NOS: 15

SOFTWARE: Patentin version 3.1
RESULT 2
US-09-833-328-5
; Sequence 5, Application US/09833328
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                                                                                                                                       1 AAGGILHLELLV 12
                                                                                                          AAGGILHLELLV 12
                                                                                                                                                                                             l Similarity 100 12; Conservative
                                                                                                                                                                                                            100.0%; Score 57; DB 10; 100.0%; Pred. No. 0.00063;
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APPLICANT: Zimmermann, Klaus
APPLICANT: Furlan, Miha
APPLICANT: Turecek, Peter
APPLICANT: Turecek, Peter
APPLICANT: Gerritsen, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
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TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
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TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
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SEQ ID NO 5

; LENGTH: 15

; TYPE: PRT

; ORGANISM: human

US-09-833-328-5
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                                                                                                                                       Matches
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/721,254
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEO ID NOS: 15
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TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence AAGG
FILE REFERENCE: 247.00CIP
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NPPLICANT: Schwarz, Hans-Peter
NPPLICANT: Schwiftinger, Friedrich
NPPLICANT: Antoine, Gerhard
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                                     1 AAGGILHLELLV 12
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1 AAGGILHLELLV 12
                                                                                                                                       12; Conservative
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Tagliavacca, Luigina
Zimmermann, Klaus
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Scheiflinger, Friedrich
Antoine, Gerhard
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Tagliavacca, Luigina
Zimmermann, Klaus
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Turecek, Peter
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APPLICANT: Antoine, Gerhard
APPLICANT: Kerschbaumer, Randolf
APPLICANT: Tagliavacca, Luigina
APPLICANT: Tagliavacca, Luigina
APPLICANT: Tagliavacca, Luigina
APPLICANT: Tagliavacca, Luigina
APPLICANT: Turecek, Peter
APPLICANT: Turecek, Peter
APPLICANT: Gerritson, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
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TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Prote;
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protes (vWF) Protes (vWF) Protes (vWF) Protes (vWF) Protes (vWF) Protes (vWF) Protes (vWF) Protes (v
                                                                                                                 ; ORGANISM: human US-09-833-328-6
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; ORGANISM: human
US-09-833-328-4
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SEQ ID NO 4
LENGTH: 148
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Best Local Similarity 100.0%;
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                                                                                                                                                                                         LENGTH: 150
TYPE: PRT
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/721,254
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Gerritsen, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF)
TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid :
FILE REFERENCE: 247.00CIP
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APPLICANT:
APPLICANT:
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APPLICANT: Schwarz, Hans-Pe
APPLICANT: Scheiflinger, Fr
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US20020136713A1
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Scheiflinger, Friedrich
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Tagliavacca, Luigina
Zimmermann, Klaus
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Scheiflinger, Friedrich
Antoine, Gerhard
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Turecek, Peter
   100.0%;
Score 57; DB 10;
Pred. No. 0.0082;
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Pred. No. 0.0081;
Mismatches 0;
                              Length 150;
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Best Local Similarity

Matches

12;

Conservative

0,

Mismatches

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COUNTRY:

ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/978,979

FILING DATE: 16-Oct-2001

CLASSIFICATION UMBER: US/60/241,469

FILING DATE: -Unknown>

PRIOR APPLICATION NUMBER: US/60/241,469

FILING DATE: -Unknown>

APPLICATION NUMBER: US/60/241,469

FILING DATE: -UNKNOWN>

APPLICATION NUMBER: US/60/241,469

FILING DATE: -UNKNOWN>

APPLICATION NUMBER: US/60/241,469

FILING DATE: -UNKNOWN>

APPLICATION NUMBER: US/60/241,469

FILING DATE: -UNKNOWN>

APPLICATION NUMBER: US/60/241,469

FILING DATE: -UNKNOWN>

AFFERENCE/DOCKET NUMBER: GI 5435p
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APPLICANT: SHEPPARD, PAUL
APPLICANT: SHEPPARD, PAUL
APPLICANT: YAWAMOTO, GAYLE
TITLE OF INVENTION: zdint5
FILE REFERENCE: 99-82
CURRENT APPLICATION NUMBER: US/09/781,080B
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 203
TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application us Patent No. US20020142439A1
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Twine, Natalie, C.
Agostino, Michael, J.
Wolfman, Neil
Morris, Elisabeth
TITLE OF INVENTION: Aggrecanase Molecules
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGILHLELLV 13
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                                                                                                                              SOFTWARE: 1
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                                                                                                                 ENGTH:
                                                                                                               1416
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Patentin

Ver. 2.1

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STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-978-979-1
                                                                                                                                                                       RESULT 9
US-09-836-712-2
                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: VARIANT
; LOCATION: (1)...(1120)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-781-080B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-781-080B-11
                                                                                                 Sequence 2, Application US/09836712
Patent No. US20010049106A1
GENERAL INFORMATION:
APPLICANT: PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 12;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING TITLE OF INVENTION: USES THEREOF FILE REFERENCE: PC10851A CURRENT APPLICATION NUMBER: US/09/836,712 CURRENT FILING DATE: 2001-04-17 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOLLOWAY, JIM
APPLICANT: SHEPPARD, PAUL
APPLICANT: YAMAMOTO, GAYLE
TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides,
TITLE OF INVENTION: Zdint5
FILE REFERENCE: 99-82
CURRENT APPLICATION NUMBER: US/09/781,080B
CURRENT FILING DATE: 2002-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (973) 683-
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                         105 AAGGILHLELLV 116
                                                                                                                                                                                                                                                            1 AAGGILHLELLV 12
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                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 0.063;
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Pred. No. 0.013;
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                                                                                                                                                                                                                                                                                                                                      DB 10;
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               Score 36; DB 10; Length 125;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.2%; Score 36; DB 10; Length 210; Best Local Similarity 100.0%; Pred, No. 46; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism:Mcphylb
US-09-272-809-11
                                                             2; Indels
                                                                                                                                                                                                                         RESULT 12
US-09-272-809-11

Sequence 11, Application US/09272809
Parent No. US-002002239A1
GENERAL INFORMATION:
APPLICANT: Lagarias, John C.
TITLE OF INVENTION: Phytofluors as fluorescent labels
FILE REFERENCE: 2500.118US0
CURRENT APPLICATION NUMBER: US/09/272,809
CURRENT FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: PRT
TYPE: PRT
CHARACTH: 210
TYPE: PRT
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US-09-833-435A-6
S-Gouence 6, Application US/09833435A
Sequence 6, Application US/09833435A
Sequence 6, Application US/09833435A
Sequence 6, Application US/09833435A
GENERAL INFORMATION:
APPLICANT: Biggard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TILLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629_200-US
CURRENT FILING DAPE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/146,237
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
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                                                             2; Mismatches
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ORGANISM: Klebsiella aerogenes
FEATURE:
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LOCATION: (1)..(1096)
OTHER INFORMATION: Pullulanase
US-09-833-435A-6
          Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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APPLICANT: Turecek, Peter
APPLICANT: Turecek, Peter
Turecek, Helena E.
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act
TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence AAGG
CURRENT APPLICATION NUMBER: US/09/833,328
PRIOR APPLICATION NUMBER: 09/721,254
PRIOR FILING DATE: 2000-11-22
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     100.0%; Score 57; DB 10; Length 1416; 100.0%; Pred. No. 0.08; tive 0; Mismatches 0; Indels 0;
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APPLICANT: Hu, Xu
APPLICANT: Hu, Xu
APPLICANT: Hu, Xu
APPLICANT: Lu, Guihua
APPLICANT: Lu, Guihua
APPLICANT: Lu, Guihua
APPLICANT: Lu, Guihua
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of Use
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR APPLICATION NUMBER: US 60/190,467
NUMBER OF SEC 1D NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%; Score 45; DB 10; Length 9; 100.0%; Pred. No. 2e+05; Live 0; Mismatches , 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Schwarz, Hans-Peter
Scheiflinger, Friedrich
Antoine, Gerhard
Kerschbaumer, Randolf
Tagliavacca, Luigina
Zimmermann, Klaus
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Patent No. US20020076775A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 9, Application US/09833328
Patent No. US20020136713A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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Ouery Match
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                  98 AAGGILHLELLV 109
                                                                                                   1 AAGGILHLELLV 12
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ORGANISM: Zea mays
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; ORGANISM: human
US-09-833-328-9
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61.4%; Score 35; DB 10; Length 1090;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels
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61.4%; Score 35; DB 9; Length 1091;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels
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Sequence 4, Application US/09262126C

Publication No. US2030013180A1

GENERAL INFORMATION:
APPLICANT: Miller, Brian S.
APPLICANT: Miller, Brian S.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2

CURRENT APPLICATION NUMBER: US/09/262,126C

CURRENT FILING DATE: 1999-03-03

CURRENT FILING DATE: 1999-03-03

CURRENT FILING DATE: 1999-03-03

SOOFWARE: FastSEC for Windows Version 3.0

SEQ ID NO 4

LENGTH: 1091

TYPE: PRT

TYPE: PRT

TYPE: PRT
Patent No. US20020081670A1

Patent No. US20020081670A1

GENERAL INFORMATION

APPLICANT: Bisgard-Franczen, Henrik

APPLICANT: Svendeen, Allan

ITLE OF INVENTION: Starch Debranching Enzymes

FILE SPERENCE: 5629.200-US

CURRENT APPLICATION NUMBER: US/09/833,435A

CURRENT APPLICATION NUMBER: 09/346,237

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

SOFTWARE: FABESEQ for Windows Version 3.0

LENGTH: 1090
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
| NAME/KEY: PEPTIDE
| LOCATION: (1)...(1090)
| OTHER INFORMATION: pullulanase
| US-09-833-435A-5
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474 SASGVTHVELL 484
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475 SASGVTHVELL 485
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